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OM protein - protein search, using sw model

Run on: December 14, 2006, 14:14:02 ; Search time 40.1309 Seconds
(without alignments)
229.018 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLVTVSDCA.....CSRFPDGRYCRSMCLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep:*

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5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	589	100.0	105	2	US-09-712-529-5 Sequence 5, Appli
2	589	100.0	105	2	US-10-212-201A-5 Sequence 5, Appli
3	589	100.0	105	2	US-10-212-355-5 Sequence 5, Appli
15	577	98.0	105	2	US-09-621-976-5350 Sequence 5350, Ap
16	488	76.1	80	2	US-09-513-999C-4898 Sequence 4698, Ap
17	303	51.4	108	2	US-09-712-529-2 Sequence 2, Appli
18	303	51.4	108	2	US-10-212-201A-2 Sequence 2, Appli
19	303	51.4	108	2	US-10-212-355-2 Sequence 2, Appli
20	107.5	18.3	224	2	US-09-161-241-14 Sequence 14, Appli
21	102	17.3	186	2	US-09-949-016-7146 Sequence 7146, Ap
22	102	17.3	207	2	US-09-161-241-13 Sequence 13, Appli
23	102	17.3	259	2	US-09-161-241-12 Sequence 12, Appli
24	102	17.3	259	2	US-09-949-016-6872 Sequence 6872, Ap
44	101	17.1	259	2	US-09-161-241-11 Sequence 11, Appli
45	100.5	17.1	215	2	US-10-104-047-2196 Sequence 2196, Ap
46	100.5	17.1	350	2	US-09-161-241-9 Sequence 9, Appli
64	100.5	17.1	375	2	US-09-949-016-7856 Sequence 7856, Ap
65	100.5	17.1	375	2	US-09-949-016-7857 Sequence 7857, Ap
66	100.5	17.1	375	2	US-09-949-016-7858 Sequence 7858, Ap
67	98.5	16.7	349	2	US-09-161-241-8 Sequence 8, Appli
68	97	16.5	266	2	US-09-161-241-10 Sequence 10, Appli
69	97	16.5	266	2	US-09-976-594-1086 Sequence 1086, Ap
77	83.5	14.2	508	2	US-10-915-160-2 Sequence 2, Appli
78	82	13.9	1342	2	US-09-561-709B-13 Sequence 13, Appli
79	81.5	13.8	446	2	US-10-104-047-2665 Sequence 2665, Ap
80	81	13.8	1964	2	US-09-467-997-1 Sequence 1, Appli

81	79	13.4	124	2	US-09-949-016-11293 Sequence 11293, A
82	78.5	13.3	163	1	US-08-219-237B-5 Sequence 5, Appli
83	78.5	13.3	163	1	US-08-477-347-13 Sequence 13, Appli
84	78.5	13.3	163	2	US-08-476-862-4 Sequence 4, Appli
85	78.5	13.3	163	2	US-08-468-560C-5 Sequence 5, Appli
86	78.5	13.3	163	2	US-09-800-903-4 Sequence 4, Appli
87	78.5	13.3	163	2	US-09-800-908-13 Sequence 13, Appli
88	78.5	13.3	163	2	US-09-884-987-5 Sequence 5, Appli
89	75.5	12.8	1101	2	US-09-561-709B-5 Sequence 5, Appli
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91	75	12.7	546	2	US-08-264-101-2 Sequence 2, Appli
92	75	12.7	651	1	US-08-765-243-2 Sequence 2, Appli
93	75	12.7	651	1	PCT-US95-07295-2 Sequence 2, Appli
94	75	12.7	651	5	PCT-US95-07295-2 Sequence 8, Appli
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98	75	12.7	3075	1	US-08-125-077-5 Sequence 5, Appli
99	74.5	12.6	451	2	US-10-915-160-6 Sequence 6, Appli
100	73	12.4	163	2	US-08-828-683A-13 Sequence 13, Appli
101	73	12.4	163	2	US-09-523-323-54 Sequence 54, Appli
102	73	12.4	164	1	US-08-232-087A-9 Sequence 9, Appli
103	73	12.4	189	2	US-09-422-680A-25 Sequence 25, Appli
104	73	12.4	227	2	US-08-974-022-48 Sequence 48, Appli
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106	73	12.4	227	2	US-08-795-447A-48 Sequence 48, Appli
107	73	12.4	227	2	US-08-974-186-48 Sequence 48, Appli
108	73	12.4	227	2	US-08-795-446B-48 Sequence 48, Appli
109	73	12.4	227	2	US-08-706-945D-134 Sequence 134, App
110	73	12.4	227	2	US-08-577-788C-48 Sequence 48, Appli
111	73	12.4	227	3	US-09-613-591F-131 Sequence 131, App
112	73	12.4	235	2	US-09-326-394-4 Sequence 4, Appli
113	73	12.4	235	2	US-09-580-235-2 Sequence 2, Appli
114	73	12.4	235	2	US-09-580-235-4 Sequence 4, Appli
115	73	12.4	235	2	US-09-580-235-6 Sequence 6, Appli
116	73	12.4	235	2	US-09-580-235-8 Sequence 8, Appli
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118	73	12.4	235	2	US-09-580-181-4 Sequence 4, Appli
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120	73	12.4	235	2	US-09-580-181-8 Sequence 8, Appli
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122	73	12.4	235	2	US-09-102-530-6 Sequence 6, Appli
123	73	12.4	235	2	US-09-102-530-8 Sequence 8, Appli
124	73	12.4	235	2	US-09-882-735A-16 Sequence 16, Appli
125	73	12.4	235	2	US-09-579-845-10 Sequence 10, Appli
126	73	12.4	235	2	US-10-360-101-226 Sequence 226, App
127	73	12.4	439	2	US-08-385-229-2 Sequence 2, Appli
128	73	12.4	461	1	US-08-650-000-2 Sequence 2, Appli
129	73	12.4	461	1	US-09-042-785A-7 Sequence 7, Appli
130	73	12.4	461	2	US-08-477-347-3 Sequence 3, Appli
131	73	12.4	461	2	US-09-006-353A-4 Sequence 4, Appli
132	73	12.4	461	2	US-08-476-862-2 Sequence 2, Appli
133	73	12.4	461	2	US-08-573-986-4 Sequence 4, Appli
134	73	12.4	461	2	US-08-406-824A-2 Sequence 2, Appli
135	73	12.4	461	2	US-09-800-909-2 Sequence 2, Appli
136	73	12.4	461	2	US-09-758-124-2 Sequence 2, Appli
137	73	12.4	461	2	US-09-800-908-3 Sequence 3, Appli
138	73	12.4	461	2	US-09-896-096A-17 Sequence 17, Appli
139	73	12.4	461	2	US-09-949-016-6019 Sequence 6019, Ap
140	73	12.4	461	2	US-10-046-433-6 Patent No. 5395760
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142	73	12.4	486	1	US-09-949-016-7840 Sequence 4, Appli
143	73	12.4	491	2	US-08-385-229-4 Sequence 1, Appli
144	73	12.4	518	1	US-09-579-845-1 Sequence 3, Appli
145	73	12.4	518	2	US-09-579-845-3 Sequence 10403, A
146	73	12.4	518	2	US-09-949-016-10403 Sequence 1076, Ap
147	73	12.3	1935	2	US-09-538-092-1076 Sequence 347, App
148	72.5	12.3	2871	2	US-09-894-882-347 Sequence 2, Appli
149	72.5	12.3	63	2	US-10-178-213-2 Sequence 88, Appli
150	72	12.2	74	2	US-09-950-933A-88 Sequence 48, Appli
151	72	12.2	101	2	US-09-171-461-48 Sequence 48, Appli
152	72	12.2	101	2	US-09-171-461-48 Sequence 48, Appli
153	71.5	12.1	453	2	US-09-171-461-48 Sequence 48, Appli

154	71.5	12.1	453	2	US-09-970-711-48	Sequence 48, Appl	227	68	11.5	455	2	US-09-527-236A-4	Sequence 4, Appl
155	71.5	12.1	470	2	US-10-915-160-4	Sequence 4, Appl	228	68	11.5	455	2	US-09-756-854-4	Sequence 4, Appl
156	71.5	12.1	575	2	US-09-949-016-11264	Sequence 11264, A	229	68	11.5	455	2	US-10-041-574-4	Sequence 4, Appl
157	71.5	12.1	575	2	US-09-949-016-11265	Sequence 11265, A	230	68	11.5	455	2	US-09-095-574-4	Sequence 4, Appl
158	71.5	12.1	575	2	US-09-949-016-11266	Sequence 11266, A	231	68	11.5	464	2	US-09-949-016-9441	Sequence 9441, Ap
159	71.5	12.1	575	2	US-09-949-016-11267	Sequence 11267, A	232	68	11.5	483	2	US-09-252-991A-19884	Sequence 19884, A
160	71.5	12.1	657	2	US-09-949-016-11365	Sequence 11365, A	233	67.5	11.5	69	2	US-09-894-882-232	Sequence 232, App
161	71.5	12.1	657	2	US-09-949-016-11366	Sequence 11366, A	234	67.5	11.5	1480	2	US-09-191-647-7	Sequence 7, Appl
162	71.5	12.1	657	2	US-09-949-016-11367	Sequence 11367, A	235	67.5	11.5	1480	2	US-03-540-245A-7	Sequence 7, Appl
163	71.5	12.1	657	2	US-09-949-016-11368	Sequence 11368, A	236	67.5	11.5	1480	2	US-09-540-153-7	Sequence 7, Appl
164	71.5	12.1	677	2	US-09-949-016-11369	Sequence 11369, A	237	67.5	11.5	1480	2	US-09-182-024A-5	Sequence 5, Appl
165	71.5	12.1	677	2	US-09-949-016-11370	Sequence 11370, A	238	67.5	11.5	1480	2	US-10-289-776-7	Sequence 7, Appl
166	71.5	12.1	677	2	US-09-949-016-11371	Sequence 11371, A	239	67.5	11.5	1480	5	PCT-US91-09055-2	Sequence 2, Appl
167	71.5	12.1	677	2	US-09-949-016-11372	Sequence 11372, A	240	67.5	11.5	1504	2	US-10-037-417-98	Sequence 98, Appl
168	71	12.1	94	2	US-09-950-933A-44	Sequence 44, Appl	241	67	11.4	1172	1	US-08-313-288B-19	Sequence 19, Appl
169	71	12.1	98	2	US-09-950-933A-50	Sequence 50, Appl	242	67	11.4	1172	1	US-09-949-016-6333	Sequence 1933, Ap
170	71	12.1	593	1	US-07-668-648-4	Sequence 4, Appl	243	67	11.4	1193	1	US-08-400-159-10	Sequence 10, Appl
171	71	12.1	593	1	US-08-429-998-4	Sequence 4, Appl	244	67	11.4	1193	2	US-08-611-729A-10	Sequence 10, Appl
172	71	12.1	593	1	US-08-431-333-4	Sequence 4, Appl	245	67	11.4	1193	2	US-09-195-524-10	Sequence 10, Appl
173	71	12.1	593	2	US-08-991-862-17	Sequence 17, Appl	246	67	11.4	1193	2	US-09-310-685-8	Sequence 8, Appl
174	71	12.1	593	2	US-08-813-156-17	Sequence 17, Appl	247	67	11.4	1219	2	US-08-882-046-5	Sequence 5, Appl
175	71	12.1	593	2	US-09-456-886-17	Sequence 17, Appl	248	67	11.4	1219	2	US-09-566-047-5	Sequence 5, Appl
176	71	12.1	593	2	US-09-824-647-17	Sequence 17, Appl	249	67	11.4	2321	2	US-09-230-652-2	Sequence 2, Appl
177	71	12.1	593	2	US-09-880-843-17	Sequence 17, Appl	250	67	11.4	2321	2	US-09-612-226B-2	Sequence 2, Appl
178	71	12.1	593	5	PCT-US91-02321-4	Sequence 4, Appl	251	67	11.4	3597	2	US-10-037-417-6	Sequence 6, Appl
179	71	12.1	613	2	US-09-949-016-9775	Sequence 9775, Ap	252	67	11.4	3600	2	US-10-037-417-2	Sequence 2, Appl
180	71	12.1	1587	2	US-09-845-583A-10	Sequence 10, Appl	253	66.5	11.3	70	2	US-09-894-882-253	Sequence 253, App
181	71	12.1	1587	2	US-09-561-709B-3	Sequence 3, Appl	254	66.5	11.3	70	2	US-09-894-882-262	Sequence 262, App
182	70	11.9	841	2	US-09-897-427A-2	Sequence 2, Appl	255	66.5	11.3	589	1	US-07-668-648-6	Sequence 2, Appl
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184	69.5	11.8	69	2	US-09-894-882-265	Sequence 265, App	257	66.5	11.3	589	1	US-08-429-998-2	Sequence 2, Appl
185	69.5	11.8	179	1	US-07-668-648-8	Sequence 8, Appl	258	66.5	11.3	589	1	US-08-429-998-6	Sequence 6, Appl
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188	69.5	11.8	179	5	PCT-US91-02321-8	Sequence 8, Appl	261	66.5	11.3	589	2	US-08-991-862-2	Sequence 2, Appl
189	69.5	11.8	3907	2	US-10-029-217A-24	Sequence 24, Appl	262	66.5	11.3	589	2	US-09-813-156-2	Sequence 2, Appl
190	69	11.7	3712	2	US-10-037-417-48	Sequence 48, Appl	263	66.5	11.3	589	2	US-09-456-886-2	Sequence 2, Appl
191	69	11.7	3712	2	US-10-037-417-51	Sequence 51, Appl	264	66.5	11.3	589	2	US-09-824-647-2	Sequence 2, Appl
192	68.5	11.6	69	2	US-09-894-882-271	Sequence 271, App	265	66.5	11.3	589	2	US-09-880-842-2	Sequence 2, Appl
193	68.5	11.6	728	2	US-09-981-392-2	Sequence 2, Appl	266	66.5	11.3	589	5	PCT-US91-02321-2	Sequence 2, Appl
194	68.5	11.6	728	2	US-09-908-323-2	Sequence 2, Appl	267	66.5	11.3	5179	5	PCT-US91-02321-6	Sequence 6, Appl
195	68.5	11.6	728	2	US-09-310-685-11	Sequence 11, Appl	268	66.5	11.3	5179	2	US-09-538-092-1258	Sequence 1258, Ap
196	68.5	11.6	729	2	US-08-872-855-8	Sequence 8, Appl	269	66	11.2	70	2	US-09-894-882-244	Sequence 244, App
197	68	11.5	122	2	US-09-489-847-189	Sequence 189, App	270	66	11.2	70	2	US-09-894-882-256	Sequence 256, App
198	68	11.5	159	1	US-08-219-237B-6	Sequence 6, Appl	271	66	11.2	70	2	US-09-894-882-353	Sequence 353, App
199	68	11.5	159	2	US-08-477-347-15	Sequence 15, Appl	272	66	11.2	158	2	US-09-832-129-39	Sequence 39, Appl
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201	68	11.5	159	2	US-08-468-560C-6	Sequence 6, Appl	274	66	11.2	1055	2	US-09-855-722-2	Sequence 2, Appl
202	68	11.5	159	2	US-08-828-683A-16	Sequence 16, Appl	275	66	11.2	1065	1	US-08-400-159-8	Sequence 8, Appl
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210	68	11.5	224	2	US-08-795-446B-50	Sequence 50, Appl	283	66	11.2	1257	2	US-09-195-524-8	Sequence 8, Appl
211	68	11.5	224	2	US-08-706-945D-137	Sequence 137, App	284	66	11.2	1257	2	US-09-310-685-6	Sequence 6, Appl
212	68	11.5	224	2	US-08-577-788C-51	Sequence 51, Appl	285	65.5	11.1	94	2	US-09-950-933A-47	Sequence 47, Appl
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215	68	11.5	317	2	US-09-823-038A-20	Sequence 20, Appl	288	65.5	11.1	182	2	US-10-104-047-3287	Sequence 3287, Ap
216	68	11.5	427	2	US-09-086-483A-4	Sequence 4, Appl	289	65.5	11.1	299	2	US-09-188-930-192	Sequence 192, App
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218	68	11.5	427	2	US-09-006-353A-5	Sequence 5, Appl	291	65.5	11.1	299	2	US-09-312-283C-192	Sequence 192, App
219	68	11.5	427	2	US-09-573-986-5	Sequence 5, Appl	292	65.5	11.1	299	2	US-09-312-283C-332	Sequence 332, App
220	68	11.5	427	2	US-09-580-212-4	Sequence 4, Appl	293	65.5	11.1	683	2	US-08-979-847B-198	Sequence 198, App
221	68	11.5	427	2	US-09-769-402-4	Sequence 4, Appl	294	65.5	11.1	683	2	US-08-979-847B-200	Sequence 200, App
222	68	11.5	427	2	US-09-748-537-13	Sequence 13, Appl	295	65.5	11.1	683	2	US-08-979-847B-208	Sequence 208, App
223	68	11.5	427	2	US-10-092-138A-24	Sequence 24, Appl	296	65.5	11.1	683	2	US-08-979-847B-210	Sequence 210, App
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225	68	11.5	427	2	US-08-681-219A-24	Sequence 24, Appl	298	65.5	11.1	722	2	US-08-981-392-12	Sequence 12, Appl
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320	65.5	11.1	768	1	US-08-979-847B-89	Sequence 89, Appl	393	64	10.9	335	2	US-09-252-991A-32163	Sequence 32163, A
321	65.5	11.1	1068	1	US-08-537-210A-2	Sequence 2, Appl	394	64	10.9	340	2	US-09-252-991A-18667	Sequence 18667, A
322	65.5	11.1	1068	2	US-09-113-825-2	Sequence 2, Appl	395	64	10.9	425	2	US-09-748-537-14	Sequence 14, Appl
323	65.5	11.1	2213	1	US-08-727-034-3	Sequence 3, Appl	396	64	10.9	459	2	US-09-605-042A-41	Sequence 41, Appl
324	65.5	11.1	2471	1	US-08-185-432-16	Sequence 16, Appl	397	64	10.9	1282	2	US-09-949-016-10099	Sequence 10099, A
325	65.5	11.1	2471	1	US-08-083-590A-19	Sequence 19, Appl	398	64	10.9	1652	2	US-09-627-650B-1	Sequence 1, Appl
326	65.5	11.1	2471	1	US-08-532-384-19	Sequence 19, Appl	399	64	10.9	1652	2	US-09-436-063C-1	Sequence 1, Appl
327	65.5	11.1	2471	2	US-08-899-232-1	Sequence 1, Appl	400	64	10.9	1917	2	US-09-627-650B-5	Sequence 5, Appl
328	65.5	11.1	2471	2	US-09-121-457-1	Sequence 1, Appl	401	64	10.9	1917	2	US-09-436-063C-5	Sequence 5, Appl
329	65.5	11.1	2556	1	US-08-185-432-17	Sequence 17, Appl	402	64	10.9	2508	2	US-09-627-650B-7	Sequence 7, Appl
330	65.5	11.1	2556	1	US-08-083-590A-20	Sequence 20, Appl	403	64	10.9	2508	2	US-09-436-063C-7	Sequence 7, Appl
331	65.5	11.1	2556	1	US-08-532-384-20	Sequence 20, Appl	404	64	10.9	2544	2	US-09-627-650B-3	Sequence 3, Appl
332	65.5	11.1	2556	2	US-08-899-232-2	Sequence 2, Appl	405	64	10.9	2544	2	US-09-436-063C-3	Sequence 3, Appl
333	65.5	11.1	2556	2	US-09-121-457-2	Sequence 2, Appl	406	64	10.9	2601	2	US-09-627-650B-9	Sequence 9, Appl
334	65.5	11.1	3635	2	US-09-845-583A-2	Sequence 2, Appl	407	64	10.9	2601	2	US-09-436-063C-9	Sequence 9, Appl
335	65.5	11.1	3635	2	US-10-037-417-47	Sequence 47, Appl	408	63.5	10.8	121	2	US-10-002-344A-257	Sequence 257, App
336	65.5	11.1	3635	2	US-10-037-182-4	Sequence 4, Appl	409	63.5	10.8	163	2	US-09-252-991A-23129	Sequence 23129, A
337	65	11.0	77	2	US-08-866-545-2	Sequence 2, Appl	410	63.5	10.8	194	2	US-09-252-991A-32646	Sequence 32646, A
338	65	11.0	77	2	US-09-627-775-2	Sequence 2, Appl	411	63.5	10.8	606	2	US-09-460-295B-12	Sequence 12, Appl
339	65	11.0	142	2	US-09-094-749-1973	Sequence 1973, Ap	412	63.5	10.8	713	2	US-08-872-855-5	Sequence 5, Appl
340	65	11.0	236	2	US-09-252-991A-25980	Sequence 25980, A	413	63.5	10.8	721	2	US-08-872-855-7	Sequence 7, Appl
341	65	11.0	383	1	US-08-597-545-2	Sequence 2, Appl	414	63.5	10.8	721	2	US-08-981-392-5	Sequence 5, Appl
342	65	11.0	383	1	US-08-457-135-2	Sequence 2, Appl	415	63.5	10.8	721	2	US-09-908-322-5	Sequence 5, Appl
343	65	11.0	575	2	US-09-482-273-159	Sequence 159, App	416	63.5	10.8	721	2	US-09-310-685-12	Sequence 12, Appl
344	65	11.0	638	2	US-08-482-273-245	Sequence 245, App	417	63.5	10.8	1128	2	US-09-627-650B-11	Sequence 11, Appl
345	65	11.0	993	1	US-08-348-143-1	Sequence 1, Appl	418	63.5	10.8	1128	2	US-09-436-063C-11	Sequence 11, Appl
346	65	11.0	993	1	US-08-571-785-1	Sequence 1, Appl	419	63.5	10.8	3647	2	US-09-949-016-10932	Sequence 10932, A
347	65	11.0	993	2	US-09-192-435-1	Sequence 1, Appl	420	63	10.7	700	2	US-09-894-882-350	Sequence 350, App
348	65	11.0	993	2	US-09-558-340-1	Sequence 1, Appl	421	63	10.7	100	2	US-09-950-933A-40	Sequence 40, Appl
349	65	11.0	1010	2	US-08-882-046-7	Sequence 7, Appl	422	63	10.7	129	2	US-10-104-047-2669	Sequence 2669, Ap
350	65	11.0	1010	2	US-09-566-047-7	Sequence 7, Appl	423	63	10.7	258	2	US-09-579-845-7	Sequence 7, Appl
351	65	11.0	1036	2	US-09-068-740A-6	Sequence 6, Appl	424	63	10.7	298	2	US-09-902-540-12595	Sequence 12595, A
352	65	11.0	1067	2	US-09-579-536C-18	Sequence 18, Appl	425	63	10.7	487	2	US-09-579-845-14	Sequence 14, Appl
353	65	11.0	1187	2	US-09-068-740A-7	Sequence 7, Appl	426	62.5	10.6	69	2	US-09-894-882-268	Sequence 268, App
354	65	11.0	1208	2	US-09-199-865-1	Sequence 1, Appl	427	62.5	10.6	70	2	US-08-469-882-235	Sequence 235, App
355	65	11.0	1208	2	US-10-213-329-1	Sequence 1, Appl	428	62.5	10.6	277	2	US-08-469-882-235	Sequence 4, Appl
356	65	11.0	1218	1	US-08-400-159-6	Sequence 6, Appl	429	62.5	10.6	297	2	US-09-270-767-44071	Sequence 44071, A
357	65	11.0	1218	2	US-08-611-729A-6	Sequence 6, Appl	430	62.5	10.6	347	2	US-09-582-337-2	Sequence 2, Appl
358	65	11.0	1218	2	US-08-882-046-2	Sequence 2, Appl	431	62.5	10.6	1080	2	US-09-904-380-2	Sequence 2, Appl
359	65	11.0	1218	2	US-09-214-278-7	Sequence 7, Appl	432	62	10.5	70	2	US-09-894-882-292	Sequence 292, App
360	65	11.0	1218	2	US-09-068-740A-11	Sequence 11, Appl	433	62	10.5	102	2	US-09-950-933A-86	Sequence 86, Appl
361	65	11.0	1218	2	US-09-855-722-7	Sequence 7, Appl	434	62	10.5	113	2	US-09-270-767-37873	Sequence 37873, A
362	65	11.0	1218	2	US-09-566-047-2	Sequence 2, Appl	435	62	10.5	113	2	US-09-270-767-53090	Sequence 53090, A
363	65	11.0	1218	2	US-09-917-254-85	Sequence 85, Appl	436	62	10.5	148	2	US-09-252-991A-32322	Sequence 32322, A
364	65	11.0	1218	2	US-09-195-524-6	Sequence 6, Appl	437	62	10.5	402	1	US-08-709-979A-3	Sequence 3, Appl
365	65	11.0	1218	2	US-09-579-536C-1	Sequence 1, Appl	438	62	10.5	402	2	US-08-709-979A-5	Sequence 5, Appl
366	65	11.0	1218	2	US-09-949-016-5902	Sequence 5902, Ap	439	62	10.5	402	1	US-08-833-642A-5	Sequence 5, Appl
367	65	11.0	1218	2	US-09-310-685-4	Sequence 4, Appl	440	62	10.5	415	1	US-08-709-974A-4	Sequence 4, Appl
368	65	11.0	1254	2	US-09-949-016-10297	Sequence 10297, A	441	62	10.5	415	2	US-09-069-632-1	Sequence 1, Appl
369	65	11.0	4654	2	US-08-476-515A-84	Sequence 84, Appl	442	62	10.5	435	1	US-08-361-920-27	Sequence 27, Appl
370	65	11.0	4655	2	US-08-652-877-84	Sequence 84, Appl	443	62	10.5	435	1	US-08-479-939-27	Sequence 27, Appl
371	65	11.0	4655	2	US-08-652-877-86	Sequence 86, Appl	444	62	10.5	435	1	US-08-483-432-27	Sequence 27, Appl
372	65	11.0	4655	2	US-08-652-877-88	Sequence 88, Appl	445	62	10.5	435	1	US-09-069-632-3	Sequence 3, Appl
373	65	11.0	4655	2	US-08-652-877-90	Sequence 90, Appl	446	62	10.5	435	2	US-08-981-392-13	Sequence 13, Appl
374	64.5	11.0	1591	2	US-09-949-002-414	Sequence 414, App	447	62	10.5	578	2	US-09-908-322-13	Sequence 13, Appl
375	64.5	11.0	1597	1	US-09-949-002-354	Sequence 354, App	448	62	10.5	578	2	US-09-939-853A-97	Sequence 97, Appl
376	64.5	11.0	2214	1	US-08-727-034-7	Sequence 7, Appl	449	62	10.5	831	2	US-09-939-853A-98	Sequence 98, Appl
377	64.5	11.0	2214	2	US-09-919-039-40	Sequence 40, Appl	450	62	10.5	831	2	US-08-313-288B-20	Sequence 20, Appl
378	64.5	11.0	2743	2	US-10-037-182-36	Sequence 36, Appl	451	62	10.5	998	1	US-08-449-645A-20	Sequence 20, Appl
379	64.5	11.0	3695	2	US-10-037-182-2	Sequence 2, Appl	452	62	10.5	998	1	US-08-702-367A-20	Sequence 20, Appl
380	64	10.9	159	1	US-08-232-087A-11	Sequence 11, Appl	453	62	10.5	998	5	PCT-US95-04681-20	Sequence 20, Appl
381	64	10.9	207	2	US-08-974-022-47	Sequence 47, Appl	454	62	10.5	998	2	US-09-959-392-4	Sequence 4, Appl
382	64	10.9	207	2	US-08-795-445A-47	Sequence 47, Appl	455	62	10.5	1113	2	US-08-313-288B-20	Sequence 20, Appl
383	64	10.9	207	2	US-08-795-447A-47	Sequence 47, Appl	456	62	10.5	1170	1	US-08-479-722B-2	Sequence 2, Appl
384	64	10.9	207	2	US-08-974-186-47	Sequence 47, Appl	457	62	10.5	1833	2	US-09-592-685-2	Sequence 2, Appl
385	64	10.9	207	2	US-08-795-446B-47	Sequence 47, Appl	458	62	10.5	1833	5	PCT-US95-02251-18	Sequence 18, Appl
386	64	10.9	207	2	US-08-706-945D-133	Sequence 133, App	459	62	10.5	1833	2	US-09-894-882-259	Sequence 259, App
387	64	10.9	207	2	US-08-577-788C-47	Sequence 47, Appl	460	61.5	10.4	69	2	US-09-270-767-33322	Sequence 33322, A
388	64	10.9	207	3	US-09-613-591F-130	Sequence 130, App	461	61.5	10.4	156	2	US-09-270-767-48539	Sequence 48539, A
389	64	10.9	235	2	US-09-902-540-15031	Sequence 2, Appl	462	61.5	10.4	156	2	US-09-904-615-78	Sequence 78, Appl
390	64	10.9	325	1	US-08-292-549-2	Sequence 2, Appl	463	61.5	10.4	180	2	US-10-054-988-78	Sequence 78, Appl
391	64	10.9	325	2	US-09-042-785A-9	Sequence 9, Appl	464	61.5	10.4	180	2		

465	61.5	10.4	277	1	US-08-147-784-2	Sequence 2, Appli	555	60.5	10.3	385	1	US-08-457-135-1	Sequence 1, Appli
466	61.5	10.4	277	2	US-08-195-967-2	Sequence 2, Appli	556	60.5	10.3	385	2	US-09-142-027A-10	Sequence 10, Appl
467	61.5	10.4	277	2	US-09-006-353A-12	Sequence 12, Appl	557	60.5	10.3	431	2	US-09-252-991A-18787	Sequence 18787, A
468	61.5	10.4	277	2	US-08-472-940-2	Sequence 2, Appli	558	60.5	10.3	515	2	US-09-635-872A-6	Sequence 6, Appli
469	61.5	10.4	277	2	US-09-573-986-12	Sequence 12, Appl	559	60.5	10.3	515	2	US-09-636-077A-6	Sequence 6, Appli
470	61.5	10.4	277	2	US-09-880-938-2	Sequence 2, Appli	560	60.5	10.3	515	2	US-09-636-060C-6	Sequence 6, Appli
471	61.5	10.4	277	2	US-09-804-200-2	Sequence 2, Appli	561	60.5	10.3	515	2	US-09-986-552-6	Sequence 6, Appli
472	61.5	10.4	277	2	US-10-046-433-3	Sequence 3, Appli	562	60.5	10.3	515	2	US-09-636-586C-6	Sequence 6, Appli
477	61.5	10.4	282	2	US-09-808-847-1	Sequence 1, Appli	563	60.5	10.3	515	2	US-10-023-894-18	Sequence 18, Appl
491	61.5	10.4	310	1	US-07-704-288C-6	Sequence 6, Appli	564	60.5	10.3	515	2	US-10-306-686-6	Sequence 6, Appli
492	61.5	10.4	310	1	US-08-379-259-6	Sequence 6, Appli	565	60.5	10.3	515	2	US-09-895-072-6	Sequence 6, Appli
493	61.5	10.4	510	2	US-10-104-047-2580	Sequence 2580, Ap	566	60.5	10.3	515	2	US-10-023-888-18	Sequence 18, Appl
494	61.5	10.4	1345	2	US-09-949-016-8313	Sequence 8313, Ap	567	60.5	10.3	520	2	US-09-068-740A-3	Sequence 3, Appli
495	61.5	10.4	2157	2	US-09-466-778-2	Sequence 2, Appli	568	60.5	10.3	563	2	US-09-248-796A-17571	Sequence 17571, A
496	61.5	10.4	2873	1	US-08-466-033-15	Sequence 15, Appl	569	60.5	10.3	702	2	US-09-068-740A-4	Sequence 4, Appli
497	61.5	10.4	2873	1	US-08-638-911A-2	Sequence 2, Appli	570	60.5	10.3	723	2	US-09-068-740A-9	Sequence 9, Appli
498	61.5	10.4	2873	1	US-08-444-733-15	Sequence 15, Appl	571	60.5	10.3	723	2	US-09-423-753-27	Sequence 27, Appl
499	61.5	10.4	2873	1	US-08-464-134-15	Sequence 15, Appl	572	60.5	10.3	723	2	US-09-641-612-6	Sequence 6, Appli
500	61.5	10.4	2873	1	US-08-461-361-15	Sequence 15, Appl	573	60.5	10.3	723	3	US-10-241-476-27	Sequence 27, Appl
501	61.5	10.4	2873	1	US-08-485-910-15	Sequence 15, Appl	575	60.5	10.3	737	2	US-08-944-457-15	Sequence 15, Appl
502	61.5	10.4	2873	5	PCT-US95-06286-15	Sequence 15, Appl	580	60.5	10.3	909	2	US-08-936-135-18	Sequence 18, Appl
503	61.5	10.4	3571	2	US-09-911-842A-2	Sequence 2, Appli	581	60.5	10.3	909	2	US-09-439-711C-18	Sequence 18, Appl
504	61	10.4	70	2	US-09-894-882-289	Sequence 289, App	582	60.5	10.3	926	2	US-08-936-135-20	Sequence 20, Appl
505	61	10.4	93	2	US-09-950-933A-95	Sequence 95, Appl	583	60.5	10.3	926	2	US-09-439-711C-20	Sequence 20, Appl
506	61	10.4	336	2	US-09-248-796A-20058	Sequence 20058, A	584	60.5	10.3	931	2	US-09-583-638-4	Sequence 4, Appli
507	61	10.4	348	1	US-08-468-847B-14	Sequence 14, Appl	585	60.5	10.3	1073	2	US-09-949-016-9771	Sequence 9771, Ap
508	61	10.4	359	2	US-09-270-767-42534	Sequence 42534, A	586	60.5	10.3	1104	1	US-08-327-832-5	Sequence 5, Appli
509	61	10.4	724	2	US-10-094-749-2240	Sequence 2240, Ap	587	60.5	10.3	1104	1	US-08-828-584-5	Sequence 5, Appli
510	61	10.4	787	1	US-08-720-484A-4	Sequence 4, Appli	588	60.5	10.3	2211	2	US-09-738-884-1	Sequence 1, Appli
511	61	10.4	787	2	US-08-953-823A-4	Sequence 4, Appli	589	60.5	10.3	2211	2	US-10-096-961A-1	Sequence 1, Appli
512	61	10.4	787	2	US-09-398-239-4	Sequence 4, Appli	590	60.5	10.3	2703	1	US-08-185-432-19	Sequence 19, Appl
513	61	10.4	787	2	US-09-560-876A-4	Sequence 4, Appli	591	60.5	10.3	2703	2	US-08-899-232-4	Sequence 4, Appli
514	61	10.4	1170	2	US-09-657-472-2	Sequence 2, Appli	592	60.5	10.3	2703	2	US-09-121-457-4	Sequence 2, Appli
515	61	10.4	1170	2	US-09-949-002-350	Sequence 350, App	593	60.5	10.3	2910	2	US-08-828-498-2	Sequence 2, Appli
516	61	10.4	1171	2	US-09-560-385A-36	Sequence 36, Appl	594	60.5	10.3	4544	1	US-08-469-658-52	Sequence 52, Appl
517	61	10.4	1192	2	US-09-560-385A-34	Sequence 34, Appl	595	60.5	10.3	4544	1	US-08-469-658-52	Sequence 52, Appl
518	61	10.4	1192	2	US-10-053-662A-32	Sequence 32, Appl	596	60	10.2	39	2	US-09-428-082B-377	Sequence 377, App
519	61	10.4	1248	2	US-08-882-046-6	Sequence 6, Appli	597	60	10.2	184	1	US-08-464-339A-2	Sequence 2, Appli
520	61	10.4	1248	2	US-09-566-047-6	Sequence 6, Appli	598	60	10.2	184	1	US-08-468-847B-18	Sequence 18, Appl
521	61	10.4	1251	5	PCT-US95-02251-3	Sequence 3, Appli	599	60	10.2	184	2	US-09-706-722A-2	Sequence 2, Appli
522	61	10.4	1252	1	US-08-199-780-3	Sequence 3, Appli	600	60	10.2	184	5	US-09-949-016-6782	Sequence 2, Appli
523	61	10.4	1252	1	US-08-316-650-3	Sequence 3, Appli	601	60	10.2	184	5	PCT-US94-14388-2	Sequence 2, Appli
524	61	10.4	2476	1	US-08-276-967-2	Sequence 2, Appli	602	60	10.2	202	2	US-09-949-016-10546	Sequence 10546, A
525	60.5	10.3	98	2	US-09-950-933A-48	Sequence 48, Appl	603	60	10.2	240	2	US-09-512-363-6	Sequence 6, Appli
526	60.5	10.3	99	2	US-09-950-933A-82	Sequence 82, Appl	604	60	10.2	240	2	US-09-176-200-6	Sequence 6, Appli
527	60.5	10.3	115	2	US-09-950-933A-39	Sequence 39, Appl	605	60	10.2	240	2	US-09-915-593-6	Sequence 6, Appli
528	60.5	10.3	141	2	US-09-248-796A-17570	Sequence 17570, A	606	60	10.2	275	2	US-09-489-039A-7372	Sequence 7372, Ap
529	60.5	10.3	170	2	US-09-252-991A-22362	Sequence 22362, A	607	60	10.2	342	2	US-09-193-562D-13	Sequence 13, Appl
530	60.5	10.3	180	2	US-09-461-688-4	Sequence 4, Appli	608	60	10.2	342	2	US-10-055-412B-13	Sequence 13, Appl
531	60.5	10.3	182	2	US-09-252-991A-25189	Sequence 25189, A	609	60	10.2	351	1	US-08-468-847B-16	Sequence 16, Appl
532	60.5	10.3	310	2	US-07-791-931-6	Sequence 6, Appli	610	60	10.2	351	2	US-09-495-448A-34	Sequence 34, Appl
533	60.5	10.3	324	1	US-08-047-413-11	Sequence 11, Appl	611	60	10.2	399	2	US-09-807-802A-9	Sequence 9, Appli
534	60.5	10.3	324	2	US-08-229-050-11	Sequence 11, Appl	612	60	10.2	623	2	US-09-807-802A-2	Sequence 2, Appli
535	60.5	10.3	324	2	US-08-801-563-11	Sequence 11, Appl	613	60	10.2	623	2	US-09-807-802A-5	Sequence 5, Appli
536	60.5	10.3	349	1	US-08-167-628-2	Sequence 2, Appli	614	60	10.2	795	2	US-09-193-562D-11	Sequence 11, Appl
537	60.5	10.3	349	1	US-08-386-680-2	Sequence 2, Appli	615	60	10.2	795	2	US-10-055-412B-11	Sequence 11, Appl
538	60.5	10.3	349	1	US-08-459-717-2	Sequence 2, Appli	616	60	10.2	821	2	US-09-193-562D-12	Sequence 12, Appl
539	60.5	10.3	349	1	US-08-712-303-2	Sequence 2, Appli	624	60	10.2	821	2	US-10-055-412B-12	Sequence 12, Appl
540	60.5	10.3	349	1	US-08-880-031-2	Sequence 2, Appli	625	60	10.2	905	2	US-09-193-562D-2	Sequence 2, Appli
541	60.5	10.3	349	2	US-09-054-368-2	Sequence 2, Appli	626	60	10.2	905	2	US-10-055-412B-2	Sequence 2, Appli
542	60.5	10.3	349	2	US-09-097-179-2	Sequence 2, Appli	627	60	10.2	1227	2	US-09-252-991A-16636	Sequence 2, Appli
543	60.5	10.3	349	2	US-09-054-274-2	Sequence 2, Appli	628	60	10.2	1523	2	US-09-182-04A-2	Sequence 2, Appli
544	60.5	10.3	349	2	US-09-080-715-2	Sequence 2, Appli	648	59.5	10.1	70	2	US-09-894-882-238	Sequence 238, App
545	60.5	10.3	349	2	US-09-056-704-2	Sequence 2, Appli	649	59.5	10.1	74	1	US-08-543-238-2	Sequence 2, Appli
546	60.5	10.3	349	2	US-09-292-036-4	Sequence 4, Appli	650	59.5	10.1	74	1	US-08-420-526-2	Sequence 2, Appli
547	60.5	10.3	349	2	US-09-253-216-26	Sequence 26, Appl	651	59.5	10.1	230	2	US-09-252-991A-25728	Sequence 25728, A
548	60.5	10.3	349	2	US-09-142-569-8	Sequence 8, Appli	652	59.5	10.1	258	2	US-09-252-991A-28812	Sequence 28812, A
549	60.5	10.3	349	2	US-09-495-448A-8	Sequence 8, Appli	653	59.5	10.1	886	2	US-09-110-116-3	Sequence 3, Appli
550	60.5	10.3	349	2	US-09-949-016-6141	Sequence 2, Appli	654	59.5	10.1	1799	2	US-09-631-603-14	Sequence 14, Appl
551	60.5	10.3	349	5	PCT-US94-08140-2	Sequence 6141, Ap	655	59.5	10.1	1799	2	US-09-845-583A-6	Sequence 6, Appli
552	60.5	10.3	349	5	PCT-US95-08140-2	Sequence 2, Appli	656	59	10.0	175	2	US-09-252-991A-30055	Sequence 30055, A
553	60.5	10.3	357	2	US-09-252-991A-31718	Sequence 31718, A	657	59	10.0	258	2	US-09-579-845-9	Sequence 9, Appli
554	60.5	10.3	385	1	US-08-597-545-1	Sequence 1, Appli	658	59	10.0	319	2	US-08-835-279-2	Sequence 2, Appli

659	59	10.0	372	2	US-09-252-991A-20108	Sequence 20108, A	732	58.5	9.9	458	2	US-09-949-016-7946	Sequence 7946, Ap
660	59	10.0	383	2	US-09-142-027A-12	Sequence 12, Appl	733	58.5	9.9	503	1	US-08-481-337A-2	Sequence 2, Appl
661	59	10.0	474	1	US-09-650-000-4	Sequence 4, Appl	734	58.5	9.9	503	1	US-08-696-268B-2	Sequence 2, Appl
662	59	10.0	474	2	US-09-042-785A-8	Sequence 8, Appl	735	58.5	9.9	503	2	US-09-382-256-2	Sequence 2, Appl
663	59	10.0	474	2	US-09-758-124-4	Sequence 4, Appl	736	58.5	9.9	503	2	US-09-395-115-2	Sequence 2, Appl
664	59	10.0	474	7	5395760-4	Patent No. 5395760	737	58.5	9.9	503	2	US-08-436-265-2	Sequence 2, Appl
665	59	10.0	621	2	US-09-046-001A-6	Sequence 6, Appl	738	58.5	9.9	503	2	US-09-679-187-2	Sequence 2, Appl
666	59	10.0	621	2	US-09-996-620-6	Sequence 6, Appl	739	58.5	9.9	503	2	US-08-448-371A-2	Sequence 2, Appl
667	59	10.0	1153	2	US-09-560-385A-16	Sequence 16, Appl	740	58.5	9.9	503	2	US-09-267-963D-2	Sequence 2, Appl
668	59	10.0	1170	2	US-09-561-709B-12	Sequence 12, Appl	741	58.5	9.9	503	2	US-09-903-068C-2	Sequence 2, Appl
669	59	10.0	1170	2	US-09-560-385A-14	Sequence 14, Appl	742	58.5	9.9	503	5	PCT-US95-05467-2	Sequence 2, Appl
670	59	10.0	1253	2	US-08-479-722B-4	Sequence 4, Appl	743	58.5	9.9	503	1	US-08-494-168-8	Sequence 8, Appl
671	59	10.0	1253	2	US-08-532-685-4	Sequence 4, Appl	744	58.5	9.9	503	1	US-09-949-016-10264	Sequence 10264, A
672	59	10.0	1404	1	US-08-400-159-2	Sequence 2, Appl	745	58.5	9.9	735	2	US-09-191-647-9	Sequence 9, Appl
673	59	10.0	1404	2	US-08-611-729A-2	Sequence 2, Appl	746	58.5	9.9	735	2	US-09-540-245A-9	Sequence 9, Appl
674	59	10.0	1404	2	US-09-195-524-2	Sequence 2, Appl	747	58.5	9.9	735	2	US-09-540-153-9	Sequence 9, Appl
675	58.5	9.9	84	3	US-10-000-986A-206	Sequence 206, App	748	58.5	9.9	735	2	US-10-289-776-9	Sequence 9, Appl
676	58.5	9.9	141	2	US-09-621-976-4236	Sequence 4236, Ap	749	58.5	9.9	787	2	US-10-000-489-70	Sequence 70, Appl
677	58.5	9.9	143	2	US-09-270-767-33302	Sequence 33302, A	750	58.5	9.9	787	2	US-09-992-095B-70	Sequence 70, Appl
678	58.5	9.9	143	2	US-09-270-767-33302	Sequence 33302, A	751	58.5	9.9	787	3	US-10-000-986A-70	Sequence 70, Appl
679	58.5	9.9	148	2	US-08-329-799-35	Sequence 35, Appl	752	58.5	9.9	909	2	US-08-936-135-8	Sequence 8, Appl
680	58.5	9.9	180	2	US-09-510-238A-286	Sequence 286, App	753	58.5	9.9	909	2	US-08-936-135-10	Sequence 10, Appl
681	58.5	9.9	189	3	US-10-000-986A-205	Sequence 205, App	754	58.5	9.9	909	2	US-09-013-895A-4	Sequence 4, Appl
682	58.5	9.9	206	2	US-09-134-000C-3471	Sequence 3471, Ap	755	58.5	9.9	909	2	US-09-448-868-4	Sequence 4, Appl
683	58.5	9.9	213	2	US-10-125-062-1	Sequence 1, Appl	756	58.5	9.9	909	2	US-09-439-711C-8	Sequence 8, Appl
684	58.5	9.9	280	2	US-08-974-022-46	Sequence 46, Appl	757	58.5	9.9	909	2	US-09-439-711C-10	Sequence 10, Appl
685	58.5	9.9	280	2	US-08-795-445A-46	Sequence 46, Appl	758	58.5	9.9	909	2	US-10-326-296-4	Sequence 4, Appl
686	58.5	9.9	280	2	US-08-795-447A-46	Sequence 46, Appl	759	58.5	9.9	914	2	US-08-936-135-12	Sequence 12, Appl
687	58.5	9.9	280	2	US-08-974-186-46	Sequence 46, Appl	760	58.5	9.9	914	2	US-09-439-711C-12	Sequence 12, Appl
688	58.5	9.9	280	2	US-08-795-446B-46	Sequence 46, Appl	761	58.5	9.9	925	2	US-09-116-473-2	Sequence 2, Appl
689	58.5	9.9	280	2	US-08-706-945D-132	Sequence 132, App	762	58.5	9.9	926	2	US-08-936-135-14	Sequence 14, Appl
690	58.5	9.9	280	2	US-08-577-788C-46	Sequence 46, Appl	763	58.5	9.9	926	2	US-09-439-711C-14	Sequence 14, Appl
691	58.5	9.9	280	3	US-09-613-591F-129	Sequence 129, App	764	58.5	9.9	931	2	US-08-936-135-16	Sequence 16, Appl
692	58.5	9.9	291	3	US-10-000-986A-204	Sequence 204, App	765	58.5	9.9	931	2	US-09-439-711C-16	Sequence 16, Appl
693	58.5	9.9	301	2	US-09-252-991A-31214	Sequence 31214, A	766	58.5	9.9	1111	1	US-08-317-450B-15	Sequence 15, Appl
694	58.5	9.9	329	2	US-10-300-819B-17	Sequence 17, Appl	767	58.5	9.9	1111	2	US-08-800-593-15	Sequence 15, Appl
695	58.5	9.9	336	2	US-08-804-166-8	Sequence 8, Appl	768	58.5	9.9	1111	2	US-09-756-071B-15	Sequence 15, Appl
696	58.5	9.9	336	2	US-08-910-991-8	Sequence 8, Appl	769	58.5	9.9	1172	2	US-09-560-385A-30	Sequence 30, Appl
697	58.5	9.9	336	2	US-09-756-186-8	Sequence 8, Appl	770	58.5	9.9	1172	2	US-09-560-385A-32	Sequence 32, Appl
698	58.5	9.9	347	2	US-09-187-478-2	Sequence 2, Appl	771	58.5	9.9	1193	1	US-08-317-450B-13	Sequence 13, Appl
699	58.5	9.9	347	2	US-09-232-036-2	Sequence 2, Appl	772	58.5	9.9	1193	2	US-08-800-593-13	Sequence 13, Appl
700	58.5	9.9	381	2	US-09-711-681-2	Sequence 2, Appl	773	58.5	9.9	1193	2	US-09-560-385A-26	Sequence 26, Appl
701	58.5	9.9	381	2	US-10-274-266-2	Sequence 2, Appl	774	58.5	9.9	1193	2	US-09-560-385A-30	Sequence 30, Appl
702	58.5	9.9	397	3	US-10-000-986A-203	Sequence 203, App	775	58.5	9.9	1193	2	US-10-053-662A-31	Sequence 31, Appl
703	58.5	9.9	426	2	US-08-747-562-37	Sequence 37, Appl	776	58.5	9.9	1193	2	US-09-756-071B-13	Sequence 13, Appl
704	58.5	9.9	453	2	US-09-086-483A-5	Sequence 5, Appl	777	58.5	9.9	1712	2	US-09-961-403-9	Sequence 9, Appl
705	58.5	9.9	453	2	US-09-580-212-5	Sequence 5, Appl	778	58.5	9.9	2254	2	US-09-949-016-9270	Sequence 9270, Ap
706	58.5	9.9	453	2	US-09-769-402-5	Sequence 5, Appl	779	58.5	9.9	4391	2	US-10-006-011A-2	Sequence 2, Appl
707	58.5	9.9	453	2	US-10-280-047-5	Sequence 5, Appl	780	58	9.8	43	2	US-09-894-882-272	Sequence 272, App
708	58.5	9.9	455	1	US-08-050-319B-25	Sequence 25, Appl	781	58	9.8	73	1	US-09-464-339A-13	Sequence 13, Appl
709	58.5	9.9	455	1	US-08-321-668-2	Sequence 2, Appl	782	58	9.8	93	1	US-08-464-339A-13	Sequence 13, Appl
710	58.5	9.9	455	1	US-08-837-941-2	Sequence 2, Appl	783	58	9.8	196	2	US-09-252-991A-31920	Sequence 31920, A
711	58.5	9.9	455	1	US-08-126-016-2	Sequence 2, Appl	784	58	9.8	234	2	US-09-902-540-15175	Sequence 15175, A
712	58.5	9.9	455	1	US-08-465-982-25	Sequence 25, Appl	785	58	9.8	525	2	US-08-688-988-10	Sequence 10, Appl
713	58.5	9.9	455	2	US-08-815-469-5	Sequence 5, Appl	786	58	9.8	540	2	US-09-786-256C-1	Sequence 1, Appl
714	58.5	9.9	455	2	US-09-006-353A-3	Sequence 3, Appl	787	58	9.8	540	2	US-09-786-256C-30	Sequence 30, Appl
715	58.5	9.9	455	2	US-09-527-236A-5	Sequence 5, Appl	788	58	9.8	673	2	US-10-104-047-2774	Sequence 2774, Ap
716	58.5	9.9	455	2	US-08-054-970-2	Sequence 2, Appl	789	58	9.8	1149	2	US-09-252-991A-25557	Sequence 25557, A
717	58.5	9.9	455	2	US-09-565-318-4	Sequence 4, Appl	790	58	9.8	1194	2	US-09-092-508-2	Sequence 2, Appl
718	58.5	9.9	455	2	US-09-573-986-3	Sequence 3, Appl	791	58	9.8	1194	2	US-09-435-115-2	Sequence 2, Appl
719	58.5	9.9	455	2	US-09-027-287-3	Sequence 3, Appl	792	58	9.8	1194	2	US-09-069-023-26	Sequence 26, Appl
720	58.5	9.9	455	2	US-09-252-656B-3	Sequence 3, Appl	793	58	9.8	1194	2	US-09-098-310-2	Sequence 2, Appl
721	58.5	9.9	455	2	US-08-406-824A-4	Sequence 4, Appl	794	58	9.8	1194	2	US-09-538-092-825	Sequence 825, App
722	58.5	9.9	455	2	US-09-523-323-3	Sequence 3, Appl	795	58	9.8	1194	2	US-09-949-016-6030	Sequence 6030, Ap
723	58.5	9.9	455	2	US-09-756-854-5	Sequence 5, Appl	796	58	9.8	1196	2	US-09-949-016-10065	Sequence 10065, A
724	58.5	9.9	455	2	US-09-557-908-5	Sequence 5, Appl	797	58	9.8	1196	2	US-09-949-016-10066	Sequence 10066, A
725	58.5	9.9	455	2	US-09-874-138-3	Sequence 3, Appl	798	58	9.8	1205	2	US-09-092-508-16	Sequence 16, Appl
726	58.5	9.9	455	2	US-09-333-966-5	Sequence 5, Appl	799	58	9.8	1205	2	US-09-435-115-16	Sequence 16, Appl
727	58.5	9.9	455	2	US-09-565-009B-3	Sequence 3, Appl	800	58	9.8	1237	2	US-09-949-016-6842	Sequence 6842, Ap
728	58.5	9.9	455	2	US-10-175-902-4	Sequence 4, Appl	801	58	9.8	1239	2	US-09-949-016-10063	Sequence 10063, Ap
729	58.5	9.9	455	2	US-10-041-574-5	Sequence 5, Appl	802	58	9.8	1239	2	US-09-949-016-10064	Sequence 10064, A
730	58.5	9.9	455	2	US-09-095-094-5	Sequence 5, Appl	803	58	9.8	1272	2	US-08-937-236-6	Sequence 6, Appl
731	58.5	9.9	455	2	US-09-314-889-5	Sequence 5, Appl	804	58	9.8	1292	2	US-08-569-214-5	Sequence 5, Appl

805	58	1392	2	US-08-569-214-6	Sequence 6, Appli	895	57.5	9.8	2446	1	US-08-551-356-2	Sequence 2, Appli
806	58	1392	2	US-08-537-236-5	Sequence 5, Appli	896	57.5	9.8	2446	5	PCT-US93-12587-2	Sequence 2, Appli
807	58	1345	1	US-08-977-767-3	Sequence 3, Appli	897	57	9.7	67	2	US-09-894-882-286	Sequence 286, App
808	57.5	63	2	US-09-950-933A-75	Sequence 75, Appl	898	57	9.7	73	2	US-09-686-332-2	Sequence 2, Appli
809	57.5	97	2	US-10-105-901A-50	Sequence 50, Appl	899	57	9.7	147	2	US-09-527-236A-19	Sequence 19, Appl
810	57.5	114	2	US-09-087-031B-12	Sequence 12, Appl	900	57	9.7	147	2	US-09-756-854-19	Sequence 19, Appl
811	57.5	132	2	US-09-523-323-55	Sequence 55, Appl	901	57	9.7	147	2	US-10-041-574-19	Sequence 19, Appl
812	57.5	187	2	US-09-248-796A-46235	Sequence 16235, A	902	57	9.7	147	2	US-09-095-094-19	Sequence 19, Appl
813	57.5	207	2	US-10-094-749-2017	Sequence 2017, Ap	903	57	9.7	181	2	US-10-094-749-1792	Sequence 1792, Ap
814	57.5	264	2	US-09-973-278-151	Sequence 151, App	904	57	9.7	240	2	US-10-006-011A-5	Sequence 5, Appli
815	57.5	265	2	US-09-227-357-153	Sequence 153, App	905	57	9.7	253	2	US-09-042-785A-4	Sequence 4, Appli
816	57.5	289	2	US-09-902-540-12179	Sequence 12179, A	906	57	9.7	254	2	US-09-422-680A-6	Sequence 6, Appli
817	57.5	293	2	US-09-134-001C-5374	Sequence 5374, Ap	907	57	9.7	290	2	US-09-422-680A-2	Sequence 2, Appli
818	57.5	320	2	US-09-183-861-22	Sequence 22, Appl	908	57	9.7	290	2	US-09-422-680A-8	Sequence 8, Appli
819	57.5	320	2	US-09-183-861-55	Sequence 55, Appl	909	57	9.7	306	2	US-09-270-767-41758	Sequence 41758, A
820	57.5	320	2	US-09-022-765-22	Sequence 22, Appl	910	57	9.7	443	1	US-08-833-963C-2	Sequence 2, Appli
821	57.5	320	2	US-09-022-765-55	Sequence 55, Appl	911	57	9.7	443	2	US-08-980-514-1	Sequence 1, Appli
822	57.5	320	2	US-09-551-974A-22	Sequence 22, Appl	912	57	9.7	466	2	US-09-949-016-7792	Sequence 7792, Ap
823	57.5	320	2	US-09-551-974A-55	Sequence 55, Appl	913	57	9.7	495	2	US-10-006-011A-4	Sequence 4, Appli
824	57.5	320	2	US-09-565-501A-22	Sequence 22, Appl	914	57	9.7	498	1	US-08-660-963-12	Sequence 12, Appl
825	57.5	320	2	US-09-565-501A-55	Sequence 55, Appl	915	57	9.7	546	2	US-10-094-749-1953	Sequence 1953, Ap
826	57.5	320	2	US-09-639-206A-22	Sequence 22, Appl	916	57	9.7	547	2	US-10-104-047-3096	Sequence 3096, Ap
827	57.5	320	2	US-09-639-206A-55	Sequence 55, Appl	917	57	9.7	564	2	US-09-949-016-11730	Sequence 11730, A
828	57.5	320	2	US-09-874-923-22	Sequence 22, Appl	918	57	9.7	571	2	US-09-460-295B-13	Sequence 13, Appl
829	57.5	320	2	US-09-874-923-55	Sequence 55, Appl	919	57	9.7	594	2	US-09-949-016-7838	Sequence 7838, Ap
830	57.5	320	2	US-08-798-841-22	Sequence 22, Appl	920	57	9.7	605	2	US-09-042-785A-23	Sequence 23, Appl
831	57.5	359	2	US-09-699-266A-11	Sequence 11, Appl	921	57	9.7	625	2	US-09-949-016-8500	Sequence 8500, Ap
832	57.5	428	2	US-09-252-991A-23863	Sequence 23863, A	922	57	9.7	654	2	US-08-979-847B-91	Sequence 91, Appl
833	57.5	443	2	US-09-461-325-147	Sequence 147, App	923	57	9.7	655	2	US-08-959-382-2	Sequence 2, Appli
834	57.5	443	2	US-10-012-542-147	Sequence 147, App	924	57	9.7	655	2	US-09-527-236A-2	Sequence 2, Appli
835	57.5	443	2	US-10-115-123-147	Sequence 147, App	925	57	9.7	655	2	US-09-314-844F-2	Sequence 2, Appli
836	57.5	503	5	PCT-US94-11328A-4	Sequence 4, Appli	926	57	9.7	655	2	US-09-756-854-2	Sequence 2, Appli
837	57.5	566	2	US-09-489-039A-14179	Sequence 14179, A	928	57	9.7	655	2	US-10-041-574-2	Sequence 2, Appli
838	57.5	581	1	US-10-104-047-2804	Sequence 2804, Ap	929	57	9.7	691	2	US-09-422-680A-4	Sequence 4, Appli
839	57.5	668	1	US-08-786-164-13	Sequence 13, Appl	936	57	9.7	705	2	US-10-006-011A-3	Sequence 3, Appli
840	57.5	709	2	US-09-874-923-121	Sequence 121, App	937	57	9.7	722	2	US-09-617-145-2	Sequence 2, Appli
841	57.5	745	2	US-10-104-047-2955	Sequence 2955, App	938	57	9.7	722	2	US-09-949-016-6418	Sequence 6418, Ap
842	57.5	750	2	US-10-104-047-2960	Sequence 2960, Ap	939	57	9.7	803	2	US-09-949-002-482	Sequence 482, App
843	57.5	750	2	US-09-270-767-42975	Sequence 42975, A	941	57	9.7	825	2	US-09-751-389-2	Sequence 2, Appli
844	57.5	767	1	US-08-874-678-2	Sequence 14, Appl	942	57	9.7	1045	2	US-09-949-016-11112	Sequence 294, App
845	57.5	767	2	US-08-643-839-2	Sequence 2, Appli	943	57	9.7	1752	2	US-09-949-002-294	Sequence 485, App
846	57.5	767	2	US-09-348-886-2	Sequence 2, Appli	944	57	9.6	1917	1	US-09-949-002-485	Sequence 56, Appl
847	57.5	767	2	US-10-105-901A-2	Sequence 2, Appli	945	56.5	9.6	57	1	US-07-609-716-56	Sequence 7, Appli
848	57.5	788	1	US-08-232-538-15	Sequence 15, Appl	946	56.5	9.6	79	2	US-10-006-011A-7	Sequence 196, App
849	57.5	810	1	US-08-786-164-15	Sequence 15, Appl	947	56.5	9.6	80	3	US-09-270-767-62424	Sequence 62424, A
850	57.5	810	1	US-08-820-170A-34	Sequence 34, Appl	948	56.5	9.6	106	2	US-10-094-749-1810	Sequence 1810, Ap
851	57.5	810	2	US-09-055-698-34	Sequence 34, Appl	949	56.5	9.6	167	2	US-09-252-991A-22671	Sequence 22671, A
852	57.5	810	2	US-09-273-565-34	Sequence 34, Appl	950	56.5	9.6	255	2	US-09-188-930-336	Sequence 336, App
853	57.5	810	2	US-09-565-538-34	Sequence 34, Appl	951	56.5	9.6	274	2	US-09-312-283C-336	Sequence 336, App
854	57.5	810	2	US-09-661-468-34	Sequence 34, Appl	952	56.5	9.6	306	2	US-09-252-991A-23169	Sequence 23169, A
855	57.5	810	2	US-09-976-165-34	Sequence 34, Appl	953	56.5	9.6	306	2	US-09-270-767-46802	Sequence 46802, A
856	57.5	880	2	US-10-104-047-2834	Sequence 2834, Ap	954	56.5	9.6	336	2	US-09-252-991A-16971	Sequence 16971, A
857	57.5	1171	1	US-08-445-135-1	Sequence 1, Appli	955	56.5	9.6	439	2	US-09-409-096-6	Sequence 6, Appli
858	57.5	1356	1	US-08-810-116-8	Sequence 8, Appli	956	56.5	9.6	570	2	US-09-252-991A-23954	Sequence 23954, A
859	57.5	1356	1	US-07-930-548A-8	Sequence 8, Appli	957	56.5	9.6	602	2	US-09-252-991A-24403	Sequence 24403, A
860	57.5	1356	2	US-09-098-707A-2	Sequence 2, Appli	958	56.5	9.6	764	2	US-09-235-451-36	Sequence 36, Appl
861	57.5	1356	2	US-09-483-539-2	Sequence 2, Appli	959	56.5	9.6	764	2	US-09-978-303-36	Sequence 36, Appl
862	57.5	1356	2	US-09-949-016-6198	Sequence 6198, Ap	960	56.5	9.6	784	2	US-09-949-016-9467	Sequence 9467, Ap
863	57.5	1356	2	US-10-100-405A-2	Sequence 2, Appli	961	56.5	9.6	830	2	US-09-562-717-33	Sequence 33, Appl
864	57.5	1356	2	US-10-022-939-2	Sequence 2, Appli	962	56.5	9.6	889	2	US-09-132-316-2	Sequence 2, Appli
865	57.5	1456	1	US-09-949-016-9853	Sequence 9853, Ap	963	56.5	9.6	889	2	US-10-137-316-2	Sequence 2, Appli
866	57.5	1940	1	US-08-644-271-30	Sequence 30, Appl	964	56.5	9.6	948	1	US-08-469-537A-101	Sequence 101, App
867	57.5	1940	2	US-09-077-955-34	Sequence 34, Appl	965	56.5	9.6	948	2	US-09-949-016-7768	Sequence 5, Appli
868	57.5	2231	1	US-10-016-283-34	Sequence 34, Appl	966	56.5	9.6	991	2	US-09-751-389-5	Sequence 4, Appli
869	57.5	2324	1	US-08-153-793-16	Sequence 16, Appl	967	56.5	9.6	1035	2	US-09-751-389-4	Sequence 2, Appli
870	57.5	2324	5	PCT-US95-08919-1	Sequence 1, Appli	968	56.5	9.6	1190	2	US-10-053-682A-2	Sequence 2, Appli
871	57.5	2327	7	US455158-1	Patent No. 5455158	969	56.5	9.6	1400	2	US-08-630-915A-37	Sequence 37, Appl
872	57.5	2355	7	US-10-360-101-235	Sequence 235, App	970	56.5	9.6	1400	2	US-08-879-957-37	Sequence 37, Appl
873	57.5	2386	1	US-09-016-366A-12	Sequence 12, Appl	971	56.5	9.6	1422	2	US-08-469-260A-82	Sequence 82, Appl
874	57.5	2386	2	US-09-961-403-1	Sequence 1, Appli	972	56.5	9.6	1422	2	US-08-488-446-82	Sequence 82, Appl
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975	56.5	9.6	1422	2	US-08-424-550B-82	Sequence 82, Appl	1048	55.5	9.4	143	2	US-09-651-236-482	Sequence 482, App
976	56.5	9.6	1551	2	US-09-549-016-6785	Sequence 6785, Ap	1049	55.5	9.4	143	2	US-09-657-279-482	Sequence 482, App
977	56.5	9.6	1616	2	US-09-538-092-1016	Sequence 1016, Ap	1050	55.5	9.4	143	2	US-10-012-896-482	Sequence 482, App
978	56.5	9.6	2088	2	US-09-548-372D-13	Sequence 13, Appl	1051	55.5	9.4	143	3	US-10-144-678A-482	Sequence 482, App
979	56.5	9.6	2088	2	US-09-548-367D-13	Sequence 13, Appl	1052	55.5	9.4	154	2	US-09-191-647-10	Sequence 10, Appl
980	56.5	9.6	2088	2	US-09-551-853D-13	Sequence 13, Appl	1053	55.5	9.4	154	2	US-09-540-245A-10	Sequence 10, Appl
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982	56.5	9.6	2088	2	US-09-548-373D-13	Sequence 13, Appl	1055	55.5	9.4	154	2	US-10-289-776-10	Sequence 10, Appl
983	56.5	9.6	2088	2	US-09-548-366F-13	Sequence 13, Appl	1056	55.5	9.4	161	2	US-09-326-394-2	Sequence 2, Appli
984	56.5	9.6	2088	2	US-09-548-368D-13	Sequence 13, Appl	1057	55.5	9.4	161	2	US-09-882-735A-2	Sequence 2, Appli
985	56.5	9.6	2712	2	US-09-086-436-30	Sequence 30, Appl	1058	55.5	9.4	203	2	US-09-252-991A-23843	Sequence 23843, A
986	56	9.5	43	2	US-09-894-882-233	Sequence 233, App	1059	55.5	9.4	227	2	US-09-252-991A-25546	Sequence 25546, A
987	56	9.5	43	2	US-09-894-882-266	Sequence 260, App	1060	55.5	9.4	233	2	US-09-252-991A-18455	Sequence 18455, A
988	56	9.5	43	2	US-09-894-882-266	Sequence 266, App	1061	55.5	9.4	240	2	US-09-252-991A-23507	Sequence 23507, A
989	56	9.5	88	2	US-09-950-933A-74	Sequence 74, Appl	1062	55.5	9.4	287	2	US-09-489-039A-9585	Sequence 9585, Ap
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991	56	9.5	143	2	US-09-252-991A-19603	Sequence 19603, A	1064	55.5	9.4	353	2	US-09-482-273-243	Sequence 243, App
992	56	9.5	169	2	US-08-630-172-11	Sequence 11, Appl	1065	55.5	9.4	367	1	US-08-514-451A-7	Sequence 7, Appli
993	56	9.5	169	2	US-09-375-419-11	Sequence 11, Appl	1066	55.5	9.4	407	2	US-09-252-991A-32423	Sequence 32423, A
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995	56	9.5	428	2	US-09-329-350-33	Sequence 33, Appl	1068	55.5	9.4	500	3	US-10-241-476-2	Sequence 2, Appli
996	56	9.5	428	2	US-08-841-636A-33	Sequence 33, Appl	1069	55.5	9.4	548	2	US-09-252-991A-28958	Sequence 28958, A
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998	56	9.5	432	1	US-08-560-098A-47	Sequence 47, Appl	1071	55.5	9.4	659	2	US-09-423-753-3	Sequence 3, Appli
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1000	56	9.5	484	2	US-09-252-991A-19511	Sequence 19511, A	1073	55.5	9.4	685	2	US-08-872-855-2	Sequence 2, Appli
1001	56	9.5	491	2	US-09-030-335-2	Sequence 2, Appli	1074	55.5	9.4	718	1	US-08-444-792-4	Sequence 4, Appli
1002	56	9.5	574	2	US-09-248-796A-15283	Sequence 15283, A	1075	55.5	9.4	788	1	US-07-728-215-32	Sequence 32, Appl
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1007	56	9.5	748	2	US-09-285-502-4	Sequence 4, Appli	1080	55.5	9.4	788	1	US-07-728-215-32	Sequence 32, Appl
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1010	56	9.5	761	2	US-09-871-385A-4	Sequence 4, Appli	1083	55.5	9.4	788	2	US-09-409-648-4	Sequence 4, Appli
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1012	56	9.5	799	2	US-09-030-335-4	Sequence 4, Appli	1085	55.5	9.4	788	2	US-10-072-838-32	Sequence 32, Appl
1013	56	9.5	826	2	US-09-949-016-9212	Sequence 9212, Ap	1086	55.5	9.4	788	2	US-10-072-841A-32	Sequence 32, Appl
1014	56	9.5	826	2	US-09-949-016-9213	Sequence 9213, Ap	1087	55.5	9.4	788	2	US-09-054-272-8	Sequence 8, Appli
1015	56	9.5	826	2	US-09-949-016-9214	Sequence 9214, Ap	1088	55.5	9.4	788	2	US-09-054-272-44	Sequence 44, Appl
1016	56	9.5	934	2	US-09-949-002-289	Sequence 289, App	1089	55.5	9.4	788	2	US-10-219-631A-32	Sequence 32, Appl
1017	56	9.5	981	2	US-09-949-002-513	Sequence 513, App	1090	55.5	9.4	788	2	US-09-949-016-5901	Sequence 5901, Ap
1018	56	9.5	1640	2	US-10-037-417-8	Sequence 8, Appli	1091	55.5	9.4	999	2	US-09-747-371-2	Sequence 2, Appli
1019	56	9.5	1656	2	US-09-949-016-7247	Sequence 7247, Ap	1092	55.5	9.4	1742	3	US-09-958-359-23	Sequence 23, Appl
1020	56	9.5	1725	2	US-09-562-702A-20	Sequence 20, Appl	1093	55.5	9.4	1765	2	US-09-562-702A-16	Sequence 16, Appl
1021	56	9.5	1725	2	US-09-561-818A-20	Sequence 12, Appl	1094	55.5	9.4	1765	2	US-09-561-818A-16	Sequence 8, Appli
1022	56	9.5	1725	2	US-10-037-182-12	Sequence 12, Appl	1095	55.5	9.4	1765	2	US-10-037-182-8	Sequence 14, Appl
1023	56	9.5	1786	2	US-09-562-702A-18	Sequence 18, Appl	1096	55.5	9.4	1786	2	US-09-562-702A-14	Sequence 14, Appl
1024	56	9.5	1786	2	US-09-561-818A-18	Sequence 18, Appl	1097	55.5	9.4	1786	2	US-09-561-818A-14	Sequence 14, Appl
1025	56	9.5	1786	2	US-10-037-182-10	Sequence 10, Appl	1098	55.5	9.4	1786	2	US-09-561-7038-9	Sequence 9, Appli
1026	56	9.5	1821	2	US-09-949-016-5938	Sequence 5938, Ap	1099	55.5	9.4	1786	2	US-09-538-092-869	Sequence 869, App
1027	56	9.5	5405	2	US-08-718-388-9	Sequence 9, Appli	1100	55.5	9.4	1786	2	US-10-037-182-6	Sequence 6, Appli
1028	55.5	9.4	44	1	US-08-050-319B-37	Sequence 37, Appl	1101	55	9.3	43	2	US-09-894-882-487	Sequence 487, App
1029	55.5	9.4	44	1	US-08-465-982-37	Sequence 37, Appl	1102	55	9.3	66	2	US-09-950-933A-73	Sequence 73, Appl
1030	55.5	9.4	80	2	US-09-621-976-71598	Sequence 7198, Ap	1103	55	9.3	82	2	US-10-178-213-464	Sequence 464, App
1031	55.5	9.4	92	1	US-07-728-215-39	Sequence 39, Appl	1104	55	9.3	113	2	US-09-826-312A-8	Sequence 8, Appli
1032	55.5	9.4	92	2	US-08-938-085A-39	Sequence 39, Appl	1105	55	9.3	113	2	US-09-542-497A-8	Sequence 8, Appli
1033	55.5	9.4	92	2	US-10-072-844-39	Sequence 39, Appl	1106	55	9.3	113	2	US-10-108-767-8	Sequence 8, Appli
1034	55.5	9.4	92	2	US-10-072-838-39	Sequence 39, Appl	1107	55	9.3	113	2	US-10-152-156-8	Sequence 8, Appli
1035	55.5	9.4	92	2	US-10-072-841A-39	Sequence 39, Appl	1108	55	9.3	113	3	US-10-835-096-8	Sequence 8, Appli
1036	55.5	9.4	92	2	US-10-219-631A-39	Sequence 39, Appl	1109	55	9.3	146	2	US-10-150-6488-32	Sequence 32, Appl
1037	55.5	9.4	139	1	US-08-466-033-177	Sequence 177, App	1110	55	9.3	150	2	US-08-334-179A-6	Sequence 6, Appli
1038	55.5	9.4	139	1	US-08-444-733-177	Sequence 177, App	1111	55	9.3	150	2	US-08-334-179A-10	Sequence 10, Appl
1039	55.5	9.4	139	1	US-08-464-134-177	Sequence 177, App	1112	55	9.3	150	2	US-09-902-540-14820	Sequence 14820, A
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1041	55.5	9.4	139	1	US-08-485-910-177	Sequence 177, App	1114	55	9.3	195	2	US-10-031-607-11	Sequence 11, Appl
1042	55.5	9.4	139	5	PCT-US95-06266-151	Sequence 151, App	1115	55	9.3	197	2	US-08-974-022-49	Sequence 49, Appl
1043	55.5	9.4	143	2	US-09-439-313-482	Sequence 482, App	1116	55	9.3	197	2	US-08-795-445A-49	Sequence 49, Appl
1044	55.5	9.4	143	2	US-09-636-215-482	Sequence 482, App	1117	55	9.3	197	2	US-08-795-447A-49	Sequence 49, Appl
1045	55.5	9.4	143	2	US-09-685-166A-482	Sequence 482, App	1118	55	9.3	197	2	US-08-974-186-49	Sequence 49, Appl
1046	55.5	9.4	143	2	US-09-679-426-482	Sequence 482, App	1119	55	9.3	197	2	US-08-795-446B-49	Sequence 49, Appl
1047	55.5	9.4	143	2	US-09-759-143-482	Sequence 482, App	1120	55	9.3	197	2	US-08-706-945D-135	Sequence 135, App

1121	55	9.3	197	2	US-08-577-788C-49	Sequence 49, Appl	1194	54.5	9.3	154	2	US-09-523-323-53	Sequence 53, Appl
1122	55	9.3	197	3	US-09-613-591F-132	Sequence 132, App	1195	54.5	9.3	157	1	US-08-050-319B-50	Sequence 50, Appl
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1127	55	9.3	374	2	US-09-252-991A-28076	Sequence 28076, A	1200	54.5	9.3	197	2	US-08-828-683A-21	Sequence 21, Appl
1128	55	9.3	388	2	US-09-489-039A-9777	Sequence 9777, Ap	1201	54.5	9.3	199	1	US-08-050-319B-48	Sequence 48, Appl
1129	55	9.3	394	2	US-10-232-858-9	Sequence 9, Appli	1202	54.5	9.3	199	1	US-08-465-982-48	Sequence 48, Appl
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1133	55	9.3	399	2	US-09-253-682-5	Sequence 5, Appli	1206	54.5	9.3	257	2	US-09-312-283C-381	Sequence 381, App
1134	55	9.3	399	2	US-09-527-657-5	Sequence 5, Appli	1207	54.5	9.3	259	2	US-09-006-353A-2	Sequence 2, Appli
1135	55	9.3	399	2	US-09-892-100-5	Sequence 5, Appli	1208	54.5	9.3	259	2	US-09-573-986-2	Sequence 3, Appli
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1137	55	9.3	537	2	US-08-937-067-11	Sequence 11, Appl	1210	54.5	9.3	299	2	US-09-134-618-4	Sequence 4, Appli
1138	55	9.3	567	1	US-08-841-483-2	Sequence 2, Appli	1211	54.5	9.3	299	2	US-09-949-016-6422	Sequence 6422, Ap
1139	55	9.3	567	2	US-09-382-911-2	Sequence 2, Appli	1212	54.5	9.3	301	2	US-09-949-016-9189	Sequence 9189, Ap
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1141	55	9.3	583	2	US-09-641-612-2	Sequence 2, Appli	1214	54.5	9.3	302	2	US-09-270-767-48543	Sequence 48543, A
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1143	55	9.3	597	2	US-09-939-853A-107	Sequence 107, App	1216	54.5	9.3	322	2	US-09-248-796A-15932	Sequence 15932, A
1144	55	9.3	619	2	US-09-949-002-442	Sequence 442, App	1217	54.5	9.3	344	2	US-10-037-417-44	Sequence 44, Appl
1145	55	9.3	717	2	US-08-872-855-9	Sequence 9, Appli	1218	54.5	9.3	357	2	US-10-037-417-46	Sequence 46, Appl
1146	55	9.3	772	2	US-09-949-016-7314	Sequence 7314, Ap	1219	54.5	9.3	385	1	US-08-361-920-23	Sequence 23, Appl
1147	55	9.3	772	2	US-09-949-016-7315	Sequence 7315, Ap	1220	54.5	9.3	385	1	US-08-479-939-23	Sequence 23, Appl
1148	55	9.3	772	2	US-09-949-016-7316	Sequence 7316, Ap	1221	54.5	9.3	385	1	US-08-483-432-23	Sequence 23, Appl
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1150	55	9.3	775	2	US-09-786-256C-15	Sequence 15, Appl	1223	54.5	9.3	442	1	US-08-208-108-2	Sequence 2, Appli
1151	55	9.3	775	2	US-09-786-256C-32	Sequence 32, Appl	1224	54.5	9.3	463	2	US-10-104-047-3058	Sequence 3058, Ap
1152	55	9.3	775	2	US-09-949-002-402	Sequence 402, App	1225	54.5	9.3	463	2	US-09-498-612-6	Sequence 6, Appli
1153	55	9.3	867	2	US-09-634-252A-6	Sequence 6, Appli	1226	54.5	9.3	468	3	US-09-497-967-7	Sequence 7, Appli
1154	55	9.3	909	2	US-09-252-991A-30503	Sequence 30503, A	1227	54.5	9.3	468	3	US-09-497-967-54	Sequence 54, Appl
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1158	55	9.3	996	2	US-09-949-016-8254	Sequence 8254, Ap	1231	54.5	9.3	575	1	US-08-424-788-2	Sequence 4, Appli
1159	55	9.3	1038	2	US-08-334-179A-2	Sequence 2, Appli	1232	54.5	9.3	575	1	US-08-110-683-4	Sequence 4, Appli
1160	55	9.3	1038	2	US-08-334-179A-8	Sequence 8, Appli	1233	54.5	9.3	575	1	US-08-477-166-4	Sequence 4, Appli
1161	55	9.3	1038	2	US-09-908-500A-2	Sequence 2, Appli	1234	54.5	9.3	575	1	US-08-472-097-4	Sequence 4, Appli
1162	55	9.3	1394	2	US-09-949-016-5971	Sequence 5971, Ap	1235	54.5	9.3	575	2	US-09-439-672-4	Sequence 4, Appli
1163	55	9.3	1394	7	5177197-30	Patent No. 5177197	1236	54.5	9.3	575	5	PCT-US93-11638-4	Sequence 4, Appli
1164	55	9.3	1431	2	US-09-842-930A-2	Sequence 2, Appli	1237	54.5	9.3	629	2	US-09-079-431B-4	Sequence 4, Appli
1165	55	9.3	1431	2	US-09-562-702A-24	Sequence 24, Appl	1238	54.5	9.3	629	2	US-09-235-451-23	Sequence 23, Appl
1166	55	9.3	1576	2	US-09-561-818A-24	Sequence 24, Appl	1239	54.5	9.3	727	2	US-09-978-303-23	Sequence 23, Appl
1167	55	9.3	1576	2	US-10-037-182-16	Sequence 16, Appl	1240	54.5	9.3	727	2	US-09-252-991A-31759	Sequence 31759, A
1168	55	9.3	1584	2	US-09-562-702A-28	Sequence 28, Appl	1241	54.5	9.3	809	2	PCT-US93-11725-2	Sequence 2, Appli
1169	55	9.3	1609	2	US-09-562-702A-22	Sequence 22, Appl	1242	54.5	9.3	889	5	PCT-US93-11725-2	Sequence 2, Appli
1170	55	9.3	1609	2	US-09-561-818A-22	Sequence 22, Appl	1243	54.5	9.3	941	1	US-08-343-760A-2	Sequence 4, Appli
1171	55	9.3	1609	2	US-09-538-092-900	Sequence 900, App	1244	54.5	9.3	941	1	US-08-500-857A-10	Sequence 10, Appl
1172	55	9.3	1609	2	US-10-037-182-14	Sequence 14, Appl	1245	54.5	9.3	955	1	US-08-343-760A-2	Sequence 2, Appli
1173	55	9.3	1617	2	US-09-562-702A-26	Sequence 26, Appl	1246	54.5	9.3	975	2	US-09-270-767-42040	Sequence 9, Appli
1174	55	9.3	2052	2	US-09-045-201A-2	Sequence 2, Appli	1247	54.5	9.3	984	1	US-08-449-645A-19	Sequence 19, Appl
1175	55	9.3	2052	2	US-09-619-062-2	Sequence 2, Appli	1248	54.5	9.3	984	1	US-08-702-367A-19	Sequence 19, Appl
1176	55	9.3	2733	2	US-09-949-016-11433	Sequence 11433, A	1249	54.5	9.3	984	2	US-09-378-759-19	Sequence 19, Appl
1177	55	9.3	3259	2	US-09-949-016-6507	Sequence 6507, Ap	1250	54.5	9.3	984	5	PCT-US95-04681-19	Sequence 19, Appl
1178	54.5	9.3	92	1	US-07-728-213-41	Sequence 41, Appl	1251	54.5	9.3	1053	2	US-09-252-991A-26140	Sequence 7, Appli
1179	54.5	9.3	92	2	US-08-938-085A-41	Sequence 41, Appl	1252	54.5	9.3	1185	2	US-09-964-956-7	Sequence 7, Appli
1180	54.5	9.3	92	2	US-10-072-844-41	Sequence 41, Appl	1253	54.5	9.3	1216	2	US-09-252-991A-26104	Sequence 26104, A
1181	54.5	9.3	92	2	US-10-072-838-41	Sequence 41, Appl	1254	54.5	9.3	1247	2	US-09-919-497-85	Sequence 85, Appl
1182	54.5	9.3	92	2	US-10-072-841A-41	Sequence 41, Appl	1255	54.5	9.3	1247	2	US-09-961-403-14	Sequence 14, Appl
1183	54.5	9.3	92	2	US-10-219-631A-41	Sequence 41, Appl	1256	54.5	9.3	1247	1	US-08-583-562B-8	Sequence 8, Appli
1184	54.5	9.3	99	2	US-09-270-767-57298	Sequence 57298, A	1257	54.5	9.3	1247	1	US-08-773-113-8	Sequence 8, Appli
1185	54.5	9.3	103	2	US-09-489-039A-7227	Sequence 7227, Ap	1258	54.5	9.3	1266	2	US-09-949-016-6082	Sequence 6082, Ap
1186	54.5	9.3	153	1	US-08-219-237B-4	Sequence 4, Appli	1259	54.5	9.3	2666	2	US-09-949-016-10857	Sequence 10857, A
1187	54.5	9.3	153	2	US-08-477-347-12	Sequence 12, Appl	1260	54	9.2	43	2	US-09-894-882-269	Sequence 269, App
1188	54.5	9.3	153	2	US-08-476-862-3	Sequence 3, Appli	1261	54	9.2	99	2	US-09-950-933A-64	Sequence 64, Appl
1189	54.5	9.3	153	2	US-08-468-560C-4	Sequence 4, Appli	1262	54	9.2	107	1	US-07-963-538B-4	Sequence 4, Appli
1190	54.5	9.3	153	2	US-09-800-909-3	Sequence 3, Appli	1263	54	9.2	107	2	US-09-461-697-322	Sequence 322, App
1191	54.5	9.3	153	2	US-09-800-908-12	Sequence 12, Appl	1264	54	9.2	120	2	US-08-974-022-42	Sequence 42, Appl
1192	54.5	9.3	153	2	US-09-884-987-4	Sequence 4, Appli	1265	54	9.2	120	2	US-08-795-445A-42	Sequence 42, Appl
1193	54.5	9.3	154	2	US-08-828-683A-12	Sequence 12, Appl	1266	54	9.2	120	2	US-08-795-447A-42	Sequence 42, Appl

1267	54	9.2	120	2	US-08-974-186-42	Sequence 42, Appl	1347	54	9.2	553	2	US-10-136-227A-24	Sequence 24, Appl
1268	54	9.2	120	2	US-08-795-446B-42	Sequence 42, Appl	1348	54	9.2	553	2	US-09-981-649A-6	Sequence 6, Appl
1269	54	9.2	120	2	US-08-706-945D-120	Sequence 120, App	1349	54	9.2	553	2	US-09-981-649A-24	Sequence 24, Appl
1270	54	9.2	120	2	US-08-577-788C-42	Sequence 42, Appl	1350	54	9.2	554	2	US-10-136-227A-32	Sequence 32, Appl
1271	54	9.2	120	3	US-09-613-591F-138	Sequence 138, App	1351	54	9.2	554	2	US-10-136-227A-32	Sequence 32, Appl
1272	54	9.2	132	1	US-08-304-051-21	Sequence 21, Appl	1352	54	9.2	554	2	US-09-981-649A-30	Sequence 30, Appl
1273	54	9.2	132	1	US-08-304-051-21	Sequence 21, Appl	1353	54	9.2	554	2	US-09-981-649A-30	Sequence 30, Appl
1274	54	9.2	132	5	PCT-US95-11445-21	Sequence 45859, A	1354	54	9.2	554	2	US-10-136-227A-32	Sequence 32, Appl
1275	54	9.2	167	2	US-09-898-659-28	Sequence 28, Appl	1355	54	9.2	559	2	US-10-136-227A-32	Sequence 32, Appl
1276	54	9.2	178	2	US-09-706-722A-7	Sequence 7, Appl	1356	54	9.2	559	2	US-09-981-649A-28	Sequence 28, Appl
1277	54	9.2	180	2	US-08-926-808C-1	Sequence 1, Appl	1357	54	9.2	572	7	5256770-7	Patent No. 5256770
1278	54	9.2	194	2	US-09-248-796A-15809	Sequence 15809, A	1358	54	9.2	575	1	US-08-261-206A-59	Sequence 59, Appl
1279	54	9.2	198	2	US-09-343-681A-7611	Sequence 7611, Ap	1359	54	9.2	575	1	US-08-312-870-1	Sequence 1, Appl
1280	54	9.2	213	2	US-09-336-536-58	Sequence 58, Appl	1360	54	9.2	575	1	US-08-170-290A-54	Sequence 54, Appl
1281	54	9.2	235	2	US-10-104-047-3131	Sequence 3131, Ap	1361	54	9.2	575	2	US-09-880-484D-2	Sequence 2, Appl
1282	54	9.2	275	1	US-08-312-870-7	Sequence 7, Appl	1362	54	9.2	575	2	US-10-438-648-2	Sequence 2, Appl
1283	54	9.2	287	1	US-07-915-934-2	Sequence 2, Appl	1363	54	9.2	575	2	US-09-949-002-296	Sequence 296, App
1284	54	9.2	287	1	US-08-325-743-2	Sequence 2, Appl	1364	54	9.2	575	7	5466668-6	Patent No. 5466668
1285	54	9.2	291	2	US-09-902-540-15052	Sequence 15052, A	1365	54	9.2	594	2	US-09-949-016-8175	Sequence 8175, Ap
1286	54	9.2	303	2	US-09-252-991A-17179	Sequence 17179, A	1366	54	9.2	600	2	US-09-422-680A-10	Sequence 10, Appl
1287	54	9.2	324	2	US-09-270-767-59483	Sequence 59483, A	1367	54	9.2	614	2	US-09-949-016-8536	Sequence 8536, Ap
1289	54	9.2	338	2	US-09-807-933B-1	Sequence 1, Appl	1368	54	9.2	640	1	US-09-605-042A-40	Sequence 40, Appl
1290	54	9.2	338	2	US-09-807-933B-7	Sequence 7, Appl	1369	54	9.2	681	2	US-08-655-345-4	Sequence 4, Appl
1297	54	9.2	352	2	US-09-270-767-44070	Sequence 44070, A	1370	54	9.2	681	2	US-09-183-275-4	Sequence 4, Appl
1298	54	9.2	376	2	US-09-540-236-3121	Sequence 3121, Ap	1371	54	9.2	681	5	PCT-US96-08407-4	Sequence 4, Appl
1299	54	9.2	394	2	US-09-523-263B-2	Sequence 2, Appl	1372	54	9.2	682	2	US-09-949-002-436	Sequence 436, App
1300	54	9.2	394	2	US-10-299-867-2	Sequence 2, Appl	1373	54	9.2	698	2	US-09-949-016-7019	Sequence 4, Appl
1301	54	9.2	446	1	US-08-307-444A-5	Sequence 5, Appl	1374	54	9.2	698	2	US-09-727-169-4	Sequence 4, Appl
1302	54	9.2	446	1	US-08-587-389-5	Sequence 5, Appl	1375	54	9.2	698	2	US-09-579-766A-4	Sequence 4, Appl
1309	54	9.2	448	1	US-08-884-072-1	Sequence 1, Appl	1376	54	9.2	698	2	US-09-726-968-4	Sequence 4, Appl
1310	54	9.2	456	1	US-08-587-389-4	Sequence 4, Appl	1377	54	9.2	721	2	US-09-815-048-2	Sequence 2, Appl
1311	54	9.2	475	1	US-08-307-444A-1	Sequence 1, Appl	1378	54	9.2	732	2	US-09-815-048-4	Sequence 4, Appl
1312	54	9.2	475	1	US-08-307-444A-2	Sequence 2, Appl	1379	54	9.2	742	2	US-09-252-991A-29239	Sequence 29239, A
1313	54	9.2	475	1	US-08-587-389-1	Sequence 1, Appl	1380	54	9.2	769	1	US-08-789-078-1	Sequence 1, Appl
1314	54	9.2	475	1	US-08-587-389-2	Sequence 2, Appl	1381	54	9.2	769	1	US-08-752-633-1	Sequence 1, Appl
1315	54	9.2	476	1	US-08-014-723-1	Sequence 1, Appl	1382	54	9.2	769	1	US-08-476-062A-45	Sequence 45, Appl
1316	54	9.2	476	1	US-08-014-723-2	Sequence 2, Appl	1383	54	9.2	769	1	US-07-728-215-31	Sequence 31, Appl
1317	54	9.2	476	1	US-08-014-723-18	Sequence 18, Appl	1384	54	9.2	769	2	US-08-938-085A-31	Sequence 31, Appl
1318	54	9.2	476	1	US-08-110-011A-1	Sequence 1, Appl	1385	54	9.2	769	2	US-10-072-844-31	Sequence 31, Appl
1319	54	9.2	476	1	US-08-110-011A-2	Sequence 2, Appl	1386	54	9.2	769	2	US-10-072-838-31	Sequence 31, Appl
1320	54	9.2	476	1	US-08-110-011A-18	Sequence 18, Appl	1387	54	9.2	769	2	US-10-072-841A-31	Sequence 31, Appl
1321	54	9.2	476	2	US-09-189-035-1	Sequence 1, Appl	1388	54	9.2	769	5	PCT-US95-04886-1	Sequence 1, Appl
1322	54	9.2	476	2	US-09-382-086-1	Sequence 1, Appl	1389	54	9.2	769	5	PCT-US96-01314-45	Sequence 45, Appl
1323	54	9.2	494	1	US-08-014-723-14	Sequence 14, Appl	1390	54	9.2	793	1	US-08-720-484A-2	Sequence 2, Appl
1324	54	9.2	494	1	US-08-014-723-16	Sequence 16, Appl	1391	54	9.2	793	2	US-08-953-823A-2	Sequence 2, Appl
1325	54	9.2	494	1	US-08-110-011A-14	Sequence 14, Appl	1392	54	9.2	793	2	US-09-293-505-15	Sequence 15, Appl
1326	54	9.2	494	1	US-08-110-011A-16	Sequence 16, Appl	1393	54	9.2	793	2	US-09-293-505-17	Sequence 17, Appl
1327	54	9.2	497	1	US-08-312-870-3	Sequence 3, Appl	1394	54	9.2	793	2	US-09-398-239-2	Sequence 2, Appl
1328	54	9.2	497	2	US-09-331-793-4	Sequence 4, Appl	1395	54	9.2	793	2	US-09-560-876A-2	Sequence 2, Appl
1329	54	9.2	498	1	US-08-733-564-2	Sequence 1, Appl	1396	54	9.2	793	2	US-09-060-939A-16	Sequence 16, Appl
1330	54	9.2	502	2	US-09-363-316B-18	Sequence 18, Appl	1397	54	9.2	793	2	US-09-060-939A-17	Sequence 17, Appl
1331	54	9.2	502	2	US-10-136-227A-18	Sequence 18, Appl	1398	54	9.2	803	2	US-09-293-505-15	Sequence 15, Appl
1332	54	9.2	502	2	US-09-981-649A-18	Sequence 18, Appl	1399	54	9.2	803	2	US-09-060-939A-15	Sequence 15, Appl
1333	54	9.2	504	2	US-09-949-016-7403	Sequence 7403, Ap	1400	54	9.2	807	1	US-08-655-345-2	Sequence 2, Appl
1334	54	9.2	512	2	US-09-252-991A-25114	Sequence 25114, A	1401	54	9.2	807	2	US-09-183-275-2	Sequence 2, Appl
1335	54	9.2	516	2	US-09-509-994-1	Sequence 1, Appl	1402	54	9.2	807	5	PCT-US96-08407-2	Sequence 2, Appl
1336	54	9.2	516	2	US-09-509-994-2	Sequence 2, Appl	1403	54	9.2	810	2	US-09-949-016-7737	Sequence 7737, Ap
1337	54	9.2	529	1	US-08-836-442-3	Sequence 3, Appl	1404	54	9.2	810	2	US-09-949-016-7738	Sequence 7738, Ap
1338	54	9.2	537	2	US-09-249-697A-4	Sequence 4, Appl	1405	54	9.2	824	2	US-09-727-169-2	Sequence 2, Appl
1339	54	9.2	537	2	US-09-363-316B-4	Sequence 4, Appl	1406	54	9.2	824	2	US-09-579-766A-2	Sequence 2, Appl
1340	54	9.2	537	2	US-10-136-227A-4	Sequence 4, Appl	1407	54	9.2	824	2	US-09-726-968-2	Sequence 2, Appl
1341	54	9.2	537	2	US-09-981-649A-4	Sequence 4, Appl	1408	54	9.2	1042	2	US-09-959-392-2	Sequence 2, Appl
1342	54	9.2	553	2	US-09-249-697A-6	Sequence 6, Appl	1409	54	9.2	1152	2	US-09-303-518D-195	Sequence 195, App
1343	54	9.2	553	2	US-09-249-697A-19	Sequence 19, Appl	1410	54	9.2	1152	2	US-08-900-230-3	Sequence 3, Appl
1344	54	9.2	553	2	US-09-363-316B-6	Sequence 6, Appl	1411	54	9.2	2362	2	US-09-949-016-8985	Sequence 8985, Ap
1345	54	9.2	553	2	US-09-363-316B-24	Sequence 24, Appl	1412	54	9.2	2523	1	US-08-185-432-18	Sequence 18, Appl
1346	54	9.2	553	2	US-10-136-227A-6	Sequence 6, Appl	1413	54	9.2	2523	2	US-08-899-232-3	Sequence 3, Appl
							1414	54	9.2	2523	2	US-09-121-457-3	Sequence 3, Appl
							1415	54	9.2	2813	2	US-09-381-261A-1	Sequence 1, Appl
							1416	54	9.2	43	2	US-09-445-480D-26	Sequence 26, Appl
							1417	53.5	9.1	70	2	US-09-894-882-295	Sequence 295, App
							1418	53.5	9.1	88	2	US-09-950-933A-56	Sequence 56, Appl
							1419	53.5	9.1	96	2	US-09-950-933A-77	Sequence 77, Appl

1420	53.5	9.1	139	2	US-09-252-991A-19187	Sequence 19187, A
1421	53.5	9.1	154	1	US-08-232-087A-10	Sequence 10, Appl
1422	53.5	9.1	157	2	US-08-872-855-6	Sequence 6, Appl
1423	53.5	9.1	157	2	US-08-981-392-68	Sequence 68, Appl
1424	53.5	9.1	157	2	US-09-621-976-4527	Sequence 4527, Ap
1425	53.5	9.1	157	2	US-09-908-322-68	Sequence 68, Appl
1426	53.5	9.1	157	2	US-09-310-685-20	Sequence 20, Appl
1427	53.5	9.1	257	2	US-09-252-991A-31868	Sequence 31868, A
1428	53.5	9.1	281	2	US-09-248-796A-15282	Sequence 15282, A
1429	53.5	9.1	328	2	US-09-253-316-28	Sequence 28, Appl
1430	53.5	9.1	328	2	US-09-961-403-2	Sequence 2, Appl
1431	53.5	9.1	328	7	5212074-4	Patent No. 5212074
1432	53.5	9.1	329	2	US-10-188-495-58	Sequence 58, Appl
1433	53.5	9.1	335	2	US-09-252-991A-23948	Sequence 23948, A
1447	53.5	9.1	353	2	US-10-188-495-56	Sequence 56, Appl
1452	53.5	9.1	385	2	US-09-252-991A-17950	Sequence 17950, A
1453	53.5	9.1	396	2	US-09-270-767-41833	Sequence 41833, A
1454	53.5	9.1	411	2	US-09-949-016-11215	Sequence 11215, A
1455	53.5	9.1	440	1	US-08-574-959A-2	Sequence 2, Appl
1456	53.5	9.1	440	2	US-09-357-014-2	Sequence 2, Appl
1457	53.5	9.1	440	2	US-09-949-016-6431	Sequence 6431, Ap
1458	53.5	9.1	473	2	US-09-303-518D-378	Sequence 378, App
1459	53.5	9.1	506	2	US-09-303-518D-546	Sequence 546, App
1460	53.5	9.1	526	2	US-09-252-991A-28761	Sequence 28761, A
1461	53.5	9.1	610	3	US-08-368-776A-3	Sequence 3, Appl
1462	53.5	9.1	610	3	US-10-073-064-3	Sequence 3, Appl
1463	53.5	9.1	610	5	PCT-US96-00419-3	Sequence 3, Appl
1464	53.5	9.1	626	2	US-08-368-776A-5	Sequence 5, Appl
1465	53.5	9.1	626	5	US-10-073-064-5	Sequence 5, Appl
1466	53.5	9.1	626	5	PCT-US96-00419-5	Sequence 5, Appl
1467	53.5	9.1	704	2	US-09-590-656-2	Sequence 2, Appl
1468	53.5	9.1	704	2	US-09-733-764-2	Sequence 2, Appl
1469	53.5	9.1	765	2	US-09-949-016-10117	Sequence 10117, A
1470	53.5	9.1	768	1	US-08-454-455-4	Sequence 4, Appl
1471	53.5	9.1	824	2	US-09-949-002-312	Sequence 312, App
1472	53.5	9.1	942	2	US-10-004-542-2	Sequence 2, Appl
1473	53.5	9.1	942	2	US-10-430-797-2	Sequence 2, Appl
1474	53.5	9.1	943	2	US-08-476-515A-12	Sequence 12, Appl
1475	53.5	9.1	944	2	US-08-652-877-12	Sequence 12, Appl
1476	53.5	9.1	975	2	US-09-751-389-8	Sequence 8, Appl
1477	53.5	9.1	977	2	US-09-590-656-1	Sequence 1, Appl
1478	53.5	9.1	977	2	US-09-733-764-1	Sequence 1, Appl
1479	53.5	9.1	993	2	US-08-368-776A-11	Sequence 11, Appl
1480	53.5	9.1	993	3	US-10-073-064-11	Sequence 11, Appl
1481	53.5	9.1	994	2	US-08-368-776A-12	Sequence 12, Appl
1482	53.5	9.1	994	3	US-10-073-064-12	Sequence 12, Appl
1483	53.5	9.1	998	2	US-08-368-776A-2	Sequence 2, Appl
1484	53.5	9.1	998	3	US-10-073-064-2	Sequence 2, Appl
1485	53.5	9.1	998	5	PCT-US96-00419-2	Sequence 2, Appl
1486	53.5	9.1	1124	1	US-08-323-474-2	Sequence 2, Appl
1487	53.5	9.1	1124	2	US-09-949-016-5946	Sequence 5946, Ap
1488	53.5	9.1	1124	5	PCT-US93-06093-2	Sequence 2, Appl
1489	53.5	9.1	1157	2	US-09-949-016-9568	Sequence 9568, Ap
1490	53.5	9.1	2123	2	US-09-949-016-7517	Sequence 7517, Ap
1491	53.5	9.1	2616	2	US-09-303-518D-879	Sequence 879, App
1492	53.5	9.1	3070	2	US-09-961-403-7	Sequence 7, Appl
1493	53.5	9.1	3088	2	US-09-562-702A-8	Sequence 8, Appl
1494	53.5	9.1	3089	2	US-09-562-702A-4	Sequence 4, Appl
1495	53.5	9.1	3110	2	US-09-562-702A-2	Sequence 2, Appl
1496	53.5	9.1	3110	2	US-09-562-702A-6	Sequence 6, Appl
1497	53.5	9.1	3110	2	US-09-561-709B-7	Sequence 7, Appl
1498	53.5	9.1	3110	2	US-09-917-254-86	Sequence 86, Appl
1499	53.5	9.1	3110	2	US-09-949-016-5937	Sequence 5937, Ap
1500	53.5	9.1	3111	1	US-08-460-309-4	Sequence 4, Appl

GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-5

Query Match 100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGSEC 60
QY 61 HPGSHKVPFFRRKRKHHTCCPLNLLCSRFPDGRYRCSDMLKNINF 105
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RESULT 2
US-10-212-201A-5
; Sequence 5, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIOR FILING DATE: US/09/712,529
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-201A-5

Query Match 100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGSEC 60
Db 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGSEC 60
QY 61 HPGSHKVPFFRRKRKHHTCCPLNLLCSRFPDGRYRCSDMLKNINF 105
Db 61 HPGSHKVPFFRRKRKHHTCCPLNLLCSRFPDGRYRCSDMLKNINF 105

RESULT 3
US-10-212-355-5
; Sequence 5, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.

ALIGNMENTS

RESULT 1
US-09-712-529-5
; Sequence 5, Application US/09712529
; Patent No. 6485938

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; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
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; LENGTH: 105
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; US-10-212-355-5

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QY 61 HPGSHKVPFRKHKHTKCPCLPNLLCSRFPDGRYRCMDLKNINF 105
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RESULT 4
; Sequence 371, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e-58; Mismatches 0; Indels 0; Gaps 0;
Matches 105; Conservative 0;

QY      1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
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QY      61 HPGSHKVPFRKRRKHHTCPLNLLCSRPDPGRYRCMDLKNINF 105
Db      61 HPGSHKVPFRKRRKHHTCPLNLLCSRPDPGRYRCMDLKNINF 105

RESULT 6
; Sequence 371, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deonoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182

;; PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGRLMCTPLGRGEEC 60
Db 1 MRGATRVSIIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGRLMCTPLGRGEEC 60
QY 61 HPGSHKVPFFRRKHKHTCPCLENLCSRPDPGRYRCMDLKNINF 105
Db 61 HPGSHKVPFFRRKHKHTCPCLENLCSRPDPGRYRCMDLKNINF 105
RESULT 7
;; Sequence 371, Application US/09992598
;; Patent No. 6956108
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Faoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumaas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC20
;; CURRENT APPLICATION NUMBER: US/09/992,598
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
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61	PRIOR APPLICATION NUMBER: 60/091978	
62	PRIOR FILING DATE: 1998-07-07	
63	PRIOR APPLICATION NUMBER: 60/091982	
64	PRIOR FILING DATE: 1998-07-07	
65	PRIOR APPLICATION NUMBER: 60/092182	
66	PRIOR FILING DATE: 1998-07-09	

Query Match	100.0%;	Score 589;	DB 2;	Length 105;
Best Local Similarity	100.0%;	Pred. No. 1.3e-58;		

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65 PRIOR APPLICATION NUMBER: 60/092182
66 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 2; Length 105;
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RESULT 9

; Sequence 371, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Nagier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C60
; CURRENT APPLICATION NUMBER: US/09/989,726
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 3; Length 105;
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Db 61 HPGSHKVPFRKRKHHTCPLNLLCSRPFDGRCRSMCLKNINP 105

RESULT 10

; Sequence 371, Application US/09997514
; Patent No. 7019116

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
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56 PRIOR FILING DATE: 1998-07-07
57 PRIOR APPLICATION NUMBER: 60/092182
58 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCPTPLGRGEEC 60

QY 61 HPGSHKVPFRKPKHHTCPLNLLCSRPDGRYRCSMDLKNINF 105
DB 61 HPGSHKVPFRKPKHHTCPLNLLCSRPDGRYRCSMDLKNINF 105

RESULT 11

Sequence 371, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC72
CURRENT APPLICATION NUMBER: US/09/989,728
CURRENT FILING DATE: 2001-11-20
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PRIOR FILING DATE: 1997-06-16
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40	PRIOR FILING DATE: 1998-07-02
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49	PRIOR APPLICATION NUMBER: 60/091978
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51	PRIOR APPLICATION NUMBER: 60/091982
52	PRIOR FILING DATE: 1998-07-07
53	PRIOR APPLICATION NUMBER: 60/092182
54	PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 105; Conservative 0; Mismatches 0; Indels

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RESULT 12
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; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C37
CURRENT APPLICATION NUMBER: US/09/997,349
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 589; DB 3; Length 105;
Best Local Similarity 100.0%; Pred No. 1.3e-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCCTPLGREGEC 60
Db 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCCTPLGREGEC 60

QY 61 HPGSHKVPFRKXKHTKTCCLNLLCSRFPDGRYRCMDLKNINF 105
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RESULT 13
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; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/089947
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09
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; Query Match 100.0%; Score 589; DB 3; Length 105;
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; Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MEGATRVSTMLLLVTVDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
Db 1 MEGATRVSTMLLLVTVDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
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RESULT 14
; Sequence 371, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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;; PRIOR APPLICATION NUMBER: 60/091978
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEGATRVSIIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECC 60

QY 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPPDGRYRCMDLKNINF 105
Db 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPPDGRYRCMDLKNINF 105

RESULT 15
US-09-621-976-5350
; Sequence 5350, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S. J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5350
; LENGTH: 105
; TYPE: PRT

;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -19...-1
;; NAME/KEY: UNSURE
;; LOCATION: 38
;; OTHER INFORMATION: Xaa = Ala, Gly
US-09-621-976-5350

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Best Local Similarity 97.1%; Pred. No. 2.9e-57;
Matches 102; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MEGATRVSIIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECC 60

QY 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPPDGRYRCMDLKNINF 105
Db 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPPDGRYRCMDLKNINF 105

Search completed: December 14, 2006, 14:15:39
Job time : 57.1309 secs

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OM protein - protein search, using sw model
Run on: December 14, 2006, 14:37:13 ; Search time 312.801 Seconds
(without alignments)
153.477 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSMILLVTVSDCA.....CSRFPDGRVRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

2589679 segs, 45716429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 1500 summaries

Database :

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1: Geneseq1980s:*
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3: Geneseq2000s:*
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5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1 ID AAY66745 standard; protein; 105 AA.

DE Membrane-bound protein/PRO1186.

PN WO963088-A2.

PD 09-DEC-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 3; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 2

ID AAB18453 standard; protein; 105 AA.

DE A human TANGO 266 polypeptide.

PN WO200052022-A1.

PD 08-SEP-2000.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 100.0%; Score 589; DB 3; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 3

ID AAB70148 standard; protein; 105 AA.

DE Human G protein-coupled receptor protein-related sequence #4.

PN WO200116309-A1.

PD 08-MAR-2001.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 4

ID AAB68427 standard; protein; 105 AA.

DE Amino acid sequence of a human Zven2 polypeptide.

PN WO200136465-A2.

PD 25-MAY-2001.

PA (ZYMO) ZYMOGENETICS INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 5

ID AAU12406 standard; protein; 105 AA.

DE Human PRO1186 polypeptide sequence.

PN WO200140466-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 6

ID AAB53096 standard; protein; 105 AA.

DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.

PN WO200236625-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 7

ID AAB65268 standard; protein; 105 AA.

DE Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.

PN WO200073454-A1.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 8

ID AAB48175 standard; protein; 105 AA.

DE Human PRO1186 polypeptide.

PN WO200075327-A1.

PD 14-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 9

ID AAB48067 standard; protein; 105 AA.

DE Human extracellular signaling molecule (EXCS) (ID 2006548CD1).

PN WO200070049-A2.

PD 23-NOV-2000.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 10

ID AAM50773 standard; protein; 105 AA.

DE Endocrine gland-derived vascular endothelial growth factor.

PN WO200200711-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 11

ID AAU3674 standard; protein; 105 AA.

DE Human PRO protein, Seq ID No 166.

PN WO200208288-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 12

ID ABB4902 standard; protein; 105 AA.

DE Human PRO1186 protein sequence SEQ ID NO:172.

PN WO200200690-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 13

ID AAO15527 standard; protein; 105 AA.

DE Human physiologically-active ZAQ ligand-related protein 3.

PN WO200257443-A1.

PD 25-JUL-2002.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 14

ID ABB06308 standard; protein; 105 AA.

DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.

PN WO200206483-A1.

PD 24-JAN-2002.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 15

ID AAB24382 standard; protein; 105 AA.

DE Human prokineticin 1 precursor protein.

PN WO200236625-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 16

ID AAB53096 standard; protein; 105 AA.

DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.

PN WO200236625-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 17

ID AAB65268 standard; protein; 105 AA.

DE Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.

PN WO200073454-A1.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 18

ID AAB48175 standard; protein; 105 AA.

DE Human PRO1186 polypeptide.

PN WO200075327-A1.

PD 14-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 19

ID AAB48067 standard; protein; 105 AA.

DE Human extracellular signaling molecule (EXCS) (ID 2006548CD1).

PN WO200070049-A2.

PD 23-NOV-2000.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 20

ID AAM50773 standard; protein; 105 AA.

DE Endocrine gland-derived vascular endothelial growth factor.

PN WO200200711-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 21

ID AAU3674 standard; protein; 105 AA.

DE Human PRO protein, Seq ID No 166.

PN WO200208288-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 22

ID ABB4902 standard; protein; 105 AA.

DE Human PRO1186 protein sequence SEQ ID NO:172.

PN WO200200690-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 23

ID AAO15527 standard; protein; 105 AA.

DE Human physiologically-active ZAQ ligand-related protein 3.

PN WO200257443-A1.

PD 25-JUL-2002.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 24

ID ABB06308 standard; protein; 105 AA.

DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.

PN WO200206483-A1.

PD 24-JAN-2002.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 25

ID AAB24382 standard; protein; 105 AA.

DE Human prokineticin 1 precursor protein.

PN WO200236625-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 26

ID AAB53096 standard; protein; 105 AA.

DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.

PN WO200236625-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 27

ID AAB65268 standard; protein; 105 AA.

DE Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.

PN WO200073454-A1.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 28

ID AAB48175 standard; protein; 105 AA.

DE Human PRO1186 polypeptide.

PN WO200075327-A1.

PD 14-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 29

ID AAB48067 standard; protein; 105 AA.

DE Human extracellular signaling molecule (EXCS) (ID 2006548CD1).

PN WO200070049-A2.

PD 23-NOV-2000.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 30

ID AAM50773 standard; protein; 105 AA.

DE Endocrine gland-derived vascular endothelial growth factor.

PN WO200200711-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;

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PD 10-MAY-2002.
PA (REGC ) UNIV CALIFORNIA.
Query Match 100.0%; Score 589; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 16
ID ABB9508 standard; protein; 105 AA.
DE Human angiogenesis related protein PRO1186 SEQ ID NO: 172.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 589; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 17
ID ADY31906 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN WO200191983-A1.
PD 13-DEC-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 18
ID ABU58083 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 19
ID ABUS9161 standard; protein; 105 AA.
DE Novel human secreted or transmembrane protein PRO1186.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 20
ID ABUS2673 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 21
ID ABO17850 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003032156-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 22
ID ABU60592 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, #151.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 23
ID ABUS0821 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 24
ID ABO33787 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 25
ID ABU13974 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 26
ID ABUS0800 standard; protein; 105 AA.
DE Human endocrine gland-derived vascular endothelial growth factor.
PN US2002192634-A1.
PD 19-DEC-2002.
PA (FERR/) FERRARA N.
PA (WATA/) WATANABE C.
PA (WOOD/) WOOD W I.
PA (SHEK/) SHEK T.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 27
ID ABUS1104 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 28
ID ABUS07603 standard; protein; 105 AA.
DE Human ZVEN2.
PN US6485938-B1.
PD 26-NOV-2002.
PA (ZYMO ) ZYMOGENETICS INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 29
ID ABUS72559 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 30
ID ABUS66804 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 31
ID ABUS9885 standard; protein; 105 AA.
DE Novel secreted and transmembrane protein PRO1186.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 32
ID ABU59308 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, #151.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 33
ID ABO26005 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 34
ID ABO25075 standard; protein; 105 AA.
DE Human secreted/transmembrane protein (PRO) #235.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 35
ID ABU82130 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1166.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 36
ID ABU59014 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, #151.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 37
ID ABU92392 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 38
ID ABU59457 standard; protein; 105 AA.
DE Novel human secreted or transmembrane protein PRO1198.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 39
ID ABU67080 standard; protein; 105 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 470.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 40
ID ABU92223 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 41
ID ABU10929 standard; protein; 105 AA.
DE Human PRO polypeptide #115.

PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 42
ID ABU81681 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 43
ID ABU88620 standard; protein; 105 AA.
DE Human secreted and transmembrane polypeptide PRO1186.
PN US2002157615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 44
ID ABO34134 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 45
ID ADA45989 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 46
ID ADA76420 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 47
ID ABJ72310 standard; protein; 105 AA.
DE Human PRO1186 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 48
ID ADA19070 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 49
ID ADA61693 standard; protein; 105 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 50
ID ADB19478 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003068796-A1.
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 51
ID ADB28019 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 52
ID ADA86498 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 53
ID ADB16062 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 54
ID ADA37882 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 55
ID ADA7848 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 56
ID ADA21568 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO1186.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 57
ID ADA10355 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, PRO1186.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 58
ID ADA67643 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068785-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 59
ID ADB30650 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 60
ID ADA85946 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 61
ID ADA17899 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 62
ID ADA97158 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 63
ID ADA79462 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 64
ID ADA87601 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 65
ID ADB16803 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 66
ID ADA28007 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 67
ID ADA91895 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 68
ID ADB14958 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 69
ID ADB18919 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
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PA US2003073211-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 79

ID ADA95394 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082695-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 80

ID ADA84842 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082708-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 81

ID ADB30098 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073214-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 82

ID ADA80626 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082761-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 83

ID ADA75868 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082703-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 84

ID ADA38812 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059780-A1.
PD 27-MAR-2003.

Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 85

ID ADA47093 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073210-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 86

ID ADB25389 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077715-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 87

ID ADA93565 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077721-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

PA US2003073211-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 79

ID ADA94134 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077722-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 80

ID ADB20030 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082691-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 81

ID ADB13342 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082710-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 82

ID ABO43383 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003044945-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 83

ID ADA94587 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059832-A1.
PD 27-MAR-2003.

Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 84

ID ADA74596 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068798-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 85

ID ADB24829 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077713-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 86

ID ADA82353 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082701-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

RESULT 87

ID ADA75316 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073216-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
Pred. No. 4e-54;

Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 88
ID ADB26915 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 89
ID ADB31202 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 90
ID ABJ72438 standard; protein; 105 AA.
DE Human PRO1186 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 91
ID ADA92933 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 92
ID ADA61130 standard; protein; 105 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 93
ID ADB24277 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 94
ID ADA96606 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 95
ID ADA81178 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 96
ID ADA96054 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 97
ID ADB26363 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 98
ID ADB21848 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 99
ID AB034333 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO 1186.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 6; Length 105;
RESULT 100
ID ADA77627 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 101
ID ADB18367 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 102
ID ADA87050 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 103
ID ADA88153 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 104
ID ADA46541 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 105
ID ADB28571 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 106
ID ADB29123 standard; protein; 105 AA.

DE Human PRO polypeptide #235.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 107
ID ABO53220 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 108
ID ADA77075 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 109
ID ADA22494 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO1186.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 110
ID ADA88705 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 111
ID ADA97710 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 112
ID ADB27467 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 113
ID ADB22400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 114
ID ABO22590 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 115
ID ADA06660 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #115.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 116

ID ABJ72140 standard; protein; 105 AA.
DE Human membrane bound receptor/protein PRO1186 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 117
ID ADA39353 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 118
ID ADA67091 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 119
ID ADB22952 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 120
ID ADB23725 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 121
ID ADA92447 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 122
ID ADB15510 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 123
ID ADB81656 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 124
ID ADB80762 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003080608-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 125
ID ADB73303 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.

PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 126
ID ADB38762 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 127
ID ADB96379 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 128
ID ADB78385 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 129
ID ADB38210 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 130
ID ADB66682 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 131
ID ADB85033 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 132
ID ADB89762 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082658-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 133
ID ADB90494 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 134
ID ADB39595 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082764-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 135
ID ADB78139 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 136
ID ADB87205 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 137
ID ADB84787 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 138
ID ADB47218 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 139
ID ADB83902 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 140
ID ADB86825 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 141
ID ADB73057 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 142
ID ADB77430 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 143
ID ADB34587 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 144
ID ADB35691 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 145
ID ADB34035 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 146
ID ADB35139 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 147
ID ADB36243 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 148
ID ADB46638 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 149
ID ADC57851 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 150
ID ADC55215 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 151
ID ADC12082 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 152
ID ADC56504 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 153
ID ADC07559 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.

PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 154
ID ADC11549 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 155
ID ADC36895 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 156
ID ADC21885 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096989-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 157
ID ADC50511 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 158
ID ADC72058 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 159
ID ADC60037 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 160
ID ADC49916 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 161
ID ADC49115 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 162
ID ADC49632 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 163
 ID ADC47493 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US200308072-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 164
 ID ADC53044 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein Seq ID470.
 PN US2003087365-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 165
 ID ADC57398 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein Seq ID470.
 PN US2003087366-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 166
 ID ADC60589 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003087367-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 167
 ID ADC51064 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003087361-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 168
 ID ADC55591 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003087362-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 169
 ID ADC54689 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein Seq ID470.
 PN US2003087363-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 170
 ID ADC53650 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein Seq ID470.
 PN US2003087364-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 171
 ID ADC59173 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein Seq ID470.
 PN US2003087359-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 172
 ID ADC56051 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein Seq ID470.
 PN US2003087360-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 173
 ID ADC58621 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein Seq ID470.
 PN US2003087346-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 174
 ID ADC14671 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003082546-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 175
 ID ADC47238 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003105288-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 176
 ID ADD08203 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003068623-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 177
 ID ADD03295 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003092104-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 178
 ID ADC90287 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003087348-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 179
 ID ADC62028 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003083461-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 180
 ID ADC69706 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194770-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4e-54;
 RESULT 181
 ID ADC48595 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.

PN US2003194773-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 182
ID ADD10124 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 183
ID ADD07670 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 184
ID ADC78113 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 185
ID ADD04699 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 186
ID ADC82561 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 187
ID ADD06348 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 188
ID ADC80655 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 189
ID ADD11162 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 190
ID ADD10461 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105011-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 191
ID ADC48043 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 192
ID ADD08741 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 193
ID ADC77867 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 194
ID ADC80103 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 195
ID ADD06990 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 196
ID ADD11421 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 197
ID ADD09572 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 198
ID ADC83237 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 199
ID ADD50830 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 200
ID ADD41285 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 201
ID ADD52424 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 202
ID ADD51076 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105230-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 203
ID ADD53164 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 204
ID ADD53716 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 205
ID ADD55344 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003077593-A1.
PD 24-APR-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 206
ID ADD69106 standard; protein; 105 AA.
DE Human ZAQ-related protein - SEQ ID 84.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 207
ID ADD37214 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 208
ID ADD56302 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 209
ID ADD51872 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 210
ID ADD02671 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 211
ID ADD50557 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 212
ID ADD02105 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 213
ID ADD54287 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 214
ID ADD54740 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 215
ID ADD50311 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 216
ID ADD51322 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 217
ID ADD92604 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 218
ID ADD91500 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199055-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 219
ID ADE04114 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 220
ID ADE26894 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 221
ID ADE32411 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 222
ID ADE22343 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 223
ID ADD79567 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US20031203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 224
ID ADE42103 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 225
ID ADE17920 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 226
ID ADD92052 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 227
ID ADE33515 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 228
ID ADE34067 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 229
ID ADD80119 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 230
ID ADD93156 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 231
ID ADE19576 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 232
ID ADE19024 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 233
ID ADE43220 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 234
ID ADD96009 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 235
ID ADE22895 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 236
ID ADD79013 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;

Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 237
ID ADE26361 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 238
ID ADE32963 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 239
ID ADE42655 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 240
ID ADD80671 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 241
ID ADD89699 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 242
ID ADE40983 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 243
ID ADE04782 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 244
ID ADE92911 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 245
ID ADF67298 standard; protein; 105 AA.
DE Human PRO1186 amino acid sequence SEQ ID NO:371.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 246

ID ADF28070 standard; protein; 105 AA.
DE Human Zven 2.
PN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYNO) ZYMOGENETICS INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 247
ID ADG21620 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 248
ID ADG23261 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 249
ID ADF97596 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 250
ID ABG75089 standard; protein; 105 AA.
DE Prokineticin 1 (PROK1).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB) BAYER PHARM CORP.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 251
ID ABG75086 standard; protein; 105 AA.
DE Human prokineticin 1 (PROK1).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB) BAYER PHARM CORP.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 252
ID ADG80660 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 253
ID ADG80108 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 254
ID ADH55400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 255
ID ADH55952 standard; protein; 105 AA.

DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 256
ID ADI3552 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 257
ID ADI64171 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 258
ID ADI65120 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 259
ID ADI63619 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 260
ID ADH82033 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 261
ID ADI00045 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 262
ID ADH81481 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 263
ID ADJ71810 standard; protein; 105 AA.
DE Human prokineticin 1 protein.
PN WQ2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 264
ID ADM82650 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087355-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 265
ID ADNI6049 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 266
ID ADNI6678 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 267
ID ADNI5497 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 268
ID ADNI4945 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 269
ID ADC48869 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 270
ID ADC81207 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 271
ID ADE21040 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 272
ID ADE05884 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 273
ID ADD76655 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;

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Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 274
ID ADD75113 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 275
ID ADD75859 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 276
ID ADD85091 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 277
ID ADD86917 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 278
ID ADE20794 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 279
ID ADE39091 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 280
ID ADD86423 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 281
ID ADD86423 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 282
ID ADE05638 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 283
ID ADD73623 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 284
ID ADE75871 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 285
ID ADD78463 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 286
ID ADE41422 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 287
ID ADE23447 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 288
ID ADE21286 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 289
ID ADD77401 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 290
ID ADE20548 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 291
ID ADD75613 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
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RESULT 292
ID ADD74129 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 293
ID ADD74375 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 294
ID ADD76105 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 295
ID ADD8597 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 296
ID ADE23999 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 297
ID ADE24642 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 298
ID ADD87467 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 299
ID ADE05146 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 300
ID ADD75359 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 301
ID ADD76903 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 302
ID ADD86671 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 303
ID ADE89333 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 304
ID ADD78139 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 305
ID ADE18472 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 306
ID ADE88781 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 307
ID ADD77647 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 308
ID ADD77893 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 309
ID ADD85351 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 310
ID ADD73883 standard; protein; 105 AA.
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DE Human PRO polypeptide #83.
PN US2003100710-A1.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 311
ID ADD74621 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 312
ID ADD77149 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 313
ID ADD85843 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 314
ID ADE05392 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 315
ID ADD74867 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 316
ID ADE94801 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 317
ID ADE91212 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 318
ID ADF35497 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 319
ID ADE95353 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199052-A1.
PD 06-NOV-2003.

PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 320
ID ADE93463 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 321
ID ADF35044 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 322
ID ADE92359 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 323
ID ADE90660 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 324
ID ADE91807 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 325
ID ADG11747 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 326
ID ADG05679 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 327
ID ADG27233 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 328
ID ADG02386 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207352-A1.
PD 06-NOV-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 329
ID ADG22172 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 330
ID ADG20242 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 331
ID ADF98148 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 332
ID ADG24365 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 333
ID ADF98719 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 334
ID ADG03550 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 335
ID ADF99271 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 336
ID ADG16856 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 337
ID ADG05315 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 338
ID ADG19582 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 339
ID ADG11296 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 340
ID ADG13419 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 341
ID ADG08476 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 342
ID ADG15646 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 343
ID ADG12075 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 344
ID ADF97044 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 345
ID ADG06229 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 346
ID ADG23813 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 347
ID ADG05315 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 347
ID ADG04102 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 348
ID ADG25003 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 349
ID ADF94632 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 350
ID ADG07300 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 351
ID ADG07852 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 352
ID ADG06728 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 353
ID ADG55347 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 354
ID ADG61011 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 355
ID ADG62115 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 356
ID ADG82316 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 357
ID ADG57555 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 358
ID ADG57003 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 359
ID ADG55899 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 360
ID ADG58659 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 361
ID ADG71025 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 362
ID ADH39072 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 363
ID ADG58107 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 364
ID ADG53691 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 365
ID ADG58659 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
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ID ADG71577 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 366
ID ADG81764 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 367
ID ADH19617 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003228636-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 368
ID ADH30726 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 369
ID ADH12093 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 370
ID ADG52515 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 371
ID ADG54243 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 372
ID ADG81212 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 373
ID ADG56451 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 374
ID ADH12717 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.

PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 375
ID ADH21110 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 376
ID ADG61563 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 377
ID ADH20150 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 378
ID ADH28650 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 379
ID ADG54795 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 380
ID ADG59835 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 381
ID ADH43605 standard; protein; 105 AA.
DE Human PRO polypeptide #86.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 382
ID ADG34162 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 383
ID ADI81259 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207361-A1.
PD 06-NOV-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 384
ID ADJ33632 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 385
ID ADH69726 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 386
ID ADG10002 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 387
ID ADI15473 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 388
ID ADG09350 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 389
ID ADI14805 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 390
ID ADI29887 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 391
ID ADI18400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 392
ID ADM27284 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004044179-A1.
PD 04-NAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 393
ID ADJ63681 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 394
ID ADJ77576 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 395
ID ADK82950 standard; protein; 105 AA.
DE Human PRO polypeptide #86.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 396
ID ADK66642 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2004041180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 397
ID ADJ65698 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 398
ID ADM27834 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 399
ID ADJ66891 standard; protein; 105 AA.
DE Human extracellular signaling molecule (EXCS) -11 protein.
PN US2004048244-A1.
PD 11-MAR-2004.
PA (TANG/) TANG Y T.
PA (YUEH/) YUE H.
PA (LALP/) LAL P.
PA (BURF/) BURFORD N.
PA (BAND/) BANDMAN O.
PA (BAUG/) BAUGHN M R.
PA (AZIM/) AZIMZAI Y.
PA (LUDA/) LIU D A M.
PA (ARVI/) ARVIZU C.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 400
ID ADN08155 standard; protein; 105 AA.
DE Human endocrine gland vascular endothelial growth factor.
PN DE10229379-A1.
PD 29-JAN-2004.
PA (SCHD ) SCHERING AG.
Query Match 100.0%; Score 589; DB 8; Length 105;
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Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 401
ID ADM44558 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 402
ID ADM41842 standard; protein; 105 AA.
DE Amino acid sequence of a human Zven2 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 403
ID ADM28420 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 404
ID ADI95902 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 405
ID ADI9454 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US20030207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 406
ID ADS86960 standard; protein; 105 AA.
DE Human Zven2 protein.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 407
ID ADS00464 standard; protein; 105 AA.
DE Human EG-VEGF, SEQ ID 8.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 408
ID ADS86475 standard; protein; 105 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 7.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 409
ID ADS75493 standard; protein; 105 AA.
DE Human prokineticin 2 receptor protein.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;

RESULT 410
ID ADS32406 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 411
ID ADT03390 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004214289-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 412
ID ADY86164 standard; protein; 105 AA.
DE Human EG-VEGF, SEQ ID NO:2.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 413
ID ADZ03441 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO1186 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 414
ID ADZ88922 standard; protein; 105 AA.
DE Human prokineticin 1 isoform.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 415
ID ABA38601 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, #183.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 416
ID AEB14187 standard; protein; 105 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 470.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE) BAKER K P.
PA (BERE) BERESENI M.
PA (DEFO) DEFORGE L.
PA (DESN) DESNOYERS L.
PA (FILV) FILVAROFF E.
PA (GAOW) GAO W.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GUEN) GUENEY A L.
PA (SHER) SHERWOOD S.
PA (SMIT) SMITH V.
PA (STEM) STEWART T A.
PA (TUNA) TUNAS D.
PA (WATA) WATANABE C K.
PA (WOOD) WOOD W I.
PA (ZHAN) ZHANG Z.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 417

ID AEB4588 standard; protein; 105 AA.
DE Human Zven2 protein, SEQ ID NO: 5.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 418
ID AEC06124 standard; protein; 105 AA.
DE Human EG-VEGF protein.
PN WO2005076972-A2.
PD 25-AUG-2005.
PA (OHIS) UNIV OHIO STATE RES FOUND.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 419
ID AED08088 standard; protein; 105 AA.
DE Human Zven2 protein.
PN US2005214800-A1.
PD 29-SEP-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 420
ID AED86385 standard; protein; 105 AA.
DE Human PRO amino acid sequence, seq id 470.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (CETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4e-54;
RESULT 421
ID AAB70147 standard; protein; 105 AA.
DE Human G protein-coupled receptor protein-related sequence #3.
PN WO200116309-A1.
PD 08-MAR-2001.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 588; DB 4; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.1e-54;
RESULT 422
ID AAM79066 standard; protein; 105 AA.
DE Human protein SEQ ID NO 1728.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 99.8%; Score 588; DB 4; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.1e-54;
RESULT 423
ID AAG79596 standard; protein; 105 AA.
DE GSP4 sequence.
PN WO200269689-A2.
PD 12-SEP-2002.
PA (GEST) GENSET.
Query Match 99.8%; Score 588; DB 5; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.1e-54;
RESULT 424
ID AAO15526 standard; protein; 105 AA.
DE Human physiologically-active ZAQ ligand-related protein 2.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 588; DB 5; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.1e-54;
RESULT 425
ID ABB06307 standard; protein; 105 AA.
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:22.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 588; DB 5; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.1e-54;
RESULT 426
ID ABP75987 standard; protein; 105 AA.

DE Human GENSET protein SEQ ID 194.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 99.8%; Score 588; DB 6; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.1e-54;
RESULT 427
ID ADD69105 standard; protein; 105 AA.
DE Human ZAQ-related protein - SEQ ID 83.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 588; DB 7; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.1e-54;
RESULT 428
ID ADS86473 standard; protein; 105 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 5.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 588; DB 8; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.1e-54;
RESULT 429
ID AED00619 standard; protein; 105 AA.
DE Human prokineticin 1 (PK1).
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 99.8%; Score 588; DB 9; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.1e-54;
RESULT 430
ID AAB18475 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide clone.
PN WO200052022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.5%; Score 586; DB 3; Length 105;
Best Local Similarity 99.0%; Pred. No. 8.2e-54;
RESULT 431
ID AAB18473 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide clone.
PN WO200052022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.5%; Score 586; DB 3; Length 105;
Best Local Similarity 99.0%; Pred. No. 8.2e-54;
RESULT 432
ID AAB18474 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide clone.
PN WO200052022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.5%; Score 586; DB 3; Length 105;
Best Local Similarity 99.0%; Pred. No. 8.2e-54;
RESULT 433
ID ABP76151 standard; protein; 105 AA.
DE Human GENSET protein SEQ ID 477.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 98.8%; Score 582; DB 6; Length 105;
Best Local Similarity 98.1%; Pred. No. 2.2e-53;
RESULT 434
ID ABP75986 standard; protein; 105 AA.
DE Human GENSET protein SEQ ID 193.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 98.8%; Score 582; DB 6; Length 105;
Best Local Similarity 98.1%; Pred. No. 2.2e-53;
RESULT 435
ID AED00616 standard; protein; 105 AA.
DE Rhesus monkey prokineticin 1 (PK1) SEQ ID NO 28.

PN WO2005091925-A2.
PA (REGC) UNIV CALIFORNIA.
Query Match 98.1%; Score 578; DB 9; Length 105;
Best Local Similarity 98.1%; Pred. No. 5.7e-53;
RESULT 436
ID ADZ88921 standard; protein; 105 AA.
DE Rhesus monkey prokineticin 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 97.1%; Score 572; DB 9; Length 105;
Best Local Similarity 97.1%; Pred. No. 2.5e-52;
RESULT 437
ID ABB99151 standard; protein; 105 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 92.5%; Score 545; DB 5; Length 105;
Best Local Similarity 89.5%; Pred. No. 1.7e-49;
RESULT 438
ID ABB06956 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:43.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 92.5%; Score 545; DB 5; Length 105;
Best Local Similarity 89.5%; Pred. No. 1.7e-49;
RESULT 439
ID ADD69154 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 132.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 92.5%; Score 545; DB 7; Length 105;
Best Local Similarity 89.5%; Pred. No. 1.7e-49;
RESULT 440
ID ADS86487 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 19.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 92.5%; Score 545; DB 8; Length 105;
Best Local Similarity 89.5%; Pred. No. 1.7e-49;
RESULT 441
ID ABB99153 standard; protein; 105 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.9%; Score 541; DB 5; Length 105;
Best Local Similarity 88.6%; Pred. No. 4.5e-49;
RESULT 442
ID ABB06958 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:47.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.9%; Score 541; DB 5; Length 105;
Best Local Similarity 88.6%; Pred. No. 4.5e-49;
RESULT 443
ID ADD69158 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 136.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.9%; Score 541; DB 7; Length 105;
Best Local Similarity 88.6%; Pred. No. 4.5e-49;
RESULT 444
ID ADS86491 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 23.
PN WO2004084945-A1.

PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.9%; Score 541; DB 8; Length 105;
Best Local Similarity 88.6%; Pred. No. 4.5e-49;
RESULT 445
ID ABB99152 standard; protein; 105 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.5%; Score 539; DB 5; Length 105;
Best Local Similarity 88.6%; Pred. No. 7.4e-49;
RESULT 446
ID ABB06957 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:45.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.5%; Score 539; DB 5; Length 105;
Best Local Similarity 88.6%; Pred. No. 7.4e-49;
RESULT 447
ID ADD69156 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 134.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.5%; Score 539; DB 7; Length 105;
Best Local Similarity 88.6%; Pred. No. 7.4e-49;
RESULT 448
ID ADS86489 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 21.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.5%; Score 539; DB 8; Length 105;
Best Local Similarity 88.6%; Pred. No. 7.4e-49;
RESULT 449
ID ABB99148 standard; protein; 105 AA.
DE Mouse ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 88.5%; Score 521; DB 5; Length 105;
Best Local Similarity 84.8%; Pred. No. 5.8e-47;
RESULT 450
ID ADD69129 standard; protein; 105 AA.
DE Murine ZAQ-related protein - SEQ ID 107.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 88.5%; Score 521; DB 7; Length 105;
Best Local Similarity 84.8%; Pred. No. 5.8e-47;
RESULT 451
ID ADS00466 standard; protein; 105 AA.
DE Murine EG-VEGF, SEQ ID 10.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 88.5%; Score 521; DB 8; Length 105;
Best Local Similarity 84.8%; Pred. No. 5.8e-47;
RESULT 452
ID ADS86479 standard; protein; 105 AA.
DE Murine ZAQ ligand protein related to eating disorders & obesity Seq 11.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 88.5%; Score 521; DB 8; Length 105;
Best Local Similarity 84.8%; Pred. No. 5.8e-47;
RESULT 453
ID ABJ05340 standard; protein; 125 AA.
DE Target fusion peptide production method-related protein #3.
PN WO200236762-A1.
PD 10-MAY-2002.

PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 85.1%; Score 501; DB 5; Length 125;
Best Local Similarity 98.9%; Pred. No. 8.9e-45;
RESULT 454
ID ABJ05339 standard; protein; 130 AA.
DE Human PTH(1-34)-ZQA ligand fusion protein.
PN WO200236762-A1.
PD 10-MAY-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 85.1%; Score 501; DB 5; Length 130;
Best Local Similarity 98.9%; Pred. No. 9.3e-45;
RESULT 455
ID AAB70146 standard; protein; 86 AA.
DE Human G protein-coupled receptor protein-related sequence #2.
PN WO200116309-A1.
PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 456
ID ABB76801 standard; protein; 86 AA.
DE Human ZAQ-1.
PN WO200208417-A1.
PD 31-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 457
ID ABJ05338 standard; protein; 86 AA.
DE Human ZAQ protein ligand.
PN WO200236762-A1.
PD 10-MAY-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 458
ID AAO15529 standard; protein; 86 AA.
DE Human physiologically-active ZAQ ligand-related protein 4.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 459
ID ABB06306 standard; protein; 86 AA.
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:21.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 460
ID AAE24383 standard; protein; 86 AA.
DE Human prokineticin 1 mature protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 84.6%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 461
ID ADD69104 standard; protein; 86 AA.
DE Human ZAQ-related protein - SEQ ID 82.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 462
ID ADO05360 standard; protein; 86 AA.
DE Human prokineticin 1 (PK1), SEQ ID NO:19.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.

Query Match 84.6%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 463
ID ADM43256 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 84.6%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 464
ID ADR24003 standard; protein; 86 AA.
DE Human ZAQ-1 ligand protein #1.
PN WO2004065419-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 465
ID ADS86471 standard; protein; 86 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 3.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 466
ID ADS75494 standard; protein; 86 AA.
DE Human prokineticin 1 receptor protein.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 84.6%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 467
ID ADW00759 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 1 (PK1).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 84.6%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 468
ID ADZ58575 standard; protein; 86 AA.
DE Human ZQA-1 amino acid sequence - SEQ ID 2.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 84.6%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 469
ID AEB45594 standard; protein; 86 AA.
DE Human Zven2 protein fragment.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 84.6%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 470
ID AED00599 standard; protein; 86 AA.
DE Partial human prokineticin 1 (PK1) SEQ ID NO 11.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 84.6%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
RESULT 471
ID AAE24395 standard; protein; 87 AA.
DE Human prokineticin 1 mutant protein #4.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 84.6%; Score 498; DB 5; Length 87;

Best Local Similarity 100.0%; Pred. No. 1.3e-44;
RESULT 472
ID ADS75509 standard; protein; 87 AA.
DE Prokineticin receptor antagonist Met PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 84.6%; Score 498; DB 8; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
RESULT 473
ID AAE24392 standard; protein; 89 AA.
DE Human prokineticin 1 mutant protein #1.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 84.6%; Score 498; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
RESULT 474
ID ADS75506 standard; protein; 89 AA.
DE Prokineticin receptor related synthetic construct protein, SEQ ID 15.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 84.6%; Score 498; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
RESULT 475
ID AAB70145 standard; protein; 86 AA.
DE Human G protein-coupled receptor protein-related sequence #1.
PN WO200116309-A1.
PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 4; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.6e-44;
RESULT 476
ID AAO15528 standard; protein; 86 AA.
DE Human physiologically-active ZAQ ligand-related protein 3.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.6e-44;
RESULT 477
ID ABB06305 standard; protein; 86 AA.
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:20.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.6e-44;
RESULT 478
ID ADD69103 standard; protein; 86 AA.
DE Human ZAQ-related protein - SEQ ID 81.
PN WO2003086860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 7; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.6e-44;
RESULT 479
ID ADR24004 standard; protein; 86 AA.
DE Human ZAQ-1 ligand protein #2.
PN WO2004065419-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 8; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.6e-44;
RESULT 480
ID ADS86469 standard; protein; 86 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 1.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 8; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.6e-44;

RESULT 481
ID ADZ58576 standard; protein; 86 AA.
DE Human ZAQ-1 amino acid sequence - SEQ ID 3.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 84.4%; Score 497; DB 9; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.6e-44;
RESULT 482
ID AAE24393 standard; protein; 85 AA.
DE Human prokineticin 1 mutant protein #2.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 83.9%; Score 494; DB 5; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
RESULT 483
ID ADS75507 standard; protein; 85 AA.
DE Prokineticin receptor antagonist dela-PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 83.9%; Score 494; DB 8; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
RESULT 484
ID ADS75511 standard; protein; 86 AA.
DE Prokineticin receptor antagonist MV PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 83.9%; Score 494; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
RESULT 485
ID AAE24394 standard; protein; 86 AA.
DE Human prokineticin 1 mutant protein #3.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 81.2%; Score 478; DB 5; Length 86;
Best Local Similarity 95.3%; Pred. No. 1.6e-42;
RESULT 486
ID ADS75508 standard; protein; 86 AA.
DE Prokineticin receptor related synthetic construct protein, SEQ ID 17.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 81.2%; Score 478; DB 8; Length 86;
Best Local Similarity 95.3%; Pred. No. 1.6e-42;
RESULT 487
ID ADZ88902 standard; protein; 82 AA.
DE Human prokineticin 1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 80.8%; Score 476; DB 9; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
RESULT 488
ID ABB99154 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 80.3%; Score 473; DB 5; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.4e-42;
RESULT 489
ID ABB06959 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:49.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 80.3%; Score 473; DB 5; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.4e-42;
RESULT 490

ID ADD9160 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 138.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 80.3%; Score 473; DB 7; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.4e-42;
RESULT 491
ID ADN3261 standard; protein; 86 AA.
DE Amino acid sequence of rat prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 80.3%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.4e-42;
RESULT 492
ID ADS96481 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 13.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 80.3%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.4e-42;
RESULT 493
ID ADS75521 standard; protein; 86 AA.
DE Modified rat prokineticin 1 receptor, SEQ ID 30.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 80.3%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.4e-42;
RESULT 494
ID ABB99156 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.6%; Score 469; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.4e-41;
RESULT 495
ID ABB06961 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:53.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.6%; Score 469; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.4e-41;
RESULT 496
ID ADD9164 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 142.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.6%; Score 469; DB 7; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.4e-41;
RESULT 497
ID ADS96485 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 17.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.6%; Score 469; DB 8; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.4e-41;
RESULT 498
ID ABB99155 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.3%; Score 467; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.3e-41;
RESULT 499
ID ABB06960 standard; protein; 86 AA.

DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:51.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.3%; Score 467; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.3e-41;
RESULT 500
ID ADD9162 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 140.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.3%; Score 467; DB 7; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.3e-41;
RESULT 501
ID ADS86483 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 15.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.3%; Score 467; DB 8; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.3e-41;
RESULT 502
ID ABB99149 standard; protein; 86 AA.
DE Mouse ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 77.2%; Score 455; DB 5; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.2e-40;
RESULT 503
ID ADD69131 standard; protein; 86 AA.
DE Murine ZAQ-related protein - SEQ ID 109.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 77.2%; Score 455; DB 7; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.2e-40;
RESULT 504
ID ADO05361 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1), SEQ ID NO:10.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 7; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.2e-40;
RESULT 505
ID ADN43259 standard; protein; 86 AA.
DE Amino acid sequence of murine prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.2e-40;
RESULT 506
ID ADS86477 standard; protein; 86 AA.
DE Murine ZAQ ligand protein related to eating disorders & obesity Seq 9.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 77.2%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.2e-40;
RESULT 507
ID ADS75519 standard; protein; 86 AA.
DE Modified mouse prokineticin 1 receptor, SEQ ID 28.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.2e-40;
RESULT 508
ID ADW00760 standard; protein; 86 AA.
DE Amino acid sequence of murine prokineticin 1 (PK1).

PN WO2004113361-A2.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.2e-40;
RESULT 509
ID ADZ88903 standard; protein; 86 AA.
DE Mouse prokineticin 1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.2e-40;
RESULT 510
ID AED00600 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1) SEQ ID NO 12.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.2e-40;
RESULT 511
ID AAY11745 standard; protein; 81 AA.
DE Human 5' EST secreted protein SEQ ID NO: 345.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GESC) GENSET.
Query Match 76.7%; Score 452; DB 2; Length 81;
Best Local Similarity 98.8%; Pred. No. 8.2e-40;
RESULT 512
ID AAG00617 standard; protein; 80 AA.
DE Human secreted protein, SEQ ID NO: 4698.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GESC) GENSET.
Query Match 76.1%; Score 448; DB 3; Length 80;
Best Local Similarity 98.8%; Pred. No. 2.1e-39;
RESULT 513
ID AAE24391 standard; protein; 86 AA.
DE Human prokineticin chimera 21 protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 5; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.1e-35;
RESULT 514
ID ADO05372 standard; protein; 86 AA.
DE PK2/PK1 chimeric protein, SEQ ID NO:21.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 7; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.1e-35;
RESULT 515
ID ADN43267 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 2 (PK2)/PK1 chimera.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.1e-35;
RESULT 516
ID ADS75505 standard; protein; 86 AA.
DE Modified human prokineticin chimeric receptor, PK2-PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.1e-35;
RESULT 517
ID ADW00765 standard; protein; 86 AA.
DE Amino acid sequence of a PK2/PK1 chimera.
PN WO2004113361-A2.

PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.1e-35;
RESULT 518
ID ADZ88908 standard; protein; 86 AA.
DE Human prokineticin 2/prokineticin 1 chimera.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.1e-35;
RESULT 519
ID AED00605 standard; protein; 86 AA.
DE Human PK2-PK1 chimera SEQ ID NO 17.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.1e-35;
RESULT 520
ID AAE24390 standard; protein; 81 AA.
DE Human prokineticin chimera 12 protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 5; Length 81;
Best Local Similarity 84.4%; Pred. No. 8.4e-32;
RESULT 521
ID ADO05371 standard; protein; 81 AA.
DE PK1/PK2 chimeric protein, SEQ ID NO:20.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 7; Length 81;
Best Local Similarity 84.4%; Pred. No. 8.4e-32;
RESULT 522
ID ADN43266 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 1 (PK1)/PK2 chimera.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 8; Length 81;
Best Local Similarity 84.4%; Pred. No. 8.4e-32;
RESULT 523
ID ADS75504 standard; protein; 81 AA.
DE Modified human prokineticin chimeric receptor, PK1-PK2.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 8; Length 81;
Best Local Similarity 84.4%; Pred. No. 8.4e-32;
RESULT 524
ID ADW00764 standard; protein; 81 AA.
DE Amino acid sequence of a PK1/PK2 chimera.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 8.4e-32;
RESULT 525
ID ADZ88907 standard; protein; 81 AA.
DE Human prokineticin 1/prokineticin 2 chimera.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 8.4e-32;
RESULT 526
ID AED00604 standard; protein; 81 AA.
DE Human PK1-PK2 chimera SEQ ID NO 16.
PN WO2005091925-A2.
PD 06-OCT-2005.

PA (REGC) UNIV CALIFORNIA.
Query Match 53.8%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 8.4e-32;
RESULT 527
ID ABG94399 standard; protein; 80 AA.
DE Dendroaspis polylepis MIT1 protein.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 528
ID ABB99160 standard; protein; 80 AA.
DE Polylepis MIT1.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 529
ID ABB06310 standard; protein; 80 AA.
DE Dendroaspis polylepis MIT1 protein sequence SEQ ID NO:34.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 530
ID ADD69043 standard; protein; 80 AA.
DE Dendroaspis polylepis MIT1-related protein.
PN WO200306680-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 531
ID ADJ71812 standard; protein; 80 AA.
DE Black mamba intestinal toxin protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 53.5%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 532
ID ADO05364 standard; protein; 80 AA.
DE Snake prokineticin orthologue MIT1, SEQ ID NO:13.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.5%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 533
ID ADS86504 standard; protein; 80 AA.
DE D polylepis MIT1 protein related to eating disorders & obesity Seq 36.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 8; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 534
ID ADW00763 standard; protein; 80 AA.
DE Amino acid sequence of snake MIT1.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.5%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 535
ID ADZ88906 standard; protein; 80 AA.
DE Snake prokineticin 1 homologue, MIT1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.

Query Match 53.5%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 536
ID AED00603 standard; protein; 80 AA.
DE Snake MIT1 SEQ ID NO 15.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.5%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.2e-25;
RESULT 537
ID ADY86167 standard; protein; 79 AA.
DE Black mamba venom protein A (VPRA), SEQ ID NO:5.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 52.9%; Score 311.5; DB 9; Length 79;
Best Local Similarity 63.6%; Pred. No. 5.1e-25;
RESULT 538
ID ADM43263 standard; protein; 81 AA.
DE Amino acid sequence of MIT1.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 52.7%; Score 310.5; DB 8; Length 81;
Best Local Similarity 62.8%; Pred. No. 6.7e-25;
RESULT 539
ID ADS75503 standard; protein; 81 AA.
DE Modified black mamba prokineticin receptor, MIT1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 52.7%; Score 310.5; DB 8; Length 81;
Best Local Similarity 62.8%; Pred. No. 6.7e-25;
RESULT 540
ID ADY86166 standard; protein; 100 AA.
DE Human Bv8 homolog protein, SEQ ID NO:4.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 52.0%; Score 306; DB 9; Length 100;
Best Local Similarity 57.0%; Pred. No. 2.5e-24;
RESULT 541
ID AAB68426 standard; protein; 108 AA.
DE Amino acid sequence of a human zvenl polypeptide.
PN WO200136465-A2.
PD 25-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 4; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 542
ID ABG94397 standard; protein; 108 AA.
DE Human GPCR ligand Bv8 protein sequence #1.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 51.4%; Score 303; DB 5; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 543
ID AAO15531 standard; protein; 108 AA.
DE Human physiologically-active ZAQ ligand-related protein 6.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 51.4%; Score 303; DB 5; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 544
ID AAE24384 standard; protein; 108 AA.
DE Human prokineticin 2 precursor protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 51.4%; Score 303; DB 5; Length 108;

Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 545
ID ABU07602 standard; protein; 108 AA.
DE Human ZVEN1.
PN US6485938-B1.
PD 26-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 6; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 546
ID AAE36789 standard; protein; 108 AA.
DE Human BV8 homologue splice variant protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 51.4%; Score 303; DB 6; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 547
ID ADD69039 standard; protein; 108 AA.
DE Human BV8-related protein - SEQ ID 17.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 51.4%; Score 303; DB 7; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 548
ID ADF28067 standard; protein; 108 AA.
DE Human Zven 1.
PN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 7; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 549
ID ABG75087 standard; protein; 108 AA.
DE Human prokineticin 2 (PROK2).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB) BAYER PHARM CORP.
Query Match 51.4%; Score 303; DB 7; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 550
ID ADJ71811 standard; protein; 108 AA.
DE Human prokineticin 2 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 51.4%; Score 303; DB 7; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 551
ID ADN41839 standard; protein; 108 AA.
DE Amino acid sequence of a human Zven1 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 8; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 552
ID ADO24421 standard; protein; 108 AA.
DE Human PRO28691 protein SEQ ID NO:60.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 51.4%; Score 303; DB 8; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 553
ID ADS86957 standard; protein; 108 AA.
DE Human Zven1 protein.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 8; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;

RESULT 554
ID ADS00460 standard; protein; 108 AA.
DE Human BV8 homologue variant #2, SEQ ID 4.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 51.4%; Score 303; DB 8; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 555
ID ADS86495 standard; protein; 108 AA.
DE Human BV8 protein related to eating disorders & obesity Seq 27.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 51.4%; Score 303; DB 8; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 556
ID ADS75496 standard; protein; 108 AA.
DE Human prokineticin 1 receptor protein isoform 2.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 51.4%; Score 303; DB 8; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 557
ID AEA23706 standard; protein; 108 AA.
DE Human PRO polypeptide SEQ ID NO 248.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 51.4%; Score 303; DB 9; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 558
ID AEB45585 standard; protein; 108 AA.
DE Human Zven1 protein, SEQ ID NO: 2.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 9; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 559
ID ABD08085 standard; protein; 108 AA.
DE Human Zven1 protein.
PN US2005214800-A1.
PD 29-SEP-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 9; Length 108;
Best Local Similarity 55.2%; Pred. No. 5.6e-24;
RESULT 560
ID ADN41861 standard; protein; 116 AA.
DE Amino acid sequence of a human Zven1 with Glu-Glu tag and Gly linker.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 8; Length 116;
Best Local Similarity 55.2%; Pred. No. 6e-24;
RESULT 561
ID ADS86981 standard; protein; 116 AA.
DE Human Zven1 protein expressed in baculovirus cell expression system.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 8; Length 116;
Best Local Similarity 55.2%; Pred. No. 6e-24;
RESULT 562
ID ADZ88897 standard; protein; 108 AA.
DE Rhesus monkey prokineticin receptor 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.9%; Score 300; DB 9; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-23;
RESULT 563

ID AED00594 standard; protein; 108 AA.
DE Rheus monkey prokineticin receptor 2 (PKR2) SEQ ID NO 6.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.9%; Score 300; DB 9; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-23;
RESULT 564
ID ABG94408 standard; protein; 107 AA.
DE Mouse GPCR ligand Bv8 protein.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 5; Length 107;
Best Local Similarity 49.0%; Pred. No. 1.9e-23;
RESULT 565
ID ABG94401 standard; protein; 107 AA.
DE Rat GPCR ligand Bv8 protein sequence #1.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 5; Length 107;
Best Local Similarity 54.0%; Pred. No. 1.9e-23;
RESULT 566
ID ABB06962 standard; protein; 107 AA.
DE Rat G protein-coupled receptor protein sequence SEQ ID NO:69.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 5; Length 107;
Best Local Similarity 54.0%; Pred. No. 1.9e-23;
RESULT 567
ID AAE36790 standard; protein; 107 AA.
DE Mouse Bv8 homologue protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 50.6%; Score 298; DB 6; Length 107;
Best Local Similarity 49.0%; Pred. No. 1.9e-23;
RESULT 568
ID ADD69059 standard; protein; 107 AA.
DE Rat Bv8-related protein - SEQ ID 37.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 7; Length 107;
Best Local Similarity 54.0%; Pred. No. 1.9e-23;
RESULT 569
ID ADD69077 standard; protein; 107 AA.
DE Murine Bv8-related protein - SEQ ID 55.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 7; Length 107;
Best Local Similarity 49.0%; Pred. No. 1.9e-23;
RESULT 570
ID ADS00462 standard; protein; 107 AA.
DE Murine Bv8 homologue, SEQ ID 6.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 50.6%; Score 298; DB 8; Length 107;
Best Local Similarity 49.0%; Pred. No. 1.9e-23;
RESULT 571
ID ADS86500 standard; protein; 107 AA.
DE Rat Bv8 protein related to eating disorders & obesity seq 32.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 8; Length 107;
Best Local Similarity 54.0%; Pred. No. 1.9e-23;
RESULT 572
ID ADS86502 standard; protein; 107 AA.

DE Murine Bv8 peptide DNA related to eating disorders & obesity Seq 34.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 8; Length 107;
Best Local Similarity 49.0%; Pred. No. 1.9e-23;
RESULT 573
ID ABG94400 standard; protein; 80 AA.
DE C-terminal Lys truncated human GPCR ligand Bv8 protein.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 5; Length 80;
Best Local Similarity 58.4%; Pred. No. 7.5e-23;
RESULT 574
ID ADD69044 standard; protein; 80 AA.
DE Human Bv8-related protein - SEQ ID 22.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 7; Length 80;
Best Local Similarity 58.4%; Pred. No. 7.5e-23;
RESULT 575
ID ABG94398 standard; protein; 81 AA.
DE Human GPCR ligand Bv8 protein sequence #2.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 5; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 576
ID AA015530 standard; protein; 81 AA.
DE Human physiologically-active ZAQ ligand-related protein 5.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 5; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 577
ID AAE24385 standard; protein; 81 AA.
DE Human prokineticin 2 mature protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 49.4%; Score 291; DB 5; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 578
ID ADD69041 standard; protein; 81 AA.
DE Human Bv8-related protein - SEQ ID 19.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 7; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 579
ID ADO05356 standard; protein; 81 AA.
DE Human major prokineticin 2 (PK2), SEQ ID NO:5.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 49.4%; Score 291; DB 7; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 580
ID ADN43258 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 2 (PK2) isoform 2.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 49.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 581
ID ADR24005 standard; protein; 81 AA.
DE Human ZAQ-1 ligand-associated protein.

PN WO2004065419-A1.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 582
ID ADS86493 standard; protein; 81 AA.
DE Human BV8 protein related to eating disorders & obesity Seq 25.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 583
ID ADS75497 standard; protein; 81 AA.
DE Human prokineticin 1 receptor protein isoform 1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 49.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 584
ID ADM00755 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 49.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 585
ID ADZ88900 standard; protein; 81 AA.
DE Human prokineticin 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 49.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 586
ID ADZ58574 standard; protein; 81 AA.
DE Human ZAQ-L-2 amino acid sequence - SEQ ID 1.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 49.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 587
ID AEB45593 standard; protein; 81 AA.
DE Human Zveni protein fragment.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 49.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 588
ID AED00597 standard; protein; 81 AA.
DE Human prokineticin receptor 2 (PKR2) SEQ ID NO 9.
PN WO200501925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 49.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 7.6e-23;
RESULT 589
ID ADJ71813 standard; protein; 96 AA.
DE Toad BV8 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 48.8%; Score 287.5; DB 7; Length 96;
Best Local Similarity 50.5%; Pred. No. 2.1e-22;
RESULT 590
ID ADS75502 standard; protein; 96 AA.
DE Modified frog prokineticin receptor, BV8.
PN WO2004087054-A2.

PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 48.8%; Score 287.5; DB 8; Length 96;
Best Local Similarity 50.5%; Pred. No. 2.1e-22;
RESULT 591
ID ADZ88901 standard; protein; 80 AA.
DE Mouse prokineticin 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 48.6%; Score 286; DB 9; Length 80;
Best Local Similarity 57.1%; Pred. No. 2.5e-22;
RESULT 592
ID AED00598 standard; protein; 80 AA.
DE Mouse/rat prokineticin receptor 2 (PKR2) SEQ ID NO 10.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 48.6%; Score 286; DB 9; Length 80;
Best Local Similarity 57.1%; Pred. No. 2.5e-22;
RESULT 593
ID ABG94402 standard; protein; 81 AA.
DE Rat GPCR ligand BV8 protein sequence #2.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 48.6%; Score 286; DB 5; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 594
ID ABB06963 standard; protein; 81 AA.
DE Rat G protein-coupled receptor protein sequence. SEQ ID NO:71.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 48.6%; Score 286; DB 5; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 595
ID ADD69061 standard; protein; 81 AA.
DE Rat BV8-related protein - SEQ ID 39.
PN WO2003086860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 48.6%; Score 286; DB 7; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 596
ID ADO05358 standard; protein; 81 AA.
DE Mouse major prokineticin 2 (PK2), SEQ ID NO:7.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 48.6%; Score 286; DB 7; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 597
ID ADN43260 standard; protein; 81 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 48.6%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 598
ID ADN43262 standard; protein; 81 AA.
DE Amino acid sequence of rat prokineticin 2 (PK2).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 48.6%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 599
ID ADS86497 standard; protein; 81 AA.
DE Rat/murine BV8 protein related to eating disorders & obesity Seq 29.
PN WO2004084945-A1.
PD 07-OCT-2004.

PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 48.0%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 600
ID ADS75520 standard; protein; 81 AA.
DE Modified mouse prokineticin 2 receptor, SEQ ID 29.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 48.6%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 601
ID ADS75522 standard; protein; 81 AA.
DE Modified rat prokineticin 2 receptor, SEQ ID 31.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 48.6%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 602
ID ADM00757 standard; protein; 81 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 48.6%; Score 286; DB 9; Length 81;
Best Local Similarity 57.1%; Pred. No. 2.6e-22;
RESULT 603
ID ADJ71808 standard; protein; 124 AA.
DE Human Bv8 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 48.0%; Score 282.5; DB 7; Length 124;
Best Local Similarity 44.4%; Pred. No. 9.4e-22;
RESULT 604
ID AAE36788 standard; protein; 129 AA.
DE Human Bv8 homologue protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 48.0%; Score 282.5; DB 6; Length 129;
Best Local Similarity 44.4%; Pred. No. 9.8e-22;
RESULT 605
ID ADJ71815 standard; protein; 129 AA.
DE Human prokineticin 2 precursor protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 48.0%; Score 282.5; DB 7; Length 129;
Best Local Similarity 44.4%; Pred. No. 9.8e-22;
RESULT 606
ID ADN41864 standard; protein; 129 AA.
DE Amino acid sequence of a longer human Zven1 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 48.0%; Score 282.5; DB 8; Length 129;
Best Local Similarity 44.4%; Pred. No. 9.8e-22;
RESULT 607
ID ADS6984 standard; protein; 129 AA.
DE Human Zven1 protein longer form.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 48.0%; Score 282.5; DB 8; Length 129;
Best Local Similarity 44.4%; Pred. No. 9.8e-22;
RESULT 608
ID ADS00458 standard; protein; 129 AA.
DE Human Bv8 homologue variant #1, SEQ ID 2.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.

Query Match 48.0%; Score 282.5; DB 8; Length 129;
Best Local Similarity 44.4%; Pred. No. 9.8e-22;
RESULT 609
ID ADN43265 standard; protein; 77 AA.
DE Amino acid sequence of a Bv8 homologue.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 47.3%; Score 278.5; DB 8; Length 77;
Best Local Similarity 61.5%; Pred. No. 1.5e-21;
RESULT 610
ID ADS75523 standard; protein; 77 AA.
DE Modified toad prokineticin receptor.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 47.3%; Score 278.5; DB 8; Length 77;
Best Local Similarity 61.5%; Pred. No. 1.5e-21;
RESULT 611
ID ADJ71809 standard; protein; 128 AA.
DE Mouse Bv8 variant 1 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 47.1%; Score 277.5; DB 7; Length 128;
Best Local Similarity 40.7%; Pred. No. 3.3e-21;
RESULT 612
ID ADN43257 standard; protein; 102 AA.
DE Amino acid sequence of human prokineticin 2 (PK2) isoform 1.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.9%; Score 270.5; DB 8; Length 102;
Best Local Similarity 45.9%; Pred. No. 1.4e-20;
RESULT 613
ID ADO05362 standard; protein; 77 AA.
DE Xenopus laevis prokineticin orthologue Bv8, SEQ ID NO:11.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 7; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.2e-20;
RESULT 614
ID ADN43264 standard; protein; 77 AA.
DE Amino acid sequence of Bv8.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 8; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.2e-20;
RESULT 615
ID ADM00761 standard; protein; 77 AA.
DE Amino acid sequence of frog Bv8.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 9; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.2e-20;
RESULT 616
ID ADZ88905 standard; protein; 77 AA.
DE Frog prokineticin 1 homologue, Bv8.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 9; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.2e-20;
RESULT 617
ID AED00602 standard; protein; 77 AA.
DE Frog Bv8 SEQ ID NO 14.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 9; Length 77;

Best Local Similarity 57.7%; Pred. No. 2.2e-20;
RESULT 618
ID ADO05359 standard; protein; 102 AA.
DE Mouse minor prokineticin 2 (PK2), SEQ ID NO:8.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.1%; Score 265.5; DB 7; Length 102;
Best Local Similarity 44.9%; Pred. No. 4.7e-20;
RESULT 619
ID ADM00758 standard; protein; 102 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.1%; Score 265.5; DB 9; Length 102;
Best Local Similarity 44.9%; Pred. No. 4.7e-20;
RESULT 620
ID ADF17105 standard; peptide; 77 AA.
DE Bombina maxima neurotrophic peptide.
PN CN1390849-A.
PD 15-JAN-2003.
PA (KUNM-) KUNMING ZOOLOGY INST CHINESE ACAD SCI.
Query Match 43.2%; Score 254.5; DB 7; Length 77;
Best Local Similarity 56.4%; Pred. No. 5.1e-19;
RESULT 621
ID ADO05357 standard; protein; 100 AA.
DE Human tissue specific (testis) prokineticin 2 (PK2), SEQ ID NO:6.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.7%; Score 251.5; DB 7; Length 100;
Best Local Similarity 44.9%; Pred. No. 1.4e-18;
RESULT 622
ID ADM00756 standard; protein; 100 AA.
DE Amino acid sequence of human prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.7%; Score 251.5; DB 9; Length 100;
Best Local Similarity 44.9%; Pred. No. 1.4e-18;
RESULT 623
ID ADO05363 standard; protein; 75 AA.
DE Toad prokineticin orthologue Bv8, SEQ ID NO:12.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.5%; Score 250.5; DB 7; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.3e-18;
RESULT 624
ID ADM00762 standard; protein; 75 AA.
DE Amino acid sequence of toad Bv8.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.5%; Score 250.5; DB 9; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.3e-18;
RESULT 625
ID ADZ88904 standard; protein; 75 AA.
DE Toad prokineticin 1 homologue, Bv8.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.5%; Score 250.5; DB 9; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.3e-18;
RESULT 626
ID AED00601 standard; protein; 75 AA.
DE Toad bv8 SEQ ID NO 13.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.5%; Score 250.5; DB 9; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.3e-18;
RESULT 627
ID ADI60152 standard; protein; 126 AA.
DE Secreted polypeptide #36.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 40.2%; Score 237; DB 7; Length 126;
Best Local Similarity 42.6%; Pred. No. 5.9e-17;
RESULT 628
ID ADJ71800 standard; protein; 126 AA.
DE Human prokineticin-like protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 40.2%; Score 237; DB 7; Length 126;
Best Local Similarity 42.6%; Pred. No. 5.9e-17;
RESULT 629
ID AED53711 standard; peptide; 56 AA.
DE Amino acid sequence of human PK2beta peptide.
PN WO2005097826-A2.
PD 20-OCT-2005.
PA (JANC) JANSSEN PHARM NV.
Query Match 31.6%; Score 186; DB 9; Length 56;
Best Local Similarity 52.7%; Pred. No. 6e-12;
RESULT 630
ID AED53712 standard; peptide; 56 AA.
DE Amino acid sequence of human PK2beta peptide #2.
PN WO2005097826-A2.
PD 20-OCT-2005.
PA (JANC) JANSSEN PHARM NV.
Query Match 31.2%; Score 184; DB 9; Length 56;
Best Local Similarity 57.4%; Pred. No. 9.7e-12;
RESULT 631
ID AAO27072 standard; peptide; 30 AA.
DE Monkey AXOR8 receptor N-terminal peptide, SEQ ID NO 20.
PN GB2378183-A.
PD 05-FEB-2003.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 26.5%; Score 156; DB 6; Length 30;
Best Local Similarity 90.0%; Pred. No. 4.5e-09;
RESULT 632
ID AEA18405 standard; peptide; 24 AA.
DE R. saharica insulin releasing peptide #1.
PN WO2005047316-A2.
PD 26-MAY-2005.
PA (UYUL-) UNIV ULSTER.
Query Match 20.4%; Score 120; DB 9; Length 24;
Best Local Similarity 91.3%; Pred. No. 2.2e-05;
RESULT 633
ID RAY44934 standard; protein; 271 AA.
DE Human dickkopf-1 homolog 3 protein.
PN WO200005714-A1.
PD 10-FEB-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 19.0%; Score 112; DB 3; Length 271;
Best Local Similarity 32.9%; Pred. No. 0.002;
RESULT 634
ID ADF28074 standard; peptide; 23 AA.
DE Human Zven polypeptide motif #2.
PN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.5%; Score 109; DB 7; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.0003;
RESULT 635
ID ADN41845 standard; peptide; 23 AA.
DE Motif found in Zvenl and Zvenl polypeptides.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.5%; Score 109; DB 8; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.0003;

PA	(BOLD//	BOLDOG F L.
PA	(BURG//	BURGESS C E.
PA	(CASM//	CASMAN S J.
PA	(CHAP//	CHAPOVAL A.
PA	(DHAN//	DHANABAL M.
PA	(EDIN//	EDINGER S R.
PA	(EISE//	EISEN A.
PA	(ELLE//	ELLERMAN K.
PA	(ETTE//	ETTENBERG S.
PA	(GANG//	GANGOLLI E A.
PA	(GERL//	GERLACH V.
PA	(GORM//	GORMAN L.
PA	(GROS//	GROSSE W M.
PA	(GUOX//	GUO X.
PA	(HACK//	HACKETT C.
PA	(JIWU//	J I W.
PA	(KEKU//	KEKUDA R.
PA	(KHRA//	KHRAMTSOV N V.
PA	(LEPL//	LEPLEY D M.
PA	(LILL//	L I L.
PA	(MACD//	MACDOUGALL J R.
PA	(MALY//	MALYANKAR U M.
PA	(MAZU//	MAZUR A.
PA	(MCQU//	MCQUEENEY K.
PA	(MEZE//	MEZES P S.
PA	(MILL//	MILLER C E.
PA	(MILLET//	MILLET I.
PA	(MISH//	MISHRA V.
PA	(PADI//	PADIGARU M.
PA	(PATY//	PATTURAJAN M.
PA	(PENAI//	PENA C E A.
PA	(PEYM//	PEYMAN J A.
PA	(RASI//	RASTELLI L.
PA	(RIEG//	RIEGER D K.
PA	(ROTH//	ROTHENBERG M E.
PA	(SHEN//	SHENOY S G.
PA	(SHIM//	SHIMKETS R A.
PA	(SMIT//	SMITHSON G.
PA	(SPAD//	SPADERNA S K.
PA	(STAR//	STARLING G.
PA	(SPYT//	SPYTEK K A.
PA	(STON//	STONE D J.
PA	(TCHE//	TCHERNEV V T.
PA	(TWOM//	TWOMLOW N.
PA	(VERN//	VERNET C A M.
PA	(ZERH//	ZERHUSEN B D.
PA	(VOSS//	VOSS E Z.
PA	(ZHON//	ZHONG M.
Query Match		
Best Local Similarity		
18.3%; Score 107.5; DB 8; Length 161;		
35.5%; Pred. No. 0.0034;		
RESULT 645		
ID	ADE28653 standard; protein; 173 AA.	
DB	Human NOV9b protein - SEQ ID 30.	
PD	WO2003040330-A2.	
PD	15-MAY-2003.	
PA	(CURA-) CURAGEN CORP.	
Query Match		
Best Local Similarity		
18.3%; Score 107.5; DB 7; Length 173;		
35.5%; Pred. No. 0.0037;		
RESULT 646		
ID	ADM93398 standard; protein; 173 AA.	
DB	Human NOVX polypeptide #15.	
PD	US2004067882-A1.	
PD	08-APR-2004.	
PA	(ALSO/) ALSOBROOK J P.	
PA	(ALVA/) ALVAREZ E.	
PA	(ANDE/) ANDERSON D W.	
PA	(BARO/) BARON M.	
PA	(BOLD/) BOLDOG F L.	
PA	(BURG/) BURGESS C E.	
PA	(CASM/) CASMAN S J.	
PA	(CHAP/) CHAPOVAL A.	
PA	(DHAN/) DHANABAL M.	
PA	(EDIN/) EDINGER S R.	

PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETTENBERG S.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCQU/) MCQUEENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHE/) TCHERNEV V T.
PA (TWOM/) TWOMLOW N.
PA (VERN/) VERNET C A M.
PA (ZERH/) ZERHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 8; Length 173;
RESULT 647 35.5%; Pred. No. 0.0037;
ID ADE28657 standard; protein; 180 AA.
DE Human NOV9d protein - SEQ ID 34.
PN WO2003040330-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 7; Length 180;
RESULT 648 35.5%; Pred. No. 0.0038;
ID ADM93402 standard; protein; 180 AA.
DE Human NOVX polypeptide #17.
PN US2004067882-A1.
PD 08-APR-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (BARO/) BARON M.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASHMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (DHAN/) DHANABAL M.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETTENBERG S.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.

PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCQU/) MCQUEENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHE/) TCHERNEV V T.
PA (TWOM/) TWOMLOW N.
PA (VERN/) VERNET C A M.
PA (ZERH/) ZERHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 8; Length 180;
RESULT 649 35.5%; Pred. No. 0.0038;
ID AAW73017 standard; protein; 224 AA.
DE Human cysteine-rich secreted protein CRSP-2.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHEAPEUTICS INC.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 2; Length 224;
RESULT 650 35.5%; Pred. No. 0.0048;
ID AAY92075 standard; protein; 224 AA.
DE Human DKR-4.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 3; Length 224;
RESULT 651 35.5%; Pred. No. 0.0048;
ID AAB08875 standard; protein; 224 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-4 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 3; Length 224;
RESULT 652 35.5%; Pred. No. 0.0048;
ID ABUS5916 standard; protein; 224 AA.
DE Human protein DKK4.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 6; Length 224;
RESULT 653 35.5%; Pred. No. 0.0048;
ID AAE34070 standard; protein; 224 AA.
DE DKK 4 protein.

PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 18.3%; Score 107.5; DB 6; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0048;
RESULT 654
ID ADE28651 standard; protein; 224 AA.
DE Human NOV9a protein - SEQ ID 28.
PN WO2003040330-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 18.3%; Score 107.5; DB 7; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0048;
RESULT 655
ID ADJ68529 standard; protein; 224 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID335.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 18.3%; Score 107.5; DB 7; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0048;
RESULT 656
ID ADN39310 standard; protein; 224 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:628.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EO3B-) EOS BIOTECHNOLOGY INC.
Query Match 18.3%; Score 107.5; DB 7; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0048;
RESULT 657
ID ADM93396 standard; protein; 224 AA.
DE Human NOVX polypeptide #14.
PN US2004067882-A1.
PD 08-APR-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (BARO/) BARON M.
PA (BOLD/) BOLDG F L.
PA (BURG/) BURGESS C E.
PA (CASH/) CASHMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (DHAN/) DHANABAL M.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETTENBERG S.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JITW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCQU/) MCQUEENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHB/) TCHERNEV V T.
PA (TWOM/) TWOMLOW N.
PA (VERN/) VERNET C A M.
PA (ZERR/) ZERRHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match 18.3%; Score 107.5; DB 8; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0048;
RESULT 658
ID AEAl6256 standard; protein; 224 AA.
DE Human Dickkopf-4 (Dkk-4) protein.
PN WO2005049797-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 18.3%; Score 107.5; DB 9; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0048;
RESULT 659
ID AEAl6254 standard; protein; 224 AA.
DE Cynomolgus monkey Dickkopf-4 (cdKk-4) protein.
PN WO2005049797-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 18.3%; Score 107.5; DB 9; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0048;
RESULT 660
ID AAW73019 standard; protein; 179 AA.
DE Human cysteine-rich secreted protein CRSP-4.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 17.3%; Score 102; DB 2; Length 179;
Best Local Similarity 31.5%; Pred. No. 0.014;
RESULT 661
ID AAB08877 standard; protein; 179 AA.
DE A partial human Dickkopf (Dkk)-2 protein.
PN WO200502047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.3%; Score 102; DB 3; Length 179;
Best Local Similarity 31.5%; Pred. No. 0.014;
RESULT 662
ID ADO35297 standard; protein; 179 AA.
DE Human Dkk2 carboxy terminal cysteine rich region.
PN US2004014209-A1.
PD 22-JAN-2004.
PA (LASS/) LASSAR A B.
PA (MERC/) MERCOLA M.
PA (GUFT/) GUPTA R.
PA (MARV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZA/) TZAHOOR E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match 17.3%; Score 102; DB 8; Length 179;
Best Local Similarity 31.5%; Pred. No. 0.014;
RESULT 663
ID AAY92074 standard; protein; 207 AA.
DE Human DKR-2 splice variant, DKR-2a.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 17.3%; Score 102; DB 3; Length 207;
Best Local Similarity 31.5%; Pred. No. 0.017;
RESULT 664
ID AAY92073 standard; protein; 259 AA.

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DE Human DKR-2.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 17.3%; Score 102; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 665
ID RAY99360 standard; protein; 259 AA.
DE Human PRO1316 (UNQ682) amino acid sequence SEQ ID NO:70.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 666
ID AAB66109 standard; protein; 259 AA.
DE Protein of the invention #21.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 4; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 667
ID AAU29148 standard; protein; 259 AA.
DE Human PRO polypeptide sequence #125.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 4; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 668
ID ABUS8524 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 669
ID ABUS8072 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 670
ID ABUS4387 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 671
ID ABR66261 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 672
ID ABR65651 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 673
ID ABUS99591 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 674
ID ABUS2830 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 675
ID ABUS9951 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 676
ID ABR68200 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 677
ID ABUS6253 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 678
ID ABUS2684 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 679
ID ABO08761 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 680
ID ABO02813 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 681
ID ABR74967 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 682
ID ABR94729 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 683
ID ABUS5702 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 684
ID ABUS98862 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
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PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 685
ID ABU98077 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 686
ID ABU91783 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 687
ID ABU9476 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 688
ID ABU86317 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 689
ID ABU67530 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036182-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 690
ID ABU80558 standard; protein; 259 AA.
DE Human PRO protein #125.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 691
ID ABR99476 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 692
ID ABR98866 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 693
ID ABO16389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027287-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 694
ID ABR92289 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003022294-A1.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 695
ID ABO18930 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044525-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 696
ID ABR78351 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 697
ID ABU85087 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 698
ID ABO00226 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 699
ID ABO11558 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 700
ID ABO02203 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 701
ID ABU55914 standard; protein; 259 AA.
DE Human protein DKK2.
PN WO20027204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 702
ID ABU88777 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 703
ID ABU83472 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 704
ID ABO06273 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003022294-A1.
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PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 705
ID ABR59309 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 706
ID ABO09371 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 707
ID ABO19235 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 708
ID ABO11253 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 709
ID ABR66871 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 710
ID ABO16084 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 711
ID ABO13790 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 712
ID ABO65693 standard; protein; 259 AA.
DE Human secreted/transmembrane protein, SEQ ID 250.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 713
ID ABO07541 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 714
ID ABO03728 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 715
ID ABR67176 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 716
ID ABO15779 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 717
ID AAE34068 standard; protein; 259 AA.
DE DKK 2 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 718
ID ABU56060 standard; protein; 259 AA.
DE Human secreted/transmembrane protein, PRO1316.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 719
ID ABU65388 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 720
ID ABU95333 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 721
ID ABU71236 standard; protein; 259 AA.
DE Human PRO1316 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 722
ID ABO07846 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 723
ID ABR70087 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 724
ID ABR69420 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;

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Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 725
ID ABO01561 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 726
ID ABU81363 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 727
ID ABR60160 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 728
ID ABR67895 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027289-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 729
ID ABR65283 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 730
ID ABR68505 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 731
ID ABR71917 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 732
ID ABU85397 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003022285-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 733
ID ABU89087 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 734
ID ABU83167 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 735
ID ABU95023 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 736
ID ABU90571 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 737
ID ABU84082 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 738
ID ABU93733 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 739
ID ABR64978 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 740
ID ABR68810 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 741
ID ABO06626 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 742
ID ABR99171 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 743
ID ABU57055 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 744
ID ABU86007 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 745
ID ABU82294 standard; protein; 259 AA.
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DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036136-A1.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 746
ID ABU87305 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 747
ID ABU81777 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 748
ID ABO08151 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003040086-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 749
ID ABU81862 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 750
ID ABU66026 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 751
ID ABR59855 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 752
ID ABU94043 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 753
ID ABU99896 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 754
ID ABR66566 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 755
ID ABR90984 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040058-A1.

PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 756
ID ABU94411 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 757
ID ABU79293 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 758
ID ABU86622 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 759
ID ABU86927 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 760
ID ABU94716 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 761
ID ABO04643 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 762
ID ABR70392 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 763
ID ABU98557 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 764
ID ABR65956 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 765
ID ABR64673 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;

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Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 766
ID ABU79598 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 767
ID ABU92989 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 768
ID ABU95948 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 769
ID ABU91168 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 770
ID ABU90261 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 771
ID ABO09676 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 772
ID ABO10948 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 773
ID ABR71002 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 774
ID ABU87610 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 775
ID ABU91478 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 776
ID ABU84692 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 777
ID ABR69782 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 778
ID ABU80159 standard; protein; 259 AA.
DE Human PRO protein #125.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 779
ID ABU93428 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 780
ID ABO09981 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 781
ID ABO09066 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 782
ID ABU10634 standard; protein; 259 AA.
DE Human secreted/transmembrane protein #125.
PN US2002127584-A1.
PD 12-SEP-2002.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 783
ID ABU95643 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 784
ID ABU96852 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 785
ID ABR70697 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040076-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
RESULT 786
ID ABO05048 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
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PN US2003008352-A1.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 787
ID ABO08456 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 788
ID ABO05663 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 789
ID ABR74052 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 790
ID ABR95644 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 791
ID ABR80941 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 792
ID ABR81246 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 793
ID ABR88544 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 794
ID ABR88544 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 795
ID ABR77365 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 796
ID ABO28849 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 797
ID ABO31594 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 798
ID ABO08011 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 799
ID ABO40491 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 800
ID ABO35916 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 801
ID ABO44055 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 802
ID ADA78002 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 803
ID ABM24850 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 804
ID ABO03118 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 805
ID ABR90374 standard; protein; 259 AA.

DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 806
ID ABM17288 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 807
ID ABR95034 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 808
ID ABR95339 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 809
ID ABO21577 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 810
ID ABR97841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 811
ID ABR87629 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 812
ID ABM77670 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 813
ID ABM27900 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 814
ID ABM06181 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 815
ID ABM03687 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 816
ID ABM35138 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 817
ID ABM26375 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 818
ID ABO48157 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 819
ID ABR92899 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 820
ID ABO24660 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 821
ID ABM11671 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 822
ID ABM02772 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 823
ID ABM16068 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 824
ID ABO27629 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 825
ID ABM29120 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 826
ID ABM07096 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 827
ID ABM21190 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 828
ID ABM09536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 829
ID ABO41406 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 830
ID ABO36221 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 831
ID ABO43750 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 832
ID ABM76450 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 833

ID ABM76146 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 834
ID ABM25765 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 835
ID ABM36070 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 836
ID ABO3423 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 837
ID ABO2508 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 838
ID ABR30679 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 839
ID ABR73747 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 840
ID ABO16999 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 841
ID ABR94424 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US200304917-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 842
ID ABR75931 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US200304929-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 843

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ID ABR71307 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 844
ID ABR93204 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 845
ID ABR91509 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 846
ID ABR87934 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 847
ID ABO33602 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 848
ID ABO27934 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 849
ID ABO30069 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 850
ID ABO33278 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 851
ID ABM04966 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 852
ID ABM08926 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054481-A1.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 853
ID ABO36526 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 854
ID ABO35611 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 855
ID ABO39576 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 856
ID ABM10451 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 857
ID ABM11976 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 858
ID ABO52122 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 859
ID ABO52427 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 860
ID ABO23745 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 861
ID ABR97231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054481-A1.
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PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 862
ID ABR87019 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 863
ID ABM11061 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 864
ID ABM28205 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 865
ID ABO32204 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 866
ID ABM15331 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 867
ID ABM06486 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 868
ID ABM04297 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 869
ID ABM22410 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 870
ID ABM07706 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068751-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 871
ID ABO40796 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 872
ID ABM35443 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 873
ID ABM33206 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 874
ID ABO52732 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 875
ID ABO50292 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 876
ID ABU99286 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 877
ID ABO04338 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036184-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 878
ID ABO05968 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 879
ID ABM19508 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 880
ID ABR97536 standard; protein; 259 AA.

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DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.021;
  RESULT 890
  ID ABM32901 standard; protein; 259 AA.
  DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
  PN US2003073185-A1.
  PD 17-APR-2003.
  PA (GETH ) GENENTECH INC.
    Query Match 17.3%; Score 102; DB 6; Length 259;
    Best Local Similarity 31.5%; Pred. No. 0.021;
    RESULT 891
    ID ABM22715 standard; protein; 259 AA.
    DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
    PN US2003087373-A1.
    PD 08-MAY-2003.
    PA (GETH ) GENENTECH INC.
      Query Match 17.3%; Score 102; DB 6; Length 259;
      Best Local Similarity 31.5%; Pred. No. 0.021;
      RESULT 892
      ID ABM74926 standard; protein; 259 AA.
      DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
      PN US2003096353-A1.
      PD 22-MAY-2003.
      PA (GETH ) GENENTECH INC.
        Query Match 17.3%; Score 102; DB 6; Length 259;
        Best Local Similarity 31.5%; Pred. No. 0.021;
        RESULT 893
        ID ADA79794 standard; protein; 259 AA.
        DE Human secreted/transmembrane protein (PRO) #125.
        PN US2003073173-A1.
        PD 17-APR-2003.
        PA (GETH ) GENENTECH INC.
          Query Match 17.3%; Score 102; DB 6; Length 259;
          Best Local Similarity 31.5%; Pred. No. 0.021;
          RESULT 894
          ID ABR96316 standard; protein; 259 AA.
          DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
          PN US2003054458-A1.
          PD 20-MAR-2003.
          PA (GETH ) GENENTECH INC.
            Query Match 17.3%; Score 102; DB 6; Length 259;
            Best Local Similarity 31.5%; Pred. No. 0.021;
            RESULT 895
            ID ABM02467 standard; protein; 259 AA.
            DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
            PN US2003059886-A1.
            PD 27-MAR-2003.
            PA (GETH ) GENENTECH INC.
              Query Match 17.3%; Score 102; DB 6; Length 259;
              Best Local Similarity 31.5%; Pred. No. 0.021;
              RESULT 896
              ID ABR86409 standard; protein; 259 AA.
              DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
              PN US2003049758-A1.
              PD 13-MAR-2003.
              PA (GETH ) GENENTECH INC.
                Query Match 17.3%; Score 102; DB 6; Length 259;
                Best Local Similarity 31.5%; Pred. No. 0.021;
                RESULT 897
                ID ABR86714 standard; protein; 259 AA.
                DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
                PN US2003049772-A1.
                PD 13-MAR-2003.
                PA (GETH ) GENENTECH INC.
                  Query Match 17.3%; Score 102; DB 6; Length 259;
                  Best Local Similarity 31.5%; Pred. No. 0.021;
                  RESULT 898
                  ID ABM16678 standard; protein; 259 AA.
                  DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
                  PN US2003064448-A1.
                  PD 03-APR-2003.
                  PA (GETH ) GENENTECH INC.
                    Query Match 17.3%; Score 102; DB 6; Length 259;
                    Best Local Similarity 31.5%; Pred. No. 0.021;
                    RESULT 899
                    ID ABO38661 standard; protein; 259 AA.
                    DE Human secreted/transmembrane protein (PRO) #125.
                    PN US2003068773-A1.

DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.021;
  RESULT 881
  ID ABR80636 standard; protein; 259 AA.
  DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
  PN US2003049740-A1.
  PD 13-MAR-2003.
  PA (GETH ) GENENTECH INC.
    Query Match 17.3%; Score 102; DB 6; Length 259;
    Best Local Similarity 31.5%; Pred. No. 0.021;
    RESULT 882
    ID ABM01247 standard; protein; 259 AA.
    DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
    PN US2003049770-A1.
    PD 13-MAR-2003.
    PA (GETH ) GENENTECH INC.
      Query Match 17.3%; Score 102; DB 6; Length 259;
      Best Local Similarity 31.5%; Pred. No. 0.021;
      RESULT 883
      ID ABR8849 standard; protein; 259 AA.
      DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
      PN US2003073169-A1.
      PD 17-APR-2003.
      PA (GETH ) GENENTECH INC.
        Query Match 17.3%; Score 102; DB 6; Length 259;
        Best Local Similarity 31.5%; Pred. No. 0.021;
        RESULT 884
        ID ABM13501 standard; protein; 259 AA.
        DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
        PN US2003064457-A1.
        PD 03-APR-2003.
        PA (GETH ) GENENTECH INC.
          Query Match 17.3%; Score 102; DB 6; Length 259;
          Best Local Similarity 31.5%; Pred. No. 0.021;
          RESULT 885
          ID ABM20885 standard; protein; 259 AA.
          DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
          PN US2003068711-A1.
          PD 10-APR-2003.
          PA (GETH ) GENENTECH INC.
            Query Match 17.3%; Score 102; DB 6; Length 259;
            Best Local Similarity 31.5%; Pred. No. 0.021;
            RESULT 886
            ID ABO42016 standard; protein; 259 AA.
            DE Human secreted/transmembrane protein (PRO) #125.
            PN US2003049745-A1.
            PD 13-MAR-2003.
            PA (GETH ) GENENTECH INC.
              Query Match 17.3%; Score 102; DB 6; Length 259;
              Best Local Similarity 31.5%; Pred. No. 0.021;
              RESULT 887
              ID ABO42626 standard; protein; 259 AA.
              DE Human secreted/transmembrane protein (PRO) #125.
              PN US2003049751-A1.
              PD 13-MAR-2003.
              PA (GETH ) GENENTECH INC.
                Query Match 17.3%; Score 102; DB 6; Length 259;
                Best Local Similarity 31.5%; Pred. No. 0.021;
                RESULT 888
                ID ABM10146 standard; protein; 259 AA.
                DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
                PN US2003067478-A1.
                PD 10-APR-2003.
                PA (GETH ) GENENTECH INC.
                  Query Match 17.3%; Score 102; DB 6; Length 259;
                  Best Local Similarity 31.5%; Pred. No. 0.021;
                  RESULT 889
                  ID ABO38661 standard; protein; 259 AA.
                  DE Human secreted/transmembrane protein (PRO) #125.
                  PN US2003068773-A1.
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ID ABM29730 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 900
ID ABO29154 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 901
ID ABM23935 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 902
ID ABM23325 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 903
ID ABM22105 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 904
ID ABO37746 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 905
ID ABM28510 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 906
ID ABM28815 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 907
ID ABM66459 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 908
ID ABM75841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104547-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 909
ID ABM34121 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 910
ID ABM34426 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 911
ID ABO20357 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 912
ID ABO21272 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 913
ID ABO22187 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 914
ID ABR96621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 915
ID ABR85799 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 916
ID ABR99781 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 917
ID ABM00332 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

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RESULT 918
ID ABO00637 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 919
ID ABO29764 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 920
ID ABO23630 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 921
ID ABO29425 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 922
ID ABO38356 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 923
ID ABO45656 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 924
ID ABO20580 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 925
ID ADA81521 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 926
ID ABO16694 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 927
ID ABO18320 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 928
ID ABO22747 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 929
ID ABO23052 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 930
ID ABR92594 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 931
ID ABR81551 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 932
ID ABM77975 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 933
ID ABR89764 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 934
ID ABM26680 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 935
ID ABM13806 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
RESULT 936
ID ABO28544 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
Pred. No. 0.021;
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RESULT 937
ID ABO30374 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 938
ID ABO07401 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 939
ID ABO03992 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 940
ID ABO37136 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 941
ID ABO41711 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 942
ID ABO35306 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 943
ID ABO25155 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 944
ID ABO47547 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 945
ID ABO47852 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 946
ID ABO48462 standard; protein; 259 AA.

DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 947
ID ABO51512 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 948
ID ABO51817 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 949
ID ABO50597 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 950
ID ABR79721 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 951
ID ABM16983 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 952
ID ABO18015 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 953
ID ABO20967 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 954
ID ABR96926 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 955
ID ABM12281 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 956
ID ABM16373 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 957
ID ABM24240 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 958
ID ABM14721 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 959
ID ABM04602 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 960
ID ABM06791 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 961
ID ABM09231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 962
ID ABO39271 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 963
ID ABM75536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 964
ID ABM25460 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 965
ID ABM19970 standard; protein; 259 AA.

DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 966
ID ABO46876 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 967
ID ABO47181 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 968
ID ADA83319 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 969
ID ABR71612 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 970
ID ABR72222 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 971
ID ABR98561 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US20030316129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 972
ID ABO06931 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 973
ID ABR84884 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 974
ID ABR73442 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 985
ID ABO30679 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
FN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 986
ID ABO30984 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
FN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 987
ID ABM27290 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
FN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 988
ID ABM30035 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
FN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 989
ID ABM05571 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
FN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 990
ID ABM15636 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
FN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 991
ID ABM08621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
FN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 992
ID ABO42321 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
FN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 993
ID ABO38051 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
FN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 994
ID ABO45961 standard; protein; 259 AA.
DE Human secreted polypeptide #125.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 995
ID ABM66764 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003058688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 996
ID ADB20362 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 997
ID ABM19665 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 998
ID ABO49377 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 999
ID ABO49682 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1000
ID ADA78614 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1001
ID ABR88239 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1002
ID ABM26985 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1003
ID ABM03382 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1004
ID ABO39881 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1005
ID ABO49987 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1006
ID ABO50902 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1007
ID ABO05358 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1008
ID ABR74662 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1009
ID ABO44455 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1010
ID ABR77141 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1011
ID ABM17898 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1012
ID ABR95949 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040073-A1.
PD 27-FEB-2003.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1013
ID ABO21882 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1014
ID ABO20052 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1015
ID ABO24355 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1016
ID ABR86104 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1017
ID ABM10756 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1018
ID ABM76755 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1019
ID ABR89459 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1020
ID ABM12586 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1021
ID ABO5876 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1022

ID ABO35001 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1023
ID ABM03077 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1024
ID ABM19055 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1025
ID ABM19360 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1026
ID ABO46571 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1027
ID ABO49072 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1028
ID ABR69115 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1029
ID ABR89154 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1030
ID ABR72527 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1031
ID ABR74357 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036161-A1.
PD 20-FEB-2003.

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PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1041
ID ABO31289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1042
ID ABM14416 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1043
ID ABM09841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1044
ID ABO38966 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1045
ID ABM34731 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1046
ID ABO51207 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1047
ID ABO04033 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1048
ID ABO10503 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1049
ID ABR77746 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1050
ID ABR78956 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054456-A1.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1032
ID ABO18625 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1033
ID ABR90331 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1034
ID ABM01552 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1035
ID ABM02162 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1036
ID ABR97324 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1037
ID ABM12891 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1038
ID ABM30645 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1039
ID ABM24545 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1040
ID ABO29459 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
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PD 20-MAR-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1051
ID ABO24050 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1052
ID ABR93814 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1053
ID ABO01857 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1054
ID ABM78280 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1055
ID ABO33479 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1056
ID ABR90069 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1057
ID ABM27595 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1058
ID ABM13196 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1059
ID ABO31899 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1060
ID ABM14111 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1061
ID ABM08316 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1062
ID ABO40186 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1063
ID ABM74621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1064
ID ABM33816 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1065
ID ABM20275 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1066
ID ABO48767 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1067
ID ABR72832 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1068
ID ABO15474 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1069
ID ABR85189 standard; protein; 259 AA.
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DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040065-A1.
PD 27-FEB-2003.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1070

ID ABO15169 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044919-A1.
PD 06-MAR-2003.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1071

ID ABO17304 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040077-A1.
PD 27-FEB-2003.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1072

ID ABM17593 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044928-A1.
PD 06-MAR-2003.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1073

ID ABR85494 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049746-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1074

ID ABN77060 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054464-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1075

ID ABO28239 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064459-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1076

ID ABM23020 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068757-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1077

ID ABM30340 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068723-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1078

ID ABM21800 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068741-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1079
ID ABM21495 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
FN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1080
ID ABM15026 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
FN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1081
ID AB041101 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
FN US2003069694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1082
ID AB036831 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
FN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1083
ID AB037441 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
FN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1084
ID ABM75231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
FN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1085
ID ABM33511 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
FN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1086
ID AB046266 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
FN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1087
ID ADA82685 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
FN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1088
ID ABM31865 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1089
ID ABM31255 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1090
ID ADB85993 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1091
ID ABM32170 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1092
ID ABM32475 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1093
ID ABM31560 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1094
ID ABM30950 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1095
ID ADC17939 standard; protein; 259 AA.
DE Human PRO polypeptide #21.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1096
ID ADD05723 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1097
ID ADD70585 standard; protein; 259 AA.

DE Human secreted/transmembrane protein PRO1316.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1098
ID ADD39662 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1099
ID ADD70108 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1100
ID ADD38229 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1101
ID ADD39185 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1102
ID ADD38708 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1103
ID ADD40139 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1104
ID ADE50360 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1105
ID ADE19972 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1106
ID ADE49883 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.

PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1107
ID ADE21441 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1108
ID ADF29866 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1109
ID ADF55759 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1110
ID ADG02718 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1111
ID ADG01425 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1112
ID ADF95600 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1113
ID ADG12415 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1114
ID ADH09075 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1115
ID ADH99263 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003065142-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1116
ID ADL32856 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1117
ID ADM30390 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1118
ID ADM39361 standard; protein; 259 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:B45.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1119
ID ADE74387 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1120
ID ADE74999 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1121
ID ADE96443 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1122
ID ADF25754 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1123
ID ADF24653 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1124
ID ADF29369 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

RESULT 1125
ID ADE96920 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1126
ID ADF96212 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1127
ID ADG04483 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1128
ID ADG00643 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1129
ID ADG82899 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1130
ID ADH02958 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1131
ID ADH03912 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1132
ID ADH03435 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1133
ID ADH26180 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1134
ID ADH33149 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1135
ID ADH04389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1136
ID ADH61390 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1137
ID ADJ54888 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1138
ID ADJ64659 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1139
ID ADM31555 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1140
ID ADM36602 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1141
ID ADM40407 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1142
ID ADL94589 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1143
ID ADO35295 standard; protein; 259 AA.
DE Human Dkk family protein Dkk2.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;

PN US2004014209-A1.
PD 22-JAN-2004.
PA (LASS/) LASSAR A B.
PA (MERC/) MERCOLA M.
PA (GUPT/) GUPTA R.
PA (MAEV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZA/) TZAHOOR E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1144
ID ADN38015 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1145
ID AED44976 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316, SEQ:70.
PN US2005181478-A1.
PD 18-AUG-2005.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
Query Match 17.3%; Score 102; DB 9; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1146
ID AED50245 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2005163766-A1.
PD 28-JUL-2005.
Query Match 17.3%; Score 102; DB 9; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.021;
RESULT 1147
ID AAB08880 standard; protein; 263 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-2 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.3%; Score 102; DB 3; Length 263;
Best Local Similarity 31.5%; Pred. No. 0.022;
RESULT 1148
ID AAY92072 standard; protein; 259 AA.
DE Murine DKR-2.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 17.1%; Score 101; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.027;
RESULT 1149
ID AEA38732 standard; protein; 272 AA.
DE Mouse dickkopf-1 (Dkk-1) protein, SEQ ID NO: 22.
PN WO2005049640-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 17.1%; Score 101; DB 9; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.029;
RESULT 1150
ID AEF80274 standard; protein; 272 AA.
DE Mouse dickkopf-1 (Dkk-1) protein sequence.
PN WO2006015373-A2.
PD 09-FEB-2006.
PA (AMGE-) AMGEN INC.
Query Match 17.1%; Score 101; DB 10; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.029;
RESULT 1151
ID ADY86168 standard; protein; 83 AA.
DE Human dickkopf-3 protein, SEQ ID NO:6.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 9; Length 83;
Best Local Similarity 37.7%; Pred. No. 0.0093;
RESULT 1152
ID ADB64042 standard; protein; 215 AA.
DE Human protein encoded by clone BRAMY20227860.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 17.1%; Score 100.5; DB 7; Length 215;
Best Local Similarity 37.7%; Pred. No. 0.025;
RESULT 1153
ID AAW73016 standard; protein; 350 AA.
DE Human cysteine-rich secreted protein CRSP-1.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 17.1%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1154
ID AAW62595 standard; protein; 350 AA.
DE Homo sapiens cerebellum and embryo specific protein.
PN WO9827932-A2.
PD 02-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 17.1%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1155
ID AAY13384 standard; protein; 350 AA.
DE Amino acid sequence of protein PRO295.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1156
ID AAY92070 standard; protein; 350 AA.
DE Human DKR-3.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 17.1%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1157
ID AAB08874 standard; protein; 350 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-3 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.1%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1158
ID ADC78556 standard; protein; 350 AA.
DE Human PRO295 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1159
ID AAB80252 standard; protein; 350 AA.
DE Human PRO295 protein.
PN WO200104311-A1.
PD 18-JAN-2001.

PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1160
ID RAG80271 standard; protein; 350 AA.
DE Human DKK-3 protein.
PN WO200163295-A2.
PD 30-AUG-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match 17.1%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1161
ID AAB87529 standard; protein; 350 AA.
DE Human PRO295.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1162
ID AAG62468 standard; protein; 350 AA.
DE Human reduced expression in immortalised cells protein.
PN WO200138528-A1.
PD 31-MAY-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 17.1%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1163
ID ABB90735 standard; protein; 350 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 202.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 17.1%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1164
ID ABG95854 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1165
ID ABB84841 standard; protein; 350 AA.
DE Human PRO295 protein sequence SEQ ID NO:50.
PN WO20020690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1166
ID ABB95447 standard; protein; 350 AA.
DE Human angiogenesis related protein PRO295 SEQ ID NO: 50.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1167
ID ABU71630 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1168
ID ABU71485 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1169
ID ABUS4442 standard; protein; 350 AA.
DE Human tumour endothelial marker TEM 4.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1170
ID ABU71931 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1171
ID ABO1814 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1172
ID ABUS0879 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1173
ID ABO33938 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1174
ID ABU71955 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1175
ID ABUS5915 standard; protein; 350 AA.
DE Human protein DKK3.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;

Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1167
ID ABU71630 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1168
ID ABU71485 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1169
ID ABUS4442 standard; protein; 350 AA.
DE Human tumour endothelial marker TEM 4.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1170
ID ABU71931 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1171
ID ABO1814 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1172
ID ABUS0879 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1173
ID ABO33938 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1174
ID ABU71955 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1175
ID ABUS5915 standard; protein; 350 AA.
DE Human protein DKK3.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;

RESULT 1176
ID ABU54387 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1177
ID ABO47402 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO295.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1178
ID ABU71509 standard; protein; 350 AA.
DE Human secreted polypeptide PRO295.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1179
ID AAE34069 standard; protein; 350 AA.
DE DKK 3 protein.
PN WO20020992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1180
ID ABU72290 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1181
ID ABU90963 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1182
ID ABO27284 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO295.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1183
ID ABU64539 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #43.
PN US2002150374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1184
ID ABU67385 standard; protein; 350 AA.
DE Human secreted protein PRO295.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1185

ID ABU92479 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003045884-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1186
ID ABO14905 standard; protein; 350 AA.
DE Human secreted / transmembrane polypeptide PRO295.
PN US2003030600-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1187
ID ABU81149 standard; protein; 350 AA.
DE Human secreted polypeptide PRO295.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1188
ID ABO53264 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1189
ID ABU98266 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1190
ID ABU89271 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1191
ID ABU82478 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1192
ID ABU69662 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1193
ID ABU96442 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1194
ID ABU72112 standard; protein; 350 AA.

DE Human PRO polypeptide #4.
PN US2003023042-A1.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1195
ID ABO14844 standard; protein; 350 AA.
DE Human secreted / transmembrane polypeptide PRO295.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1196
ID ADB29441 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1197
ID ADB17065 standard; protein; 350 AA.
DE Human transmembrane PRO polypeptide (SeqID 8).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1198
ID ABO44242 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1199
ID ADA18297 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1200
ID ABO32796 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1201
ID ADA19870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003059394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1202
ID ADB17253 standard; protein; 350 AA.
DE Human transmembrane PRO polypeptide (SeqID 8).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1203
ID ABO34856 standard; protein; 350 AA.
DE Human PRO polypeptide #41.

PN US2003044793-A1.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1204
ID ADA16272 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1205
ID ADA20042 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1206
ID ABO34170 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1207
ID ADA42417 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1208
ID ABO17534 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1209
ID ADA00339 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1210
ID ADA16696 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1211
ID ADA13125 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1212
ID ADA41993 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082540-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1213
ID ADA17340 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1214
ID ADA2843 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1215
ID ABO17595 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1216
ID ADB9581 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1217
ID ADB7762 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1218
ID ADB74898 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1219
ID ADB68260 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1220
ID ADB68067 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1221
ID ADB90884 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003083473-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1222
ID ADC28544 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1223
ID ADC39744 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1224
ID ADC40258 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1225
ID ADC19082 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1226
ID ADC34382 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1227
ID ADC29437 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1228
ID ADC28968 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1229
ID ADC40853 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1230
ID ADC19510 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1231
ID ADC06964 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003080602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1232
ID ADC17143 standard; protein; 350 AA.
DE Mammalian PRO polypeptide (SeqID 8).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1233
ID ADC33958 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1234
ID ADC13028 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1235
ID ADC14841 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1236
ID ADC52336 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1237
ID ADC12480 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1238
ID ADD10339 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1239
ID ADD05035 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1240
ID ADD11299 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1241
ID ADD04041 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1242
ID ADD03617 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1243
ID ADD37092 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1244
ID ADD36012 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1245
ID ADE34869 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1246
ID ADG01013 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1247
ID ADG08565 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1248
ID ADF95187 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;

RESULT 1249
ID ADH24040 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1250
ID ADH34066 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1251
ID ADH29899 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1252
ID ADH23870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1253
ID ADH5274 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1254
ID ADH24550 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1255
ID ADH37406 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1256
ID ADH01995 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1257
ID ADH37576 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1258
ID ADH59352 standard; protein; 350 AA.

ID ADH5614 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1259
ID ADH24210 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1260
ID ADH38504 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1261
ID ADH3625 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1262
ID ADH29433 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1263
ID ADH27549 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1264
ID ADH37746 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1265
ID ADH37923 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1266
ID ADH57343 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1267
ID ADH59352 standard; protein; 350 AA.

DE Human secreted/transmembrane protein, #45.
PN US2003039972-A1.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1268
ID ADH53485 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1269
ID ADH53655 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1270
ID ADH51991 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1271
ID ADH49846 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1272
ID ADI25356 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1273
ID ADH90149 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1274
ID ADI25526 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1275
ID ADH97700 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1276
ID ADI38131 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003181673-A1.

PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1277
ID ADI03548 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1278
ID ADI11905 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1279
ID ADH89979 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1280
ID ADH98380 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1281
ID ADI11055 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1282
ID ADI11565 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1283
ID ADH98210 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1284
ID ADH98550 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1285
ID ADH98040 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181673-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1286
ID ADI05028 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1287
ID ADI03378 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1288
ID ADI04773 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1289
ID ADH78227 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1290
ID ADI19571 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1291
ID ADH90319 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1292
ID ADI03038 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1293
ID ADH77887 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1294
ID ADH97870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181674-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1295
ID ADI01255 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1296
ID ADI01950 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1297
ID ADI03208 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1298
ID ADI11395 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1299
ID ADI02297 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1300
ID ADI11735 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1301
ID ADI05372 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1302
ID ADH79444 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1303
ID ADI19401 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1304
ID ADI05202 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US200318167-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1305
ID ADH79614 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1306
ID ADI01440 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1307
ID ADI01610 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1308
ID ADI01780 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1309
ID ADH79784 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1310
ID ADI04602 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1311
ID ADI02738 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1312
ID ADH78057 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1313
ID ADH78057 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1314
ID ADI25866 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1315
ID ADK65378 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1316
ID ADH98720 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1317
ID ADH79961 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1318
ID ADJ26399 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1319
ID ADJ93692 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1320
ID ADP65205 standard; protein; 350 AA.
DE Human dickkopf homologue 3, RIG-like 7-1, RIG-like 5-6.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1321
ID ADC52146 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;

RESULT 1322
ID ADE79314 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003155025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1323
ID ADE79738 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1324
ID ADE73414 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003129593-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1325
ID ADE41300 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1326
ID ADE73949 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1327
ID ADE9503 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1328
ID ADE98622 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1329
ID ADE99049 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1330
ID ADG40519 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOMSKI P J.
PA (GURN/) GURNEY A L.

PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1331
ID ADF73913 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1332
ID ADF73489 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1333
ID ADH06578 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1334
ID ADH06408 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1335
ID ADG68829 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1336
ID ADH27719 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1337
ID ADH25060 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1338
ID ADH33692 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1339
ID ADG92332 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003027145-A1.

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PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1340
ID ADH02335 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1341
ID ADH07942 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1342
ID ADG6339 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1343
ID ADH3160 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1344
ID ADG92759 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1345
ID ADG83900 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1346
ID ADG85444 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003168846-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1347
ID ADH06238 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1348
ID ADH30068 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1349
ID ADH24380 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1350
ID ADG69509 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1351
ID ADH07772 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1352
ID ADG85784 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1353
ID ADH39330 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1354
ID ADH33522 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1355
ID ADH33862 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1356
ID ADH01072 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1357
ID ADG69679 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1358
ID ADH02165 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1359
ID ADG69169 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1360
ID ADG85954 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1361
ID ADH24890 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1362
ID ADH39507 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1363
ID ADH02505 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1364
ID ADG68999 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1365
ID ADH07602 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1366
ID ADG66124 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;

Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1367
ID ADH24720 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1368
ID ADH25768 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1369
ID ADH38334 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1370
ID ADH20548 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1371
ID ADH57173 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1372
ID ADH43483 standard; protein; 350 AA.
DE Human PRO polypeptide #25.
PN US200324984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1373
ID ADH07403 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1374
ID ADH52161 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1375
ID ADH59948 standard; protein; 350 AA.

DE Human secreted/transmembrane protein, #45.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1376
ID ADH49527 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1377
ID ADH06976 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1378
ID ADH90489 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1379
ID ADI11225 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1380
ID ADI18718 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1381
ID ADH98890 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190696-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1382
ID ADI65438 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1383
ID ADI02120 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1384
ID ADH90659 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1385
ID ADI37697 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1386
ID ADH97497 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1387
ID ADI65865 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1388
ID ADH60608 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1389
ID ADJ99665 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1390
ID ADL08858 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1391
ID ADJ98534 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;

RESULT 1392
ID ADJ98704 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1393
ID ADH78863 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1394
ID ADJ99097 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1395
ID ADJ99267 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1396
ID ADJ98885 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1397
ID ADH79033 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1398
ID ADK00893 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1399
ID ADK14414 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1400
ID ADM25199 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003086233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1401

ID ADM29949 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1402
ID ADK82828 standard; protein; 350 AA.
DE Human PRO polypeptide #25.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1403
ID ADM80863 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1404
ID ADO06271 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1405
ID ADR11123 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1406
ID ADR18032 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FLIV/) FLIVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANT/) PAN J.
PA (PAON/) PAONT N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1407
ID ADS74671 standard; protein; 350 AA.
DE Human secreted/transmembrane protein #45.

PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLMAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1408
ID ADT03708 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH/) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1409
ID ADY77703 standard; protein; 350 AA.
DE Neoplastic disease detection protein PRO295.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (MATA/) MATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 9; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1410
ID AEA37946 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH/) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 9; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1411
ID AED23980 standard; protein; 350 AA.
DE Human secreted protein PRO 295, SEQ ID 236.
PN US2005219004-A1.
PD 29-SEP-2005.
PA (GETH/) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 9; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1412
ID AEE69149 standard; protein; 350 AA.
DE Integrin homologous PRO295 protein, SEQ ID 236.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH/) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1413
ID AEF12534 standard; protein; 350 AA.
DE Human PRO295 protein SEQ ID NO:8.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH/) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1414
ID AEF74223 standard; protein; 350 AA.
DE Human PRO295 protein SEQ ID NO:8.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (MATA/) MATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 17.1%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1415
ID AEF68232 standard; protein; 350 AA.
DE Human Dickkopf homolog 3 (DKK-3) protein.
PN WO2006010534-A1.
PD 02-FEB-2006.
PA (HOFF/) HOFFMANN LA ROCHE & CO AG F.
Query Match 17.1%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.042;
RESULT 1416
ID AAW73021 standard; protein; 349 AA.
DE Mouse cysteine-rich secreted protein-1.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 16.7%; Score 98.5; DB 2; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.069;
RESULT 1417
ID AAY92069 standard; protein; 349 AA.
DE Murine DKK-3.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 16.7%; Score 98.5; DB 3; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.069;
RESULT 1418
ID AAB08879 standard; protein; 349 AA.
DE A murine Dickkopf (DKK)-3 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.7%; Score 98.5; DB 3; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.069;
RESULT 1419
ID AEF68233 standard; protein; 349 AA.
DE Murine Dickkopf homolog 3 (DKK-3) protein.
PN WO2006010534-A1.
PD 02-FEB-2006.
PA (HOFF/) HOFFMANN LA ROCHE & CO AG F.
Query Match 16.7%; Score 98.5; DB 10; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.069;
RESULT 1420
ID ADE82539 standard; protein; 84 AA.
DE Antibody that binds to DKK #6.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.

PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 84;
Best Local Similarity 32.3%; Pred. No. 0.022;
RESULT 1421
ID ADE82541 standard; protein; 107 AA.
DE Antibody that binds to DKK #8.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 107;
Best Local Similarity 32.3%; Pred. No. 0.028;
RESULT 1422
ID ADU66981 standard; protein; 108 AA.
DE Human DPK-1 LRP-6 binding domain.
PN US200423516-A1.
PD 25-NOV-2004.
PA (PROC/) PROCKOP D.
PA (SEKI/) SEKIYA I.
PA (GREG/) GREGORY C.
PA (SPER/) SPERS J.
PA (SMIT/) SMITH J.
PA (POCH/) POCHAMPALLY R.
Query Match 16.5%; Score 97; DB 8; Length 108;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1423
ID AD251669 standard; protein; 108 AA.
DE Dickkopf-1 LDL receptor-related protein 6 binding site.
PN US2005084494-A1.
PD 21-APR-2005.
PA (PROC/) PROCKOP D.
PA (GREG/) GREGORY C.
PA (GUNN/) GUNN W.
Query Match 16.5%; Score 97; DB 9; Length 108;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1424
ID ADE82538 standard; protein; 128 AA.
DE Antibody that binds to DKK #5.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 128;
Best Local Similarity 32.3%; Pred. No. 0.034;
RESULT 1425
ID ADE82540 standard; protein; 149 AA.
DE Antibody that binds to DKK #7.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 149;
Best Local Similarity 32.3%; Pred. No. 0.04;
RESULT 1426
ID ADB99065 standard; protein; 151 AA.
DE LRP5 constrained peptide OST264.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 151;
Best Local Similarity 32.3%; Pred. No. 0.041;
RESULT 1427
ID ADE82633 standard; protein; 151 AA.
DE LRP5 peptide aptamer #10.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 151;
Best Local Similarity 32.3%; Pred. No. 0.041;
RESULT 1428
ID ADE82537 standard; protein; 170 AA.
DE Antibody that binds to DKK #4.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 170;
Best Local Similarity 32.3%; Pred. No. 0.046;
RESULT 1429
ID ADB99066 standard; protein; 172 AA.
DE LRP5 constrained peptide OST265.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 172;
Best Local Similarity 32.3%; Pred. No. 0.047;
RESULT 1430
ID ADE82634 standard; protein; 172 AA.
DE LRP5 peptide aptamer #11.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 172;
Best Local Similarity 32.3%; Pred. No. 0.047;
RESULT 1431
ID ADO35296 standard; protein; 180 AA.
DE Human DKK1 carboxy terminal cysteine rich region.
PN US2004014209-A1.
PD 22-JAN-2004.
PA (LASS/) LASSAR A B.
PA (MERC/) MERCOLA M.
PA (GUPT/) GUPTA R.
PA (MARV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZA/) TZAHOE E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match 16.5%; Score 97; DB 8; Length 180;
Best Local Similarity 32.3%; Pred. No. 0.045;
RESULT 1432
ID ADE82535 standard; protein; 212 AA.
DE Antibody that binds to DKK #2.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 212;
Best Local Similarity 32.3%; Pred. No. 0.058;
RESULT 1433
ID ADE82534 standard; protein; 233 AA.
DE Antibody that binds to DKK #1.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 233;
Best Local Similarity 32.3%; Pred. No. 0.064;
RESULT 1434
ID AEA38731 standard; protein; 265 AA.
DE Human dickkopf-1 (DKK-1) protein, SEQ ID NO: 21 #1.
PN WO2005049640-A2.
PD 02-JUN-2005.
PA (MERT) MERT & CO INC.
Query Match 16.5%; Score 97; DB 9; Length 265;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1435
ID AAW73018 standard; protein; 266 AA.
DE Human cysteine-rich secreted protein CRSP-3.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 16.5%; Score 97; DB 2; Length 266;

Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1436
ID AAY41757 standard; protein; 266 AA.
DE Human PRO1008 protein sequence.
PN W09946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 2; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1437
ID AAY92071 standard; protein; 266 AA.
DE Human DKR-1.
PN W0200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 16.5%; Score 97; DB 3; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1438
ID AAB44313 standard; protein; 266 AA.
DE Human PRO1008 (UNQ492) protein sequence SEQ ID NO:456.
PN W0200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 3; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1439
ID AAB08876 standard; protein; 266 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-1 protein.
PN W0200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.5%; Score 97; DB 3; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1440
ID AAU13385 standard; protein; 266 AA.
DE Human PRO1008 polypeptide sequence.
PN W0200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 4; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1441
ID AAM78517 standard; protein; 266 AA.
DE Human protein SEQ ID NO 1179.
PN W0200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.5%; Score 97; DB 4; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1442
ID ABO17829 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1443
ID ABO25259 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1444
ID ABU81083 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1445
ID ABU72265 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1446
ID ABU66783 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1447
ID ABU55913 standard; protein; 266 AA.
DE Human protein DK1.
PN W0200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1448
ID ABU84945 standard; protein; 266 AA.
DE Human secreted and transmembrane PRO polypeptide #21.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1449
ID AAE34067 standard; protein; 266 AA.
DE DK1 protein.
PN W0200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1450
ID ABU59864 standard; protein; 266 AA.
DE Novel secreted and transmembrane protein PRO1008.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1451
ID ABU61143 standard; protein; 266 AA.
DE Human PRO1008 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1452
ID ABU57630 standard; protein; 266 AA.
DE Differentially expressed breast cancer associated protein #17.
PN US2002156263-A1.
PD 24-OCT-2002.
PA (CHEN/) CHEN H.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1453
ID ABO25054 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #214.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1454

ID ABR01793 standard; protein; 266 AA.
DE Human cancer-related protein, 151P.C7A.
PN W0200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1455
ID ABU80412 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO1008.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1456
ID ABU67059 standard; protein; 266 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 428.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1457
ID ADA45947 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003023328-A1.
PD 30-JAN-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1458
ID ADA76378 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1459
ID ADA19028 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1460
ID ADA61651 standard; protein; 266 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1461
ID ADH19436 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1462
ID ADB27977 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1463
ID ADA86456 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1464
ID ADB16020 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1465
ID ADA47806 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1466
ID ADA67601 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1467
ID ADB30608 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1468
ID ADA85904 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1469
ID ADA97116 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1470
ID ADA79420 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1471
ID ADA87559 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GENH-) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1472
ID ADB16761 standard; protein; 266 AA.
DE Human PRO polypeptide #214.

PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1473
ID ADA91853 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1474
ID ADB14916 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1475
ID ADA24995 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1476
ID ADB18877 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1477
ID ADA94092 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1478
ID ADB19988 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1479
ID ADB13300 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1480
ID ABO43362 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1481
ID ABO19714 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003050240-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1482
ID ADA12656 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO1008.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1483
ID ADA74554 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1484
ID ADB24787 standard; protein; 266 AA.
DE Human PRO polypeptide SEQ ID NO 428.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1485
ID ADA82311 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1486
ID ADA75274 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1487
ID ADA85352 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1488
ID ADA94800 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1489
ID ADB31056 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1490
ID ADA80584 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082761-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1491
ID ADA75826 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1492
ID ADA47051 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1493
ID ADB25347 standard; protein; 266 AA.
DE Human PRO polypeptide SEQ ID NO 428.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1494
ID ADA93523 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1495
ID ADB26873 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1496
ID ADB31160 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1497
ID ADA61088 standard; protein; 266 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1498
ID ADB24235 standard; protein; 266 AA.
DE Human PRO polypeptide SEQ ID NO 428.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1499
ID ADA96564 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;
RESULT 1500
ID ADA81136 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.074;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 14, 2006, 14:30:22 : Search time 138.534 Seconds
(without alignments)
351.087 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MGRATRVSMILLVTVDCA.....CSRFPPGRYRCMSMDLNINP 105

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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16	589	100.0	105	3	US-09-965-528-11
29	589	100.0	105	3	US-09-997-428-371
33	589	100.0	105	3	US-09-796-753-64
75	589	100.0	105	3	US-09-969-984-11
76	589	100.0	105	4	US-10-016-481-2
77	589	100.0	105	4	US-10-027-603-2
100	589	100.0	105	4	US-10-132-812-16
259	589	100.0	105	4	US-10-223-085-172
265	589	100.0	105	4	US-10-219-065-166
293	589	100.0	105	4	US-10-223-084-172
294	589	100.0	105	4	US-10-223-088-172
295	589	100.0	105	4	US-10-223-090-172
300	589	100.0	105	4	US-10-212-355-5
301	589	100.0	105	4	US-10-223-087-172
302	589	100.0	105	4	US-10-323-157-2
304	589	100.0	105	4	US-10-223-083-172
307	589	100.0	105	4	US-10-223-089-172
356	589	100.0	105	4	US-10-212-201-5
467	589	100.0	105	4	US-10-223-081-172
501	589	100.0	105	4	US-10-323-082-172
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632	589	100.0	105	4	US-10-680-755A-5
633	589	100.0	105	4	US-10-680-800A-5
641	589	100.0	105	5	US-10-713-567-2

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647	589	100.0	105	5	US-10-912-907-2
648	589	100.0	105	5	US-10-692-299-2
649	589	100.0	105	5	US-10-415-724-2
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693	589	84.6	86	4	US-10-333-192-21
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697	589	84.6	86	5	US-10-912-907-3
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703	589	84.6	87	4	US-10-016-481-18
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705	589	84.6	87	5	US-10-713-567-18
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722	589	83.9	85	5	US-10-415-724-16
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728	478	81.2	86	5	US-10-811-328-17	Sequence 17, Appl	801	303	51.4	108	4	US-10-212-201-2	Sequence 2, Appl1
729	478	81.2	86	5	US-10-912-907-17	Sequence 17, Appl	802	303	51.4	108	4	US-10-467-019-17	Sequence 17, Appl
730	478	81.2	86	5	US-10-415-724-17	Sequence 17, Appl	803	303	51.4	108	4	US-10-680-755A-2	Sequence 2, Appl1
731	476	80.8	82	5	US-10-977-113-11	Sequence 11, Appl	804	303	51.4	108	4	US-10-680-800A-2	Sequence 2, Appl1
732	473	80.3	86	4	US-10-470-951-37	Sequence 37, Appl	805	303	51.4	108	5	US-10-713-567-5	Sequence 5, Appl1
733	473	80.3	86	4	US-10-362-504-49	Sequence 49, Appl	806	303	51.4	108	5	US-10-811-328-5	Sequence 5, Appl1
734	473	80.3	86	4	US-10-680-554-10	Sequence 10, Appl	807	303	51.4	108	5	US-10-912-907-5	Sequence 5, Appl1
735	473	80.3	86	5	US-10-713-567-30	Sequence 30, Appl	808	303	51.4	108	5	US-10-415-724-5	Sequence 5, Appl1
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737	473	80.3	86	5	US-10-503-554A-138	Sequence 138, Appl	810	303	51.4	108	5	US-10-503-554A-17	Sequence 17, Appl
738	469	79.6	86	4	US-10-470-951-41	Sequence 41, Appl	811	303	51.4	108	5	US-10-982-168-2	Sequence 2, Appl1
739	469	79.6	86	4	US-10-362-504-53	Sequence 53, Appl	812	303	51.4	108	5	US-10-504-554-6	Sequence 6, Appl1
740	469	79.6	86	5	US-10-503-554A-142	Sequence 142, App	813	303	51.4	116	4	US-10-680-755A-26	Sequence 26, Appl
741	467	79.3	86	4	US-10-470-951-39	Sequence 39, Appl	814	303	51.4	116	4	US-10-680-800A-36	Sequence 36, Appl
742	467	79.3	86	4	US-10-362-504-51	Sequence 51, Appl	815	300	50.9	108	5	US-10-713-567-34	Sequence 34, Appl
743	467	79.3	86	5	US-10-503-554A-140	Sequence 140, App	816	300	50.9	108	6	US-10-977-113-6	Sequence 6, Appl1
744	467	79.3	86	4	US-10-417-426-10	Sequence 10, Appl	817	300	50.9	108	6	US-11-073-420-6	Sequence 6, Appl1
745	455	77.2	86	4	US-10-470-951-8	Sequence 8, Appl1	818	298	50.6	107	4	US-10-132-812-10	Sequence 10, Appl
746	455	77.2	86	5	US-10-680-554-8	Sequence 8, Appl1	819	298	50.6	107	4	US-10-231-411-6	Sequence 6, Appl1
747	455	77.2	86	5	US-10-713-567-28	Sequence 28, Appl	820	298	50.6	107	4	US-10-467-019-37	Sequence 37, Appl
748	455	77.2	86	5	US-10-811-328-28	Sequence 28, Appl	821	298	50.6	107	4	US-10-467-019-35	Sequence 35, Appl
749	455	77.2	86	5	US-10-977-113-12	Sequence 12, Appl	822	298	50.6	107	4	US-10-362-504-69	Sequence 69, Appl
750	455	77.2	86	5	US-10-871-152-23	Sequence 23, Appl	823	298	50.6	107	5	US-10-503-554A-37	Sequence 37, Appl
751	455	77.2	86	5	US-10-503-554A-109	Sequence 109, App	824	298	50.6	107	5	US-10-503-554A-55	Sequence 55, Appl
752	455	77.2	86	6	US-11-073-420-12	Sequence 12, Appl	825	291	49.4	80	4	US-10-467-019-22	Sequence 22, Appl
753	455	77.2	86	4	US-10-016-481-14	Sequence 14, Appl	826	291	49.4	80	5	US-10-503-554A-22	Sequence 22, Appl
754	455	77.2	86	4	US-10-323-157-14	Sequence 14, Appl	827	291	49.4	81	4	US-10-016-481-6	Sequence 6, Appl1
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756	455	77.2	86	5	US-10-680-554-16	Sequence 16, Appl	829	291	49.4	81	4	US-10-417-426-5	Sequence 5, Appl1
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771	455	77.2	86	5	US-10-415-724-13	Sequence 13, Appl	844	287.5	48.8	96	5	US-10-811-328-11	Sequence 11, Appl
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773	455	77.2	86	5	US-10-871-152-27	Sequence 27, Appl	846	287.5	48.8	96	5	US-10-415-724-11	Sequence 11, Appl
774	455	77.2	86	4	US-11-073-420-16	Sequence 16, Appl	847	286	48.6	80	5	US-10-977-113-10	Sequence 10, Appl
775	455	77.2	86	4	US-10-417-426-13	Sequence 13, Appl	848	286	48.6	80	6	US-11-073-420-10	Sequence 10, Appl
776	455	77.2	86	4	US-10-467-019-21	Sequence 21, Appl	849	286	48.6	81	4	US-10-417-426-7	Sequence 7, Appl1
777	455	77.2	86	4	US-10-470-951-64	Sequence 64, Appl	850	286	48.6	81	4	US-10-467-019-39	Sequence 39, Appl1
778	455	77.2	86	4	US-10-333-192-34	Sequence 34, Appl	851	286	48.6	81	4	US-10-362-504-71	Sequence 71, Appl
779	455	77.2	86	5	US-10-977-113-15	Sequence 15, Appl	852	286	48.6	81	5	US-10-680-554-9	Sequence 9, Appl1
780	455	77.2	86	5	US-10-871-152-26	Sequence 26, Appl	853	286	48.6	81	5	US-10-680-554-11	Sequence 11, Appl
781	455	77.2	86	5	US-10-503-554A-21	Sequence 21, Appl	854	286	48.6	81	5	US-10-713-567-29	Sequence 29, Appl
782	455	77.2	86	6	US-11-073-420-15	Sequence 15, Appl	855	286	48.6	81	5	US-10-811-328-31	Sequence 31, Appl
783	455	77.2	86	3	US-09-886-242A-5	Sequence 5, Appl1	856	286	48.6	81	5	US-10-811-328-29	Sequence 29, Appl
784	455	77.2	86	4	US-10-027-603-5	Sequence 5, Appl1	857	286	48.6	81	5	US-10-811-328-31	Sequence 31, Appl
785	455	77.2	86	5	US-10-692-299-5	Sequence 5, Appl1	858	286	48.6	81	5	US-10-871-152-20	Sequence 20, Appl
786	455	77.2	86	4	US-10-016-481-12	Sequence 12, Appl	859	286	48.6	81	5	US-10-503-554A-39	Sequence 39, Appl
787	455	77.2	86	4	US-10-132-812-11	Sequence 12, Appl	860	284	48.2	129	4	US-11-073-420-37	Sequence 37, Appl
788	455	77.2	86	4	US-10-323-157-12	Sequence 12, Appl	861	282.5	48.0	129	4	US-10-132-812-14	Sequence 14, Appl
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791	455	77.2	86	5	US-10-811-328-12	Sequence 12, Appl	864	282.5	48.0	129	4	US-10-680-800A-29	Sequence 29, Appl
792	455	77.2	86	5	US-10-912-907-12	Sequence 12, Appl	865	278.5	47.3	77	5	US-10-680-554-14	Sequence 14, Appl
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794	455	77.2	86	3	US-09-886-242A-4	Sequence 4, Appl1	867	270.5	45.9	102	5	US-10-811-328-32	Sequence 32, Appl
795	455	77.2	86	3	US-10-027-603-4	Sequence 4, Appl1	868	270.5	45.9	102	5	US-10-680-554-6	Sequence 6, Appl1
796	455	77.2	86	3	US-10-692-299-4	Sequence 4, Appl1	869	267.5	45.4	77	5	US-10-417-426-11	Sequence 11, Appl
797	455	77.2	86	3	US-10-016-481-5	Sequence 5, Appl1	870	267.5	45.4	77	5	US-10-680-554-13	Sequence 13, Appl
798	455	77.2	86	3	US-10-231-411-4	Sequence 4, Appl1	871	267.5	45.4	77	5	US-10-977-113-14	Sequence 14, Appl
799	455	77.2	86	3	US-10-212-355-2	Sequence 2, Appl1	872	267.5	45.4	77	5	US-10-871-152-24	Sequence 24, Appl

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875	265.5	45.1	102	5	US-10-871-152-21	Sequence 21, Appl
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877	251.5	42.7	100	5	US-10-871-152-19	Sequence 19, Appl
878	250.5	42.5	75	4	US-10-417-426-12	Sequence 12, Appl
879	250.5	42.5	75	5	US-10-977-113-13	Sequence 13, Appl
880	250.5	42.5	75	5	US-10-871-152-25	Sequence 25, Appl
881	250.5	42.5	75	6	US-11-073-420-13	Sequence 13, Appl
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884	109	18.5	23	4	US-10-680-800A-9	Sequence 9, Appl
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886	107.5	18.3	173	4	US-10-287-971-30	Sequence 30, Appl
887	107.5	18.3	180	4	US-10-287-971-34	Sequence 34, Appl
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892	107.5	18.3	224	4	US-10-287-971-28	Sequence 28, Appl
893	107.5	18.3	224	4	US-10-408-765A-335	Sequence 335, Appl
894	107.5	18.3	224	5	US-10-819-054-5	Sequence 5, Appl
895	107.5	18.3	224	5	US-10-998-271-14	Sequence 14, Appl
896	107.5	18.3	224	6	US-11-255-790-5	Sequence 5, Appl
897	107.5	18.3	344	4	US-10-201-310-3	Sequence 3, Appl
898	107.5	18.3	350	3	US-09-972-473-38	Sequence 38, Appl
899	107.5	18.3	350	3	US-09-972-473-38	Sequence 38, Appl
900	107.5	18.3	350	5	US-10-819-054-38	Sequence 38, Appl
901	107.5	18.3	350	6	US-11-255-790-38	Sequence 38, Appl
902	105.5	17.9	223	6	US-10-271-628-4	Sequence 4, Appl
903	105.5	17.9	223	6	US-11-056-562-4	Sequence 4, Appl
904	102	17.3	179	3	US-09-972-473-11	Sequence 11, Appl
905	102	17.3	179	3	US-09-972-473-11	Sequence 11, Appl
906	102	17.3	179	4	US-10-351-275-6	Sequence 6, Appl
907	102	17.3	179	5	US-10-819-054-11	Sequence 11, Appl
908	102	17.3	179	6	US-11-255-790-11	Sequence 11, Appl
909	102	17.3	207	3	US-09-976-736-13	Sequence 13, Appl
910	102	17.3	207	5	US-10-898-271-13	Sequence 13, Appl
911	102	17.3	259	3	US-09-976-736-12	Sequence 12, Appl
1356	102	17.3	259	4	US-10-271-628-2	Sequence 2, Appl
1408	102	17.3	259	4	US-10-174-587-250	Sequence 250, Appl
1448	102	17.3	259	4	US-10-013-909A-70	Sequence 70, Appl
1487	102	17.3	259	4	US-10-295-027-679	Sequence 679, Appl
1490	102	17.3	259	4	US-10-351-275-4	Sequence 4, Appl

Search completed: December 14, 2006, 14:36:52
Job time : 162.034 secs

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OM protein - protein search, using sw model

Run on: December 14, 2006, 14:06:11, Search time 26.9372 Seconds
(without alignments)
375.049 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLVTVSDCA.....CSRFPDGRVRCMSMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 80:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.5	17.1	350	2 JC7188	RRIC protein - hum
2	88.5	15.0	640	2 T08179	LRG5 protein - Chl
3	83	14.1	1101	2 T16840	hypothetical prote
4	81	13.8	1964	2 T09059	notch4 - mouse
5	79	13.4	112	1 XLHU	colipase precursor
6	77.5	13.2	473	2 A56175	adhesive plaque pr
7	77	13.1	251	2 A55035	cysteine-rich prot
8	75.5	12.8	1574	2 T13954	MEGF6 protein - ra
9	75	12.7	734	2 JC4861	fertilin beta cha
10	75	12.7	2318	2 S45306	notch 3 protein -
11	75	12.7	2531	2 T31070	notch homolog - se
12	74	12.6	112	2 I51909	colipase precursor
13	74	12.6	1620	2 T27283	hypothetical prote
14	73	12.4	461	2 A53556	tumor necrosis fac
15	73	12.4	3075	2 S14458	laminin alpha-1 ch
16	72.5	12.3	643	2 T25473	hypothetical prote
17	72.5	12.3	2871	2 A55567	fibrillin I - bovi
18	72.5	12.3	3002	2 A47221	fibrillin I precu
19	72	12.2	1639	1 MWFPB2	laminin gamma-1 ch
20	71.5	12.1	591	2 I48141	acroganin - guine
21	71.5	12.1	601	2 B36346	fibulin I precu
22	71.5	12.1	683	2 C36346	fibulin I precu
23	71.5	12.1	1178	1 A39804	thrombospondin pre
24	71.5	12.1	1854	2 T13576	hypothetical prote
25	71	12.1	286	2 S34665	collagen, cuticula
26	71	12.1	593	1 GYHU	granulin precursor
27	70.5	12.0	1847	2 T18308	probable vitellog
28	70.5	12.0	2871	2 A55624	fibrillin-1 precu
29	69.5	11.8	802	2 T24293	hypothetical prote

30	69.5	11.8	949	2 T24294	hypothetical prote
31	69.5	11.8	2352	2 T30201	Notch homolog prot
32	69.5	11.8	4545	1 S25111	alpha-2-macroglobu
33	69	11.7	2918	2 A54105	fibrillin-2 precu
34	69	11.7	3133	2 S52093	hemocytin - silkw
35	69	11.7	3712	2 S18253	laminin alpha-1 ch
36	68.5	11.6	728	2 I50719	C-Delta-1 - chicke
37	68.5	11.6	850	2 T14450	serine/threonine k
38	68.5	11.6	884	2 T18649	hypothetical prote
39	68.5	11.6	1172	2 A42587	thrombospondin 2 p
40	68.5	11.6	1376	2 G00043	osteonidogen - hum
41	68	11.5	112	2 A46717	colipase precursor
42	68	11.5	345	2 T25138	hypothetical prote
43	68	11.5	358	2 T25137	hypothetical prote
44	68	11.5	427	1 GQHUN	nerve growth facto
45	68	11.5	547	2 A33901	mannosyl-oligosacc
46	68	11.5	586	1 MWBEDE	65K early nonstruc
47	68	11.5	1119	2 A88481	protein C16A3.6 [i
48	68	11.5	1150	2 A41641	mannosyl-oligosacc
49	68	11.5	2215	2 T00348	LRI1 protein - mou
50	68	11.5	5147	1 IJPFMT	cadherin-related t
51	67.5	11.5	108	2 C88450	protein P21H1.4 [
52	67.5	11.5	895	2 T49010	hypothetical prote
53	67.5	11.5	1184	2 A55184	fibulin-2 precu
54	67.5	11.5	1469	2 B36665	slit protein 2 pre
55	67.5	11.5	1480	2 A36665	slit protein 1 pre
56	67.5	11.5	1687	2 T30176	EGF repeat transme
57	67	11.4	237	2 S45463	probable membrane
58	67	11.4	993	2 I48653	mouse developmenta
59	67	11.4	1172	1 TSHUP2	thrombospondin 2 p
60	67	11.4	1220	2 A56136	Jagged protein pre
61	67	11.4	1722	2 E89753	protein FilC7.4 [i
62	67	11.4	2321	2 S78549	notch3 protein - h
63	67	11.4	2437	2 S42612	transmembrane prot
64	67	11.4	2825	2 T14271	Doc4 protein, stre
65	67	11.4	2907	2 A57278	fibrillin-2 precu
66	66.5	11.3	589	2 C38128	epithelin/granulin
67	66.5	11.3	589	2 B38128	epithelin/granulin
68	66.5	11.3	1111	2 T26972	hypothetical prote
69	66.5	11.3	1221	2 A49457	fibulin-2 precu
70	66.5	11.3	3020	2 A49332	mucin 2 precursor,
71	66	11.2	1327	2 D70759	probable otss prot
72	66	11.2	1743	2 T26859	hypothetical prote
73	65.5	11.1	459	2 I48854	gene murine tumou
74	65.5	11.1	722	2 I48324	DELTA-like 1 - mou
75	65.5	11.1	2555	2 A40043	notch protein homo
76	65.5	11.1	3635	2 T10053	laminin alpha 5 ch
77	65	11.0	143	2 B21761	high cysteine chor
78	65	11.0	302	2 S65021	chitinase (EC 3.2.
79	65	11.0	328	2 S42152	urinary plasminoge
80	65	11.0	339	2 T07000	chitinase (EC 3.2.
81	65	11.0	329	2 T06999	chitinase (EC 3.2.
82	65	11.0	1295	2 A32901	glp1 protein precu
83	65	11.0	2139	2 A35672	crumbs protein - f
84	64.5	11.0	191	2 H71370	hypothetical prote
85	64.5	11.0	823	2 S18968	cyrtichestin precu
86	64.5	11.0	1790	1 MWFPB1	laminin beta-1 cha
87	64	10.9	117	2 H72706	hypothetical prote
88	64	10.9	130	1 KRSH3A	keratin high-sulfu
89	64	10.9	178	2 A23219	high-cysteine chor
90	64	10.9	217	2 A98196	hypothetical prote
91	64	10.9	225	2 A86043	probable transposa
92	64	10.9	325	2 B43692	T2 protein - rabbi
93	64	10.9	425	1 A26431	nerve growth facto
94	64	10.9	587	1 WMBETE	65K early nonstruc
95	64	10.9	723	2 PN0509	integrin beta-3 ch
96	64	10.9	1143	2 T22952	hypothetical prote
97	64	10.9	1984	2 T13171	probable vitellog
98	63.5	10.8	682	2 A69170	UDP-N-acetylmuram
99	63.5	10.8	782	2 A61625	tenascin-like prot
100	63.5	10.8	905	2 T23229	hypothetical prote
101	63.5	10.8	3707	2 S18252	heparan sulfate pr
102	63.5	10.8	5376	2 T42215	zonadhesin - mouse

103	63	10.7	95	1	XLPG2	colipase II precu	176	60	10.2	351	2	S20078	NOV protein - chic
104	63	10.7	350	2	T37511	probable phosphopr	177	60	10.2	419	2	S41607	atrolysin A (EC 3.
105	63	10.7	369	1	B64921	conserved hypothet	178	60	10.2	419	2	A59414	metalloproteinase
106	63	10.7	369	2	A85771	hypothetical prote	179	60	10.2	589	2	T43210	fibulin-1D precurs
107	63	10.7	369	2	E90922	hypothetical prote	180	60	10.2	837	1	A29512	LDL receptor precu
108	63	10.7	689	2	T42760	fibulin, splice fo	181	60	10.2	869	1	JC4858	VLDL receptor prec
109	63	10.7	712	2	T42990	fibulin 1, splice	182	60	10.2	905	2	T02205	Lu-ECAM-1 protein
110	63	10.7	735	2	G02937	fibulin, splice fo	183	60	10.2	906	2	JE0237	apolipoprotein E r
111	62.5	10.6	308	2	JC7125	epidermal growth f	184	60	10.2	1142	2	T30272	hypothetical prote
112	62.5	10.6	360	2	AH2272	fructose-bisphosph	185	60	10.2	1203	2	A49175	Motch B protein -
113	62.5	10.6	645	2	T22178	hypothetical prote	186	60	10.2	1357	2	T16860	hypothetical prote
114	62.5	10.6	685	2	S78040	fibulin, splice fo	187	60	10.2	1547	2	JQ0096	hypothetical 176K
115	62.5	10.6	705	2	S34968	fibulin, splice fo	188	60	10.2	1607	2	T43212	insulin-like growt
116	62.5	10.6	895	1	IJXUCP	EP-cadherin precu	189	60	10.2	1680	2	A43434	furin (EC 3.4.21.7
117	62.5	10.6	907	2	T27317	hypothetical prote	190	59.5	10.1	128	2	S32936	sporulation initia
118	62.5	10.6	4135	2	T42629	hypothetical prote	191	59.5	10.1	186	2	T32656	hypothetical prote
119	62	10.5	92	1	S36658	tenascin-X - bovin	192	59.5	10.1	886	2	A57172	probable hormone r
120	62	10.5	491	2	T21421	proteinase inhibit	193	59.5	10.1	925	2	T37475	lipoprotein recept
121	62	10.5	988	2	S37627	hypothetical prote	194	59.5	10.1	952	2	T18900	disintegrin and me
122	62	10.5	1113	2	JE0315	protein-tyrosine k	195	59.5	10.1	1245	1	MMMSND	nidogen precursor
123	62	10.5	1170	1	TSHUP1	low-density lipopr	196	59.5	10.1	2823	2	F87908	protein T22A3.8 [i
124	62	10.5	1170	2	A40558	thrombospondin 1 p	197	59.5	10.1	2823	2	T23064	hypothetical prote
125	62	10.5	1522	2	H88380	thrombospondin 1 p	198	59.5	10.1	3102	2	T43291	laminin alpha chai
126	62	10.5	1523	2	T13953	protein T22P7.3 [i	199	59	10.0	96	2	SI4018	keratin high-sulfu
127	62	10.5	1599	2	T16210	MEGF5 protein - ra	200	59	10.0	131	1	KRSHA3	keratin high-sulfu
128	62	10.5	2195	2	T34264	hypothetical prote	201	59	10.0	132	1	KRGT3J	keratin heavy chain
129	61.5	10.4	83	2	T26545	hypothetical prote	202	59	10.0	141	2	S54236	agglutinin isolect
130	61.5	10.4	220	2	A95956	hypothetical prote	203	59	10.0	186	2	A28401	probable CCH-type
131	61.5	10.4	277	2	I37552	hypothetical prote	204	59	10.0	315	2	B84654	follistatin - Afri
132	61.5	10.4	322	1	S37144	OX40 homolog - hum	205	59	10.0	319	2	A53502	follistatin - Afri
133	61.5	10.4	373	2	T34126	chitinase (EC 3.2.	206	59	10.0	474	2	B38634	tumor necrosis fac
134	61.5	10.4	1373	2	JE0095	hypothetical prote	207	59	10.0	616	2	T29234	hypothetical prote
135	61.5	10.4	2150	2	T32497	gastric mucin MUC5	208	59	10.0	670	2	T49510	fibroin-3 related
136	61.5	10.4	2471	2	A49128	hypothetical prote	209	59	10.0	737	2	PQ0219	RNA-2 polypeptide
137	61.5	10.4	2946	2	T15940	cell-fate determin	210	59	10.0	930	2	T34334	hypothetical prote
138	61.5	10.4	4006	2	T09070	probable tenascin	211	59	10.0	1106	2	T18739	hypothetical prote
139	61	10.4	93	2	JE0159	Gibberellin-stimul	212	59	10.0	1170	2	A53612	laminin B1k chain
140	61	10.4	95	2	S53510	pancreatic colipase	213	59	10.0	1360	2	P96596	hypothetical prote
141	61	10.4	95	2	T42112	hypothetical prote	214	59	10.0	1408	2	S16148	gene serrate prote
142	61	10.4	111	2	I48204	colipase - nutria	215	59	10.0	1429	2	S06434	nudel protein prec
143	61	10.4	269	2	T26957	hypothetical prote	216	59	10.0	2616	2	A57096	laminin alpha-1 ch
144	61	10.4	283	2	B88597	protein Y47D3B.6 [217	59	10.0	3084	1	MMMSA	hypothetical prote
145	61	10.4	309	2	B86937	conserved hypothet	218	58.5	9.9	220	2	T21730	hypothetical prote
146	61	10.4	383	2	D88633	protein F56B3.2 [i	219	58.5	9.9	236	2	T05695	pathogenesis-relat
147	61	10.4	451	2	T30603	perlecan homolog 2	220	58.5	9.9	287	1	S75925	DNA-formamidopyrim
148	61	10.4	593	1	S25062	triacylglycerol li	221	58.5	9.9	297	2	H69609	hypothetical prote
149	61	10.4	601	2	A27030	DIF-induced presta	222	58.5	9.9	316	2	S65020	chitinase (EC 3.2.
150	61	10.4	738	2	S40992	hypothetical prote	223	58.5	9.9	329	2	S08627	chitinase (EC 3.2.
151	61	10.4	739	2	B88553	protein K04H4.2b [224	58.5	9.9	358	2	T34128	hypothetical prote
152	61	10.4	1192	2	S69000	laminin gamma 2 ch	225	58.5	9.9	455	1	GQHUT1	tumor necrosis fac
153	61	10.4	1251	2	A57293	latent transformin	226	58.5	9.9	496	2	S51668	tyrosine kinase -
154	61	10.4	1955	1	AGCH	agrin precursor -	227	58.5	9.9	503	2	A49431	activin/TGF-beta-1
155	61	10.4	2476	2	T34022	zonadhesin - pig	228	58.5	9.9	601	2	D89711	protein F40E10.4 [
156	60.5	10.3	90	2	S69487	bombaxin B-7 precu	229	58.5	9.9	601	2	T22025	hypothetical prote
157	60.5	10.3	96	2	C86649	hypothetical prote	230	58.5	9.9	717	2	SI2100	hypothetical prote
158	60.5	10.3	99	2	S60231	gibberellin-regula	231	58.5	9.9	772	2	S32659	transferrin precu
159	60.5	10.3	129	2	A72606	hypothetical prote	232	58.5	9.9	962	1	TVBE14	integrin beta 2 ch
160	60.5	10.3	289	2	A84812	probable aquaporin	233	58.5	9.9	1193	2	A44018	106.6K protein kin
161	60.5	10.3	324	2	S20981	chitinase (EC 3.2.	234	58.5	9.9	1297	2	T30274	laminin B2t chain
162	60.5	10.3	349	2	A40551	connective tissue	235	58.5	9.9	1712	1	CGHU2B	proteoliasin - se
163	60.5	10.3	370	2	AE0289	conserved hypothet	236	58.5	9.9	1712	2	A38261	masking protein pr
164	60.5	10.3	385	2	S53718	homeotic protein d	237	58.5	9.9	3507	2	T34513	hypothetical prote
165	60.5	10.3	385	2	A54785	preadipocyte facto	238	58.5	9.9	3566	1	A40701	tenascin-X precurs
166	60.5	10.3	387	2	B49175	Motch A protein -	239	58.5	9.9	4391	2	A38096	antimicrobial pept
167	60.5	10.3	574	2	B88465	protein B0244.8 [i	240	58	9.8	46	2	A44794	probable ferredoxi
168	60.5	10.3	680	2	PN0510	integrin beta-3 ch	241	58	9.8	170	2	H83404	hypothetical prote
169	60.5	10.3	1104	2	I38869	transcription fact	242	58	9.8	234	2	T44731	4-amino-4-deoxycho
170	60.5	10.3	2531	2	A46019	notch-1 protein -	243	58	9.8	268	2	AF0195	hypothetical prote
171	60.5	10.3	2703	1	A24420	notch protein - fr	244	58	9.8	354	2	T22274	delta-like homeoti
172	60.5	10.3	4544	1	S02392	alpha-2-macroglobu	245	58	9.8	383	2	S53716	cartilage oligomer
173	60	10.2	102	2	S26409	protein 108 precu	246	58	9.8	755	2	A44315	hypothetical prote
174	60	10.2	233	2	S46639	hypothetical prote	247	58	9.8	798	2	T22793	hypothetical prote
175	60	10.2	263	2	T27641	hypothetical prote	248	58	9.8	891	2	H86306	F20223.20 protein

249	58	9.8	898	2	T14764	hypothetical prote	322	56.5	9.6	1622	2	JB0378	DNA (cytosine-5-) -
250	58	9.8	984	2	T00326	hypothetical prote	323	56.5	9.6	3623	2	T08618	intrinsic factor-B
251	58	9.8	1194	2	T03818	apoptotic proteina	324	56.5	9.6	4753	1	A47437	LDL-receptor-relat
252	58	9.8	1217	1	EGMSG	epidermal growth f	325	56	9.5	254	2	I48603	insulin-like growt
253	58	9.8	1292	2	T09329	galactose binding	326	56	9.5	264	2	T52104	GATA-binding trans
254	58	9.8	1311	2	T33757	hypothetical prote	327	56	9.5	265	2	H84867	probable endochiti
255	58	9.8	1428	2	T08852	hypothetical prote	328	56	9.5	320	2	T14624	hypothetical prote
256	58	9.8	1522	2	T00028	lustrin A - Califo	329	56	9.5	335	2	S03212	hypothetical prote
257	57.5	9.8	196	2	T26943	brain-specific ang	330	56	9.5	377	2	T52606	hypothetical prote
258	57.5	9.8	279	2	C70458	diaminopimelate ep	331	56	9.5	391	2	C86347	squamosa promoter -
259	57.5	9.8	306	2	S51361	folliculin-relate	332	56	9.5	434	1	A35005	r24J8.6 protein -
260	57.5	9.8	375	1	S66272	alcohol dehydrogen	333	56	9.5	442	1	UKPG	u-plasminogen acti
261	57.5	9.8	458	2	AF0631	probable 4-hydroxy	334	56	9.5	478	2	S47040	gene fts2 protein
262	57.5	9.8	568	2	F86291	hypothetical prote	335	56	9.5	491	2	S52920	disintegrin (EC 3.
263	57.5	9.8	686	2	S43562	K08E5.3 protein -	336	56	9.5	548	2	T16642	hypothetical prote
264	57.5	9.8	710	2	T46589	ropy-2 protein [im	337	56	9.5	801	2	T52605	squamosa promoter
265	57.5	9.8	810	2	T10756	Nel-homolog protei	338	56	9.5	849	1	T05181	S-receptor kinase
266	57.5	9.8	1036	2	T17405	scavenger receptor	339	56	9.5	894	1	A34372	complement C6 prec
267	57.5	9.8	1046	2	A26838	prestalk protein p	340	56	9.5	1136	1	S57845	protein-tyrosine k
268	57.5	9.8	1356	2	JC1402	protein-tyrosine k	341	56	9.5	1661	2	T43260	RNA polymerase (EC
269	57.5	9.8	1801	1	MMRTS	laminin beta-2 cha	342	56	9.5	1786	1	MMSB1	laminin beta-1 cha
270	57.5	9.8	1959	1	AGRT	agrin - rat	343	56	9.5	1797	2	A55677	laminin beta-2 cha
271	57.5	9.8	2265	1	FNBO	fibronectin - bovi	344	56	9.5	2531	2	T16743	hypothetical prote
272	57.5	9.8	2386	1	FNHU	fibronectin precu	345	56	9.5	3191	2	T22945	hypothetical prote
273	57.5	9.8	2481	2	A43908	fibronectin - Afri	346	55.5	9.4	99	2	S40012	fill protein - gar
274	57.5	9.8	2767	1	UIHU	thyroglobulin prec	347	55.5	9.4	106	2	A72581	hypothetical prote
275	57.5	9.8	4543	1	A53102	alpha-2-macroglobu	348	55.5	9.4	151	2	T20071	hypothetical prote
276	57	9.7	98	2	A75393	conserved hypothet	349	55.5	9.4	264	2	A84868	probable endochiti
277	57	9.7	153	2	A60585	thyroglobulin - sl	350	55.5	9.4	290	2	T21185	hypothetical prote
278	57	9.7	175	2	C82886	lactoylglutathione	351	55.5	9.4	291	1	JN0064	insulin-like growt
279	57	9.7	212	2	T05936	agglutinin isolect	352	55.5	9.4	292	2	C88072	protein ZK1240.8 [
280	57	9.7	250	1	A49053	CD27 antigen precu	353	55.5	9.4	309	2	T28708	hypothetical prote
281	57	9.7	268	1	G71271	probable ABC trans	354	55.5	9.4	416	1	JNR006	nerve growth facto
282	57	9.7	334	2	S20982	chitinase (EC 3.2.	355	55.5	9.4	471	1	KHRZOB	oryzain (EC 3.4.22
283	57	9.7	334	2	D70918	hypothetical prote	356	55.5	9.4	503	2	D70926	hypothetical prote
284	57	9.7	356	2	A25918	thrombomodulin - b	357	55.5	9.4	513	1	RGBYC6	cell division cont
285	57	9.7	414	2	T24563	hypothetical prote	358	55.5	9.4	569	2	T50711	urease (EC 3.5.1.5
286	57	9.7	468	2	T48686	hypothetical prote	359	55.5	9.4	580	2	A46538	lg heavy chain, se
287	57	9.7	513	2	D88991	protein apx-1 (imp	360	55.5	9.4	674	2	T15524	hypothetical prote
288	57	9.7	514	2	T10559	hypothetical prote	361	55.5	9.4	680	2	T39858	hypothetical prote
289	57	9.7	571	2	S24789	Jararagin C precu	362	55.5	9.4	685	2	JC7570	Delta-4 protein -
290	57	9.7	609	2	S55270	catrocollastatin p	363	55.5	9.4	775	2	A61228	collagen alpha 2(I
291	57	9.7	773	2	JQ2187	P87 protein - Card	364	55.5	9.4	788	2	A26547	platelet glycoprot
292	57	9.7	779	2	H71301	probable membrane-	365	55.5	9.4	1039	2	T14802	phytochrome B - so
293	57	9.7	917	2	JC7799	PARIS-1 protein -	366	55.5	9.4	1296	2	T16859	hypothetical prote
294	57	9.7	964	2	JC5545	integrin beta-4 pr	367	55.5	9.4	1746	1	S19694	tenascin precursor
295	57	9.7	1107	2	T15884	hypothetical prote	368	55.5	9.4	1786	1	MMRUB1	laminin beta-1 cha
296	57	9.7	1548	2	S34583	serine proteinase	369	55.5	9.4	2477	2	S14428	fibronectin precu
297	57	9.7	1820	2	A55494	latent transformin	370	55.5	9.4	3570	2	T45025	intrinsic factor-B
298	57	9.7	1875	2	A36429	integrin beta-4 ch	371	55.5	9.4	3623	2	T09456	mucin MUC5B, trach
299	56.5	9.6	113	2	S11532	colicin E1 immunit	372	55	9.3	163	1	H83499	ferredoxin protein
300	56.5	9.6	258	2	T32542	hypothetical prote	373	55	9.3	171	2	S66858	probable membrane
301	56.5	9.6	318	2	S65019	chitinase (EC 3.2.	374	55	9.3	226	2	A12564	hypothetical prote
302	56.5	9.6	409	2	A86240	protein F20B24.10	375	55	9.3	268	2	S25311	chitinase (EC 3.2.
303	56.5	9.6	443	2	T08905	hypothetical prote	376	55	9.3	269	2	S75243	hypothetical prote
304	56.5	9.6	446	2	T31644	hypothetical prote	377	55	9.3	305	2	A46476	B cell-associated
305	56.5	9.6	682	2	T12968	hypothetical prote	378	55	9.3	318	2	E87929	protein T22H2.6 [i
306	56.5	9.6	753	2	B36268	platelet glycoprot	379	55	9.3	323	2	A99211	hypothetical prote
307	56.5	9.6	778	2	A60798	platelet glycoprot	380	55	9.3	324	2	S56694	chitinase (EC 3.2.
308	56.5	9.6	788	2	I77349	platelet glycoprot	381	55	9.3	341	2	AE2445	hypothetical prote
309	56.5	9.6	938	2	I49071	protein kinase - m	382	55	9.3	343	2	S45321	folliculin - mous
310	56.5	9.6	948	2	S51605	receptor-like tyro	383	55	9.3	357	2	T32881	hypothetical prote
311	56.5	9.6	1106	2	T44598	gene shuttle craft	384	55	9.3	396	1	KXBOZ	plasma protein Z -
312	56.5	9.6	1106	2	T13938	hypothetical prote	385	55	9.3	416	2	T25101	hypothetical prote
313	56.5	9.6	1391	2	T24006	hypothetical prote	386	55	9.3	512	2	T06713	probable cytochrom
314	56.5	9.6	1458	2	A45665	adult-specific bru	387	55	9.3	531	2	B83422	probable serine/th
315	56.5	9.6	1490	2	JC5145	DNA (cytosine-5-) -	388	55	9.3	599	2	JC8009	choline dehydrogen
316	56.5	9.6	1495	2	S22610	DNA (cytosine-5-) -	389	55	9.3	748	2	S66129	disintegrin (EC 3.
317	56.5	9.6	1537	2	JC4172	DNA (cytosine-5-) -	390	55	9.3	850	2	S56015	gastric mucin MUC5
318	56.5	9.6	1557	2	T28811	hypothetical prote	391	55	9.3	853	2	B85429	beta-galactosidase
319	56.5	9.6	1572	2	T00027	brain-specific ang	392	55	9.3	863	1	S51789	VLDL receptor prec
320	56.5	9.6	1584	2	T22674	hypothetical prote	393	55	9.3	865	2	B69074	probable formate d
321	56.5	9.6	1612	2	JC5210	DNA (cytosine-5-) -	394	55	9.3	961	1	TSHUP4	thrombospondin 4 p

395	55	9.3	1038	2	I38935	bone morphogenetic	468	54	9.2	537	2	JC7127	frizzled protein 4
396	55	9.3	1038	2	JCS527	bone morphogenetic	469	54	9.2	558	2	TL7324	hypothetical prote
397	55	9.3	1064	2	A40136	fibropellin Ia - s	470	54	9.2	575	1	THRUB	thrombospondin pre
398	55	9.3	1133	1	EGRT	epidermal growth f	471	54	9.2	595	2	T39228	beta-transducin -
399	55	9.3	1207	1	EGHU	epidermal growth f	472	54	9.2	640	1	A30452	uromodulin precurs
400	55	9.3	1394	2	A35626	transforming growth	473	54	9.2	685	2	C56591	E75 B steroid rece
401	55	9.3	1531	2	T42218	glit-1 protein hom	474	54	9.2	732	2	JC4194	lanosterol synthas
402	55	9.3	1609	1	MMHUB2	laminin gamma-1 ch	475	54	9.2	737	2	S65758	nitrate reductase
403	55	9.3	1808	2	TL5099	hypothetical prote	476	54	9.2	756	2	S47656	tMDC 11 protein -
404	55	9.3	2129	2	I18290	FIVE finger-contai	477	54	9.2	769	1	IGHULM	leukocyte adhesion
405	55	9.3	3025	2	I52300	probable cell-surf	478	54	9.2	790	2	A39627	protein-tyrosine k
406	55	9.3	3229	1	S27852	giantin - human	479	54	9.2	793	2	JCS539	Smoothed protein
407	55	9.3	3229	1	A56539	giantin - human	480	54	9.2	794	2	F88508	protein H14A12.6 l
408	55	9.3	4660	2	T42737	gp330 protein prec	481	54	9.2	809	2	S55344	outer envelope mem
409	54.5	9.3	57	2	C46654	growth modulatory	482	54	9.2	838	2	T20125	hypothetical prote
410	54.5	9.3	63	2	S08572	chymotrypsin/elast	483	54	9.2	977	2	T00014	DAP-1-alpha protei
411	54.5	9.3	90	2	S69488	bombyxin B-7 precu	484	54	9.2	1052	2	B49120	protein-tyrosine k
412	54.5	9.3	92	2	D37057	epithelial cell gl	485	54	9.2	1364	2	T51920	probable xanthine
413	54.5	9.3	103	4	S59331	hypothetical prote	486	54	9.2	1364	2	T00250	MEG2 protein - hu
414	54.5	9.3	120	2	T31000	cysteine-rich prot	487	54	9.2	2524	2	A35844	Xotch protein - Af
415	54.5	9.3	131	1	KRG73M	keratin high-sulfu	488	54	9.2	2531	2	SL1818	notch protein homo
416	54.5	9.3	221	2	C34768	ORF2 protein - Orf	489	54	9.2	2652	1	VFIH2	genome polyprotein
417	54.5	9.3	226	2	JC4868	ribonuclease S2 (E	490	54	9.2	2813	1	VMHU	von Willebrand fac
418	54.5	9.3	243	2	T31144	hypothetical prote	491	54	9.2	3175	1	RRWVEV	genome polyprotein
419	54.5	9.3	248	2	T19913	hypothetical prote	492	54	9.2	4351	2	T00252	MEG1 protein - ra
420	54.5	9.3	289	2	A12128	Arp-binding protei	493	54	9.1	57	2	A46654	growth modulatory
421	54.5	9.3	306	2	S38251	folliculin-relate	494	54	9.1	96	2	S43910	Gibberellin-regula
422	54.5	9.3	310	2	A60967	insulin-like growt	495	53.5	9.1	109	2	S67091	probable membrane
423	54.5	9.3	317	2	I46916	insulin-like growt	496	53.5	9.1	125	2	S24831	hypothetical prote
424	54.5	9.3	318	2	S43317	chitinase (EC 3.2.	497	53.5	9.1	135	2	AH2100	hypothetical prote
425	54.5	9.3	386	2	S52035	probable alcohol d	498	53.5	9.1	202	1	A44247	C4b-binding protei
426	54.5	9.3	419	2	E71519	probable ATPase -	499	53.5	9.1	232	2	H69315	cytochrome-c3 hydr
427	54.5	9.3	442	2	JC4978	oxidative stress p	500	53.5	9.1	266	2	B72532	hypothetical prote
428	54.5	9.3	442	2	T40420	probable acid phos	501	53.5	9.1	273	2	F69199	conserved hypotet
429	54.5	9.3	462	2	T02538	hypothetical prote	502	53.5	9.1	280	2	T33519	hypothetical prote
430	54.5	9.3	530	2	C95334	TRM23a transposase	503	53.5	9.1	294	2	T23916	hypothetical prote
431	54.5	9.3	575	2	A49667	interleukin-10 rec	504	53.5	9.1	297	2	S06267	surface antigen H
432	54.5	9.3	644	2	A36325	epidermal growth f	505	53.5	9.1	314	2	T32985	hypothetical prote
433	54.5	9.3	711	2	S43464	ecdysteroid-induce	506	53.5	9.1	328	1	A41927	insulin-like growt
434	54.5	9.3	761	2	JCS759	brain-specific ser	507	53.5	9.1	346	2	JA0159	cysteine proteinas
435	54.5	9.3	788	2	I51530	integrin beta-3 su	508	53.5	9.1	354	2	A82850	fimbrial adhesin p
436	54.5	9.3	862	1	QRMSLD	LDL receptor precu	509	53.5	9.1	373	2	AH0693	conserved hypotet
437	54.5	9.3	941	1	A55195	chordin precursor	510	53.5	9.1	390	2	S46540	methionine adenosy
438	54.5	9.3	949	2	T44577	hypothetical prote	511	53.5	9.1	396	1	TRYXB4	alpha-lytic protei
439	54.5	9.3	955	2	A45441	thrombospondin 4 -	512	53.5	9.1	424	2	SL1676	spore coat protein
440	54.5	9.3	984	1	A34076	hypothetical prote	513	53.5	9.1	466	2	T06416	hypothetical prote
441	54.5	9.3	1143	2	T10636	protein-tyrosine k	514	53.5	9.1	473	2	C81984	hypothetical prote
442	54.5	9.3	1204	2	A96676	hypothetical prote	515	53.5	9.1	509	2	T02864	probable lipopolys
443	54.5	9.3	1237	2	A34598	ecdysone-induced p	516	53.5	9.1	584	2	I50419	probable Zn finger
444	54.5	9.3	1247	1	MMHUND	nidogen precursor	517	53.5	9.1	605	2	JCS673	s-glycerin precurs
445	54.5	9.3	1332	2	T23024	hypothetical prote	518	53.5	9.1	610	2	I48612	receptor tyrosine
446	54.5	9.3	1369	2	S70713	protein-tyrosine k	519	53.5	9.1	624	2	T00044	developmental kina
447	54.5	9.3	1386	2	T00257	hypothetical prote	520	53.5	9.1	626	2	I48614	developmental kina
448	54.5	9.3	1443	2	S05979	steroid hormone re	521	53.5	9.1	704	2	B84685	hypothetical prote
449	54.5	9.3	2647	2	A37098	gelation factor AB	522	53.5	9.1	753	2	G02173	semaphorin III fam
450	54.5	9.3	3051	2	S42373	hypothetical prote	523	53.5	9.1	768	2	B41029	integrin beta-8 ch
451	54.5	9.3	7962	2	I38346	elastic titin - hu	524	53.5	9.1	774	1	RRVETC	RNA-directed RNA p
452	54	9.2	132	1	TIHUSP	antileukoproteinas	525	53.5	9.1	792	2	T42963	hypothetical prote
453	54	9.2	148	2	G82223	pilB-related prote	526	53.5	9.1	957	2	TL5976	hypothetical prote
454	54	9.2	212	2	S09623	agglutinin isolect	527	53.5	9.1	977	2	JCS672	tyrosine kinase Mp
455	54	9.2	213	1	AEWT2	agglutinin isolect	528	53.5	9.1	998	2	JCS672	receptor tyrosine
456	54	9.2	216	2	JX0265	platelet aggregati	529	53.5	9.1	1124	1	I58388	protein-tyrosine k
457	54	9.2	229	2	T43325	hypothetical prote	530	53.5	9.1	1201	2	A57369	anillin - fruit fl
458	54	9.2	252	2	T46247	hypothetical prote	531	53.5	9.1	1328	2	T43060	agrin - electric r
459	54	9.2	287	2	A41257	apoptosis protein	532	53.5	9.1	1474	2	D88550	mucin 2, intestina
460	54	9.2	349	2	A85303	probable transcrip	533	53.5	9.1	1513	2	A54895	dominant autoantig
461	54	9.2	349	2	T04272	hypothetical prote	534	53.5	9.1	1650	2	S53457	189.6K hypotetica
462	54	9.2	415	2	T32467	hypothetical prote	535	53.5	9.1	1678	2	D86481	collagen alpha 2(I
463	54	9.2	424	2	T39524	hypothetical prote	536	53.5	9.1	1707	2	A33526	collagen type IV a
464	54	9.2	496	1	ALPGP	alpha-amylase (EC	537	53.5	9.1	1761	2	T13990	hypothetical prote
465	54	9.2	496	1	ALPGP	alpha-amylase (EC	538	53.5	9.1	2180	2	T29764	gamma-zeathionin 2
466	54	9.2	502	2	T20130	hypothetical prote	539	53	9.0	47	2	B58319	metallothionein A
467	54	9.2	534	2	A29677	complement C9 prec	540	53	9.0	64	2	A25775	

541	53	9.0	77	2	S29563	endothelin 2 precu	614	52.5	8.9	397	2	S26731	neuro-D4 protein -
542	53	9.0	141	2	T08790	hypothetical prote	615	52.5	8.9	403	2	T26326	hypothetical prote
543	53	9.0	156	2	T43957	hypothetical prote	616	52.5	8.9	407	1	KFB07	coagulation factor
544	53	9.0	177	2	B71682	probable ubiquinol	617	52.5	8.9	418	2	E90925	probable enzyme EC
545	53	9.0	240	2	A39842	insulin-like growt	618	52.5	8.9	418	2	A85774	probable enzyme EC
546	53	9.0	255	2	T38426	lymphocyte activat	619	52.5	8.9	418	2	B64924	hypothetical prote
547	53	9.0	272	1	G69587	L-arabinose operon	620	52.5	8.9	431	2	T37621	hypothetical prote
548	53	9.0	309	2	T22402	hypothetical prote	621	52.5	8.9	473	2	C81039	lipopolysaccharide
549	53	9.0	343	2	T49067	zinc finger protei	622	52.5	8.9	474	2	T27297	hypothetical prote
550	53	9.0	345	2	T34998	probable transmem	623	52.5	8.9	559	2	C85073	probable transposo
551	53	9.0	393	1	A48357	nonstructural prot	624	52.5	8.9	740	2	A71141	hypothetical prote
552	53	9.0	393	2	S40123	polygalacturonase	625	52.5	8.9	747	2	T39744	conserved hypothet
553	53	9.0	404	2	C86396	hypothetical prote	626	52.5	8.9	788	2	A37057	integrin beta-6 ch
554	53	9.0	413	2	T34123	hypothetical prote	627	52.5	8.9	826	2	A60385	monocyte surface a
555	53	9.0	429	2	T21113	hypothetical prote	628	52.5	8.9	873	1	A49729	VLDL receptor prec
556	53	9.0	460	2	B87455	DNA repair protein	629	52.5	8.9	898	2	S47489	receptor tyrosine
557	53	9.0	469	1	NMIV27	exo-alpha-sialidas	630	52.5	8.9	909	1	ORXL12	LDL receptor 2 pre
558	53	9.0	493	2	JC5486	membrane glycoprot	631	52.5	8.9	1106	2	T04015	hypothetical prote
559	53	9.0	524	2	S38539	disintegrin-like m	632	52.5	8.9	2027	2	S60123	hypothetical prote
560	53	9.0	527	2	S03974	amine oxidase (fla	633	52.5	8.9	2056	2	G88564	protein R10811.1 [
561	53	9.0	551	2	S51941	prunin 1 precursor	634	52	8.8	75	1	GSFF8	salivary glue prot
562	53	9.0	578	2	S50446	VAC8 protein - yea	635	52	8.8	90	2	B86560	9 kDa-Cysteine-ric
563	53	9.0	613	2	A88448	protein C45G9.6 [i	636	52	8.8	90	2	A72064	cysteine rich oute
564	53	9.0	636	2	H64429	DNA-directed RNA p	637	52	8.8	107	2	T49527	hypothetical prote
565	53	9.0	664	1	JX0336	succinate dehydrog	638	52	8.8	127	2	G84999	hypothetical prote
566	53	9.0	670	2	T65967	disintegrin-like m	639	52	8.8	181	1	MNXRRD	nonstructural prot
567	53	9.0	684	2	T39595	phospholipase C -	640	52	8.8	189	2	JC6064	RNA-binding protei
568	53	9.0	711	1	A47136	macrophage-stimula	641	52	8.8	191	2	T50306	hypothetical prote
569	53	9.0	725	2	T35114	probable kinase/ph	642	52	8.8	197	2	S56662	protease inhibit
570	53	9.0	861	2	A48825	Notch homolog Motc	643	52	8.8	213	1	D70416	phosphoglycolate p
571	53	9.0	874	2	B70914	probable dnab prot	644	52	8.8	221	2	G69420	hydrogenase expres
572	53	9.0	922	2	T23573	hypothetical prote	645	52	8.8	227	1	LNK2	lectin precursor -
573	53	9.0	1069	2	T42681	hypothetical prote	646	52	8.8	281	2	I39199	C2H2-150 - human
574	53	9.0	1168	2	I56985	kalinin B1 - mouse	647	52	8.8	317	2	AP2129	hypothetical prote
575	53	9.0	1354	2	T13363	phosphoribosylform	648	52	8.8	325	2	AI3096	protease import
576	53	9.0	1360	2	T33922	hypothetical prote	649	52	8.8	325	2	H98189	probable proteinase
577	53	9.0	1416	2	E88550	protein ZC84.1 [im	650	52	8.8	327	2	T09687	chitinase (EC 3.2.
578	53	9.0	1737	2	T00209	MEGF8 protein - hu	651	52	8.8	347	2	T32768	hypothetical prote
579	53	9.0	1748	1	JN0786	integrin beta-4 ch	652	52	8.8	348	1	S32484	L-iditol 2-dehydro
580	53	9.0	1798	2	S53869	laminin beta-2 cha	653	52	8.8	348	2	A40578	beta IG-M2 protein
581	53	9.0	1807	2	JC6319	integrin beta-4 ch	654	52	8.8	348	2	AF0295	conserved hypothte
582	53	9.0	2017	1	A36014	myosin heavy chain	655	52	8.8	393	2	D86168	hypothetical prote
583	53	9.0	2057	2	S61477	myosin II heavy ch	656	52	8.8	435	2	I54182	tumor necrosis fac
584	53	9.0	2262	2	T30890	calcium channel al	657	52	8.8	435	2	S40993	hypothetical prote
585	53	9.0	2844	2	S28291	hypothetical prote	658	52	8.8	456	1	KXBO	protein C (activat
586	53	9.0	3106	1	S53868	laminin alpha-2 ch	659	52	8.8	467	2	D86485	protein F28J9.13 [
587	53	9.0	4307	2	T20721	hypothetical prote	660	52	8.8	475	2	S54996	reverse transcript
588	52.5	8.9	70	2	A55824	drosomycin precurs	661	52	8.8	475	2	I53417	type I serine-thre
589	52.5	8.9	77	2	S47158	metallothionein II	662	52	8.8	505	2	T48811	hypothetical prote
590	52.5	8.9	99	2	S60230	gibberellin-regula	663	52	8.8	541	2	I49281	fertilin alpha pre
591	52.5	8.9	101	2	C35834	isocitrate dehydro	664	52	8.8	600	2	T16761	hypothetical prote
592	52.5	8.9	154	2	A86086	hypothetical prote	665	52	8.8	635	2	C81861	hypothetical prote
593	52.5	8.9	163	2	E91238	hypothetical prote	666	52	8.8	656	2	S49745	probable membrane
594	52.5	8.9	203	2	T02696	probable disease r	667	52	8.8	716	1	JC5061	macrophage-stimula
595	52.5	8.9	236	2	B98315	exsB protein [limp	668	52	8.8	736	2	S47645	TMDC I protein - c
596	52.5	8.9	236	2	A12967	succinoglycan bios	669	52	8.8	786	2	T31793	hypothetical prote
597	52.5	8.9	250	2	T01779	trypsin (EC 3.4.21	670	52	8.8	873	1	I48952	VLDL receptor prec
598	52.5	8.9	250	2	S31384	trypsin (EC 3.4.21	671	52	8.8	873	1	QRREVD	VLDL receptor prec
599	52.5	8.9	252	2	AB1030	probable membrane	672	52	8.8	883	2	H95953	probable bifunctio
600	52.5	8.9	253	2	T49971	hypothetical prote	673	52	8.8	909	1	QRXL11	LDL receptor 1 pre
601	52.5	8.9	255	2	T44991	oxidoreductase [im	674	52	8.8	961	2	A55380	faciogenital dyspl
602	52.5	8.9	261	2	S17889	class II histocomp	675	52	8.8	1162	2	T21557	hypothetical prote
603	52.5	8.9	278	2	H96611	hypothetical prote	676	52	8.8	1172	2	C70619	probable lyxX prot
604	52.5	8.9	280	2	D82017	hypothetical prote	677	52	8.8	1188	2	D86236	protein FL4N23.5 [
605	52.5	8.9	282	2	S50031	prostacyclin-stimu	678	52	8.8	1197	1	VGURF	M polyprotein - Ri
606	52.5	8.9	287	2	T09035	hypothetical prote	679	52	8.8	1299	2	T43251	furin (EC 3.4.21.7
607	52.5	8.9	288	2	D81002	conserved hypothet	680	52	8.8	1300	2	A36502	insulin receptor-r
608	52.5	8.9	349	2	S47093	hypothetical prote	681	52	8.8	1321	2	JE0352	mucin MUC5B, trach
609	52.5	8.9	362	2	G96735	probable proline-r	682	52	8.8	1358	1	XOCHDH	xanthine dehydroge
610	52.5	8.9	370	2	AE3479	alcohol dehydrogen	683	52	8.8	1435	2	T01075	polyprotein - hepa
611	52.5	8.9	372	2	A42778	agglutinin precurs	684	52	8.8	2451	1	A28372	insulin-like growt
612	52.5	8.9	375	1	S62640	alcohol dehydrogen	685	52	8.8	3672	2	T23433	hypothetical prote
613	52.5	8.9	387	2	T38449	extracellular prot	686	52	8.8	3704	2	T37316	probable laminin a

687	51.5	8.7	46	2	I48947	cellular disintegr	760	51	8.7	257	2	I38025	keratin-like prote
688	51.5	8.7	77	2	AF2564	hypothetical prote	761	51	8.7	259	1	IOHUL	insulin-like growt
689	51.5	8.7	87	2	JN0670	Na+-channel-blocki	762	51	8.7	260	2	S11562	probable MASH-1 pr
690	51.5	8.7	144	2	S54244	Ig mu heavy chain	763	51	8.7	261	2	S51678	chitinase (EC 3.2.
691	51.5	8.7	214	2	T51027	hypothetical prote	764	51	8.7	269	2	T36639	probable substrate
692	51.5	8.7	221	2	S59832	hypothetical prote	765	51	8.7	274	2	T18768	hypothetical prote
693	51.5	8.7	238	2	E85597	arginine 3rd trans	766	51	8.7	284	2	A28008	tropoin T, cardia
694	51.5	8.7	238	2	A90747	arginine 3rd trans	767	51	8.7	297	2	T45705	hypothetical prote
695	51.5	8.7	245	2	T49889	zinc finger transc	768	51	8.7	313	2	S44208	extracellular matr
696	51.5	8.7	251	2	G96006	probable SUR1-like	769	51	8.7	319	2	D97081	ketopantoate reduc
697	51.5	8.7	261	2	A55242	MHC class II histo	770	51	8.7	330	2	D87068	hypothetical prote
698	51.5	8.7	281	2	AE0671	N-hydroxyarylamine	771	51	8.7	332	2	T21458	hypothetical prote
699	51.5	8.7	281	2	A38090	N-hydroxyarylamine	772	51	8.7	342	2	A83263	dihydroorotate deh
700	51.5	8.7	282	2	A48516	surfactant protein	773	51	8.7	353	2	T27800	hypothetical prote
701	51.5	8.7	284	2	JC7686	activator of cAMP-	774	51	8.7	374	1	A53142	alcohol dehydrogen
702	51.5	8.7	323	2	T27450	hypothetical prote	775	51	8.7	374	1	S35669	alcohol dehydrogen
703	51.5	8.7	326	2	S14266	uracil-DNA glycosy	776	51	8.7	375	1	DEHOAL	probable FMN-depen
704	51.5	8.7	335	2	A39579	c-myc promoter-bin	777	51	8.7	381	2	H95288	cystathionine gamm
705	51.5	8.7	335	2	A39579	hypothetical prote	778	51	8.7	388	2	A82045	S-adenosylmethioni
706	51.5	8.7	394	2	T24860	hypothetical prote	779	51	8.7	394	2	AE2211	3-dehydroquinat s
707	51.5	8.7	410	2	T47926	hypothetical prote	780	51	8.7	394	2	AH1858	succinylornithine
708	51.5	8.7	414	2	H95843	hypothetical prote	781	51	8.7	406	2	D64934	acetylornithine de
709	51.5	8.7	451	2	T20798	hypothetical prote	782	51	8.7	406	2	B85784	acetylornithine de
710	51.5	8.7	480	1	A30065	trigamin precursor	783	51	8.7	406	2	F90935	copper transport p
711	51.5	8.7	485	2	S36772	E-selectin - bovin	784	51	8.7	406	2	A53010	hypothetical prote
712	51.5	8.7	488	2	T47697	Regulator of chrom	785	51	8.7	417	2	T45857	coagulation factor
713	51.5	8.7	497	2	T27012	hypothetical prote	786	51	8.7	452	1	A30351	polysialacturonase
714	51.5	8.7	518	2	T13120	hypothetical prote	787	51	8.7	460	2	T17011	activin A receptor
715	51.5	8.7	523	2	F71302	asparagine-tRNA li	788	51	8.7	505	2	I38859	hypothetical prote
716	51.5	8.7	523	2	T49386	hypothetical prote	789	51	8.7	525	2	T35084	hypothetical prote
717	51.5	8.7	585	2	S43572	COSB5.5 protein (c	790	51	8.7	560	1	JC4795	plasma hyaluronan-
718	51.5	8.7	591	2	T48596	protein COSB5.5 (i	791	51	8.7	560	2	D69587	Li-ribulokinase ara
719	51.5	8.7	592	2	T21536	ankyrin-like prote	792	51	8.7	573	2	JC4335	anti-mullerian hor
720	51.5	8.7	675	1	KXMS5	hypothetical prote	793	51	8.7	604	2	D71377	phenylalanine-tRNA
721	51.5	8.7	686	2	JC7569	Delta-4 protein -	794	51	8.7	651	2	JC7705	death receptor-6 -
722	51.5	8.7	719	2	T00266	hypothetical prote	795	51	8.7	735	2	S77385	nitrate reductase
723	51.5	8.7	730	2	E87451	isoquinoline l-oxi	796	51	8.7	735	2	A59434	dimethylamine dehy
724	51.5	8.7	740	2	A75011	hypothetical prote	797	51	8.7	736	2	S57961	protein C34G6.2 (i
725	51.5	8.7	765	2	T15447	hypothetical prote	798	51	8.7	751	2	F87789	von Willebrand fac
726	51.5	8.7	765	2	I48967	brain-specific kin	799	51	8.7	780	2	A34102	LDL receptor precu
727	51.5	8.7	899	2	G02428	subtilisin-like pr	800	51	8.7	854	1	QRHYLD	hypothetical prote
728	51.5	8.7	915	2	JC6148	subtilisin-like pr	801	51	8.7	915	2	T21773	hypothetical prote
729	51.5	8.7	962	2	JC5571	subtilisin-like pr	802	51	8.7	927	2	T21772	hypothetical prote
730	51.5	8.7	972	2	A30363	glycoprotein GP330	803	51	8.7	1345	2	B71608	DNA-directed RNA p
731	51.5	8.7	975	2	JC5570	subtilisin-like pr	804	51	8.7	1356	2	A45445	janusin precursor,
732	51.5	8.7	981	2	A41401	mineralocorticoid	805	51	8.7	1379	2	T37752	hypothetical serin
733	51.5	8.7	984	2	A29513	G9a protein - huma	806	51	8.7	1700	2	S08167	Balbani ring 3 pr
734	51.5	8.7	1001	2	S30385	sog protein - frui	807	51	8.7	2233	2	T28669	surface protease 51
735	51.5	8.7	1038	2	T13177	hypothetical prote	808	51	8.7	2254	2	T09053	low voltage-activa
736	51.5	8.7	1057	2	S09112	GRPase-activating	809	51	8.7	2415	1	A35086	aggreacan precursor
737	51.5	8.7	1165	2	S27809	polycomb protein e	810	51	8.7	3766	2	T29165	hypothetical prote
738	51.5	8.7	2023	2	T13154	G-cadherin - sea u	811	51	8.7	3766	2	T03099	mucin, submaxillar
739	51.5	8.7	2809	2	T30213	hypothetical prote	812	50.5	8.6	47	2	S69145	gamma-thionin Si-a
740	51.5	8.7	2895	2	H85362	hypothetical prote	813	50.5	8.6	62	2	I51538	metallothionein -
741	51.5	8.7	3512	2	T17121	CPY protein - midg	814	50.5	8.6	90	2	PC2137	hypothetical 90 pr
742	51	8.7	84	2	JN0469	85K MKK-20 recogni	815	50.5	8.6	90	2	PC2136	LiMi protein - tru
743	51	8.7	87	2	A39439	small cysteine-ric	816	50.5	8.6	118	2	S38491	Ig heavy chain - h
744	51	8.7	114	1	S22168	lipid transfer pro	817	50.5	8.6	122	2	T28977	hypothetical prote
745	51	8.7	120	2	JQ1740	hypothetical 12.7K	818	50.5	8.6	124	2	A21761	high-cysteine chor
746	51	8.7	137	2	T15609	hypothetical prote	819	50.5	8.6	144	2	A42585	trypsin inhibitor
747	51	8.7	142	2	A71097	hypothetical prote	820	50.5	8.6	151	2	T34245	hypothetical prote
748	51	8.7	146	2	D86419	hypothetical prote	821	50.5	8.6	153	1	XKPOC1	proteinase inhibit
749	51	8.7	150	2	D87652	hypothetical prote	822	50.5	8.6	154	2	E87530	isoquinoline l-oxi
750	51	8.7	168	2	T49250	zinc finger protei	823	50.5	8.6	185	2	T34807	probable transcrip
751	51	8.7	169	2	T03033	probable cytochrom	824	50.5	8.6	201	2	T07011	proteinase inhibit
752	51	8.7	187	2	H69956	5-formyltetrahydro	825	50.5	8.6	214	2	T19930	hypothetical prote
753	51	8.7	205	2	T27278	hypothetical prote	826	50.5	8.6	230	2	T34854	hypothetical prote
754	51	8.7	206	2	S18250	collagen alpha 1(I	827	50.5	8.6	237	2	D75027	dihydroorotate deh
755	51	8.7	216	2	S05575	sporozoite antigen	828	50.5	8.6	256	2	B32393	T-cell antigen 4-1
756	51	8.7	226	2	B71478	probable phosphogl	829	50.5	8.6	260	1	A46517	CD27 antigen precu
757	51	8.7	233	2	B69202	endonuclease III -	830	50.5	8.6	266	1	A35037	insulin-like growt
758	51	8.7	240	2	T47864	GATA transcription	831	50.5	8.6	267	2	F87665	hypothetical prote
759	51	8.7	253	2	T25768	hypothetical prote	832	50.5	8.6	272	2	H95314	probable transposa

833	50.5	8.6	283	2	T23785	hypothetical prote	906	50	8.5	298	2	T33046	hypothetical prote
834	50.5	8.6	284	2	T29715	hypothetical prote	907	50	8.5	302	1	TPCHTC	tropoin T, cardia
835	50.5	8.6	304	2	T30716	hypothetical prote	908	50	8.5	308	2	S51362	follietatin-relate
836	50.5	8.6	308	2	T37286	collagen 40 - Caen	909	50	8.5	334	2	H69076	hypothetical prote
837	50.5	8.6	316	2	H95293	probable cyclodeam	910	50	8.5	351	2	S50754	hypothetical prote
838	50.5	8.6	323	1	S5E2AC	cysteine synthase	911	50	8.5	353	2	D96596	hypothetical prote
839	50.5	8.6	323	2	F91039	cysteine synthase	912	50	8.5	359	2	T02833	threonine aldolase
840	50.5	8.6	323	2	A85884	cysteine synthase	913	50	8.5	372	2	AE3184	alcohol dehydrogen
841	50.5	8.6	324	2	T25154	hypothetical prote	914	50	8.5	384	2	T19513	hypothetical prote
842	50.5	8.6	346	2	A64448	hypothetical prote	915	50	8.5	385	2	T31493	hypothetical prote
843	50.5	8.6	376	2	D95370	probable oxidoredu	916	50	8.5	408	2	AB0710	succinylornithine
844	50.5	8.6	389	2	S73633	glutamate N-acetyl	917	50	8.5	424	2	S72695	L-aspartate oxidas
845	50.5	8.6	390	2	S49491	methionine adenosyl	918	50	8.5	425	2	D88115	protein F53C3.11 [
846	50.5	8.6	390	2	G84785	probable s-adenosyl	919	50	8.5	427	2	E84966	serine-tRNA ligase
847	50.5	8.6	398	2	A35281	integumentary muc	920	50	8.5	431	1	A39588	NADH2 dehydrogenas
848	50.5	8.6	428	2	S45361	LR847 protein - fr	921	50	8.5	449	2	B82802	conserved hypotet
849	50.5	8.6	473	2	H84550	probable obtusifol	922	50	8.5	450	2	T14352	WD-repeat protein
850	50.5	8.6	475	2	S54989	reverse transcript	923	50	8.5	459	2	D96833	hypothetical prote
851	50.5	8.6	475	2	S54993	reverse transcript	924	50	8.5	476	2	T01812	activin type I rec
852	50.5	8.6	475	2	S54994	reverse transcript	925	50	8.5	478	2	JQ1301	hemorrhagic protei
853	50.5	8.6	484	2	T25944	hypothetical prote	926	50	8.5	481	2	JC4342	fibrinolytic prote
854	50.5	8.6	538	2	E84863	hypothetical prote	927	50	8.5	481	2	S43125	trimucin precursor
855	50.5	8.6	559	1	CSHU	complement C9 prec	928	50	8.5	487	2	T80183	activin type I rec
856	50.5	8.6	603	2	JC5063	prostaglandin-endo	929	50	8.5	493	2	JC5621	epidermal growth f
857	50.5	8.6	604	2	F87936	protein M01G12.12	930	50	8.5	511	2	T34359	hypothetical prote
858	50.5	8.6	604	2	T23669	hypothetical prote	931	50	8.5	526	2	D71334	conserved hypotet
859	50.5	8.6	618	2	D71055	probable indolegry	932	50	8.5	541	2	T49108	pectinesterase lik
860	50.5	8.6	657	2	D71351	probable prinosoma	933	50	8.5	575	2	S35786	glycoprotein 9E -
861	50.5	8.6	758	2	S51748	lethal (2) denticiel	934	50	8.5	581	2	B54665	netrin-2 precursor
862	50.5	8.6	769	2	A41029	integrin beta-8 ch	935	50	8.5	610	2	S64126	cell division cont
863	50.5	8.6	812	2	A35206	glycosyl transfera	936	50	8.5	642	2	D69085	transcription cont
864	50.5	8.6	821	2	T02419	Mutator-like trans	937	50	8.5	647	2	T43952	hypothetical prote
865	50.5	8.6	855	2	JC7731	membrane-bound arg	938	50	8.5	665	1	A42792	succinate dehydrog
866	50.5	8.6	856	2	T24215	polycarb protein E	939	50	8.5	665	2	F71310	probable periplasm
867	50.5	8.6	898	2	T01503	hypothetical prote	940	50	8.5	669	2	T06702	hypothetical prote
868	50.5	8.6	951	2	T45726	hypothetical prote	941	50	8.5	686	2	B75267	prolyl endopeptida
869	50.5	8.6	955	2	S56649	pyruvate, phosphat	942	50	8.5	686	2	T25987	hypothetical prote
870	50.5	8.6	987	2	A54092	protein-tyrosine k	943	50	8.5	704	2	T03478	probable DNA-direc
871	50.5	8.6	1018	2	T19693	hypothetical prote	944	50	8.5	759	2	T44142	hypothetical prote
872	50.5	8.6	1019	1	A56318	enteropeptidase (E	945	50	8.5	775	2	S28284	DRI protein (impor
873	50.5	8.6	1045	2	S55253	sucrose-phosphate	946	50	8.5	780	2	T27941	hypothetical prote
874	50.5	8.6	1053	2	S46199	probable complemen	947	50	8.5	782	2	E88556	hypothetical prote
875	50.5	8.6	1087	2	S28282	hypothetical prote	948	50	8.5	887	2	S57430	protein B0464.5c [
876	50.5	8.6	1164	2	T06144	disease resistance	949	50	8.5	889	2	T23299	probable formate d
877	50.5	8.6	1193	2	A86193	hypothetical prote	950	50	8.5	916	2	G75417	hypothetical prote
878	50.5	8.6	1237	2	T46609	calcium-activated	951	50	8.5	1054	2	A61221	SNF2/Rad54 helicase
879	50.5	8.6	1384	2	T02748	hypothetical prote	952	50	8.5	1054	2	T30933	probable calcium t
880	50.5	8.6	1551	1	A43364	M polyprotein prec	953	50	8.5	1093	2	F88556	chitinase (EC 3.2.
881	50.5	8.6	1627	2	S65464	pregnancy-associat	954	50	8.5	1108	2	JC4037	alpha-mannosidase
882	50.5	8.6	2225	2	T26063	hypothetical prote	955	50	8.5	1113	2	S50613	hypothetical prote
883	50.5	8.6	2599	2	A96616	unknown protein F1	956	50	8.5	1206	1	VGVURV	M polyprotein - Ri
884	50	8.5	44	2	I48942	cellular disintegr	957	50	8.5	1210	2	A53183	epidermal growth f
885	50	8.5	87	2	JN0669	Na+-channel-blocki	958	50	8.5	1280	2	A39117	170K lectin precu
886	50	8.5	96	1	XLHOB	colipase B precurs	959	50	8.5	1391	2	S73652	RNA polymerase bet
887	50	8.5	98	2	S42596	hypothetical prote	960	50	8.5	1481	1	OZDOP3	pyrimidine synthe
888	50	8.5	98	2	AG3416	hypothetical prote	961	50	8.5	1613	2	J80272	low density lipopr
889	50	8.5	100	2	T17962	hypothetical prote	962	50	8.5	1661	2	T31330	head-activator bin
890	50	8.5	103	2	T25294	hypothetical prote	963	50	8.5	2120	2	T30243	alpha-tectorin - c
891	50	8.5	113	2	T07855	translation elonga	964	50	8.5	2499	1	A30788	mannose 6-phosphat
892	50	8.5	131	2	A37791	nifu protein (impo	965	50	8.5	2910	2	T42214	otocogelin - mouse
893	50	8.5	147	2	JC7237	receptor-activity-	966	50	8.5	3005	2	T08841	polyprotein - dour
894	50	8.5	176	2	T31796	hypothetical prote	967	49.5	8.4	61	2	C81079	hypothetical prote
895	50	8.5	193	2	PQ0503	surface protein -	968	49.5	8.4	73	2	E35982	trigramin gamma -
896	50	8.5	193	2	T16566	hypothetical prote	969	49.5	8.4	73	2	D35982	trigramin beta-2 -
897	50	8.5	204	2	T35410	probable DNA-bind	970	49.5	8.4	73	2	A23731	alobabrin - green
898	50	8.5	233	2	T471136	hypothetical prote	971	49.5	8.4	74	2	S05594	pseudothionin St1
899	50	8.5	239	1	Q4ECTD	hypothetical 26.3K	972	49.5	8.4	90	1	IPMTB1	bombyxin B-1 precu
900	50	8.5	249	2	E69546	conserved hypotet	973	49.5	8.4	90	1	IPMTB2	bombyxin B-2 precu
901	50	8.5	256	2	T06649	hypothetical prote	974	49.5	8.4	109	2	E84202	ferredoxin [impor
902	50	8.5	269	2	A81998	dihydrodipicolinat	975	49.5	8.4	118	2	T45791	non-specific lipid
903	50	8.5	282	1	YPD01	prestalk D11 prote	976	49.5	8.4	119	2	T07984	lipid transfer pro
904	50	8.5	288	2	S46536	chitinase (EC 3.2.	977	49.5	8.4	134	1	WYMS	whay acidic protei
905	50	8.5	297	2	T46590	probable regulator	978	49.5	8.4	138	2	A05215	hypothetical prote

979	49.5	8.4	142	2	S54243	Ig mu heavy chain	1052	49.5	8.4	1745	2	A46431	tight junction-ass
980	49.5	8.4	142	2	H72600	hypothetical prote	1053	49.5	8.4	2025	2	T03884	hypothetical prote
981	49.5	8.4	147	2	G83586	hypothetical prote	1054	49.5	8.4	2149	2	T47655	hypothetical prote
982	49.5	8.4	163	2	B83445	probable oxidoredu	1055	49.5	8.4	2156	1	RRVUNE	genome polypeptid
983	49.5	8.4	165	2	E95890	probable oxidoredu	1056	49.5	8.4	2406	2	A54148	odz protein - frui
984	49.5	8.4	170	2	T51042	hypothetical prote	1057	49.5	8.4	2515	2	S47008	tenascin-like prot
985	49.5	8.4	176	2	T48699	hypothetical prote	1058	49.5	8.4	3562	2	A47171	chondroitin sulfat
986	49.5	8.4	202	2	T24524	hypothetical prote	1059	49.5	8.4	63	2	A34905	metallothionein 1
987	49.5	8.4	208	2	C96348	deoxyphosphogluco	1060	49.5	8.4	65	2	S03858	carboxypeptidase A
988	49.5	8.4	213	2	E71212	hypothetical prote	1061	49.5	8.4	67	2	PC4008	hypothetical prote
989	49.5	8.4	246	2	E70556	probable respirato	1062	49.5	8.4	72	2	A42325	orf 5' to pheC - p
990	49.5	8.4	256	2	JC4627	fibroblast growth	1063	49.5	8.4	74	1	GSFF7	salivary glue prot
991	49.5	8.4	257	2	T50658	expansin 9 [import	1064	49.5	8.4	74	2	T24715	hypothetical prote
992	49.5	8.4	274	2	G84353	hypothetical prote	1065	49.5	8.4	93	2	S72363	pancreatic ribonuc
993	49.5	8.4	285	2	T06434	plasma membrane in	1066	49.5	8.4	96	2	B96701	protein FlA21.1 [
994	49.5	8.4	305	2	I48601	insulin-like growt	1067	49.5	8.4	116	2	H63338	hypothetical prote
995	49.5	8.4	320	2	G70866	anaerobic sulfite	1068	49.5	8.4	117	2	A24178	when acidic protei
996	49.5	8.4	357	2	C72022	UDP-N-acetylglucos	1069	49.5	8.4	127	1	NRBOK2	pancreatic-type ri
997	49.5	8.4	357	2	F86603	peptidoglycan tran	1070	49.5	8.4	131	2	H71651	iron-sulfur cofact
998	49.5	8.4	357	2	S72734	DNA-binding protei	1071	49.5	8.4	132	2	T20463	hypothetical prote
999	49.5	8.4	369	2	JN0450	conglutinin precu	1072	49.5	8.4	134	2	S54906	Ig heavy chain V r
1000	49.5	8.4	371	2	I45878	alcohol dehydrogen	1073	49.5	8.4	145	1	PSKF2U	phospholipase A2 (
1001	49.5	8.4	375	1	DEMGA	site-specific DNA-	1074	49.5	8.4	155	2	S59155	NADH2 dehydrogenas
1002	49.5	8.4	379	1	F64633	type II DNA modifi	1075	49.5	8.4	191	2	S09635	pABA protein - Ser
1003	49.5	8.4	381	2	A71882	hypothetical prote	1076	49.5	8.4	193	2	PQ0504	surface protein -
1004	49.5	8.4	397	2	T22332	probable FAD-link	1077	49.5	8.4	195	2	H70719	omega-conotoxin re
1005	49.5	8.4	408	2	H87193	transporter, proba	1078	49.5	8.4	203	2	H75434	hypothetical prote
1006	49.5	8.4	411	2	A87390	hypothetical prote	1079	49.5	8.4	213	2	I36929	ZNF80 homolog - gr
1007	49.5	8.4	416	2	T32458	3-oxoacyl-(acyl ca	1080	49.5	8.4	219	2	E82825	hypothetical prote
1008	49.5	8.4	420	2	AH2711	probable solute-bi	1081	49.5	8.4	221	2	T02923	probable oxalate o
1009	49.5	8.4	428	2	AF0302	probable solute-bi	1082	49.5	8.4	239	2	F83366	conserved hypotet
1010	49.5	8.4	442	2	F97493	probable cytochrom	1083	49.5	8.4	247	2	S13813	trypsin (EC 3.4.21
1011	49.5	8.4	483	2	T06712	probable cytochrom	1084	49.5	8.4	295	2	T04483	probable ring fing
1012	49.5	8.4	490	2	T06711	tumor necrosis fac	1085	49.5	8.4	300	2	T43748	hypothetical prote
1013	49.5	8.4	501	2	S56163	amine oxidase (fla	1086	49.5	8.4	302	2	T26513	hypothetical prote
1014	49.5	8.4	526	2	JT0528	low density lipopr	1087	49.5	8.4	325	2	E95349	hypothetical prote
1015	49.5	8.4	527	2	JE0373	glucuronosyltransf	1088	49.5	8.4	358	2	T33484	hypothetical prote
1016	49.5	8.4	530	2	C47113	hypothetical prote	1089	49.5	8.4	375	1	A60004	matrix protein - m
1017	49.5	8.4	554	2	B85072	probable cytosolic	1090	49.5	8.4	375	2	MFNZMS	fibromodulin precu
1018	49.5	8.4	573	2	H96744	MYB-related transc	1091	49.5	8.4	375	2	S05390	45K WW domain-cont
1019	49.5	8.4	608	2	T02684	uromodulin precurs	1092	49.5	8.4	386	2	JC7508	oligogalacturonid
1020	49.5	8.4	642	1	S52111	P-selectin precurs	1093	49.5	8.4	388	2	QJ0189	Runt domain contai
1021	49.5	8.4	646	2	JN0473	probable CHP-rich	1094	49.5	8.4	415	2	S60078	hypothetical prote
1022	49.5	8.4	651	2	F85024	hypothetical prote	1095	49.5	8.4	430	2	T46317	surface antigen se
1023	49.5	8.4	661	2	T42754	adhesion-type prot	1096	49.5	8.4	439	2	A36385	hypothetical prote
1024	49.5	8.4	679	2	A40351	Kallmann syndrome	1097	49.5	8.4	453	2	T01114	glucokinase (EC 2.7
1025	49.5	8.4	680	2	S17982	protein MEDEA [imp	1098	49.5	8.4	465	2	I49693	hexokinase (EC 2.7
1026	49.5	8.4	689	2	T52060	NADH2 dehydrogenas	1099	49.5	8.4	465	2	A31810	neurexin I-beta pr
1027	49.5	8.4	741	2	T13042	NADH2 dehydrogenas	1100	49.5	8.4	468	2	B40228	cationic amino aci
1028	49.5	8.4	741	2	T13658	NADH2 dehydrogenas	1101	49.5	8.4	469	2	G86638	membrane-bound rib
1029	49.5	8.4	744	2	T13757	probable protein k	1102	49.5	8.4	476	2	A44170	probable cytochrom
1030	49.5	8.4	756	2	S60966	ribonucleoside-dip	1103	49.5	8.4	490	2	T08714	hexokinase (EC 2.7
1031	49.5	8.4	825	2	S55060	probable beta-gala	1104	49.5	8.4	498	2	S12061	hypothetical prote
1032	49.5	8.4	826	1	Q08B11	late expression fa	1105	49.5	8.4	500	2	H96570	nicotinic acetylch
1033	49.5	8.4	853	2	T04600	receptor-like tyro	1106	49.5	8.4	524	2	JH0174	probable aminopept
1034	49.5	8.4	874	2	T30398	fertilin alpha-I -	1107	49.5	8.4	530	2	T44889	probable transcript
1035	49.5	8.4	893	2	S51603	subtilisin-like pr	1108	49.5	8.4	525	2	T41663	importin alpha - t
1036	49.5	8.4	905	2	S55059	telencephalin prec	1109	49.5	8.4	527	2	T04329	60K cysteine-rich
1037	49.5	8.4	915	1	A48225	endopeptidase Clp	1110	49.5	8.4	556	1	S12602	60 kDa Cysteine-ri
1038	49.5	8.4	917	2	I48950	protein-tyrosine k	1111	49.5	8.4	556	2	E95289	conserved hypotet
1039	49.5	8.4	926	1	A35905	receptor tyrosine-t	1112	49.5	8.4	568	2	JC5629	mullerian-inhibiti
1040	49.5	8.4	988	2	I50611	receptor tyrosine-t	1113	49.5	8.4	586	2	D69250	RNAse L-inhibitor
1041	49.5	8.4	998	2	I58351	DNA-directed RNA p	1114	49.5	8.4	592	2	B83231	probable short-cha
1042	49.5	8.4	1005	2	S49015	DNA-directed RNA p	1115	49.5	8.4	593	2	A35281	coagulation factor
1043	49.5	8.4	1188	2	T05846	hypothetical prote	1116	49.5	8.4	603	2	A38630	prostaglandin-endo
1044	49.5	8.4	1191	2	S65068	structural polypro	1117	49.5	8.4	606	2	A54665	netrin-1 precursor
1045	49.5	8.4	1221	2	T23472	protein-tyrosine k	1118	49.5	8.4	616	2	A55796	ecarin precursor -
1046	49.5	8.4	1255	1	B44213	hypothetical prote	1119	49.5	8.4	642	2	S53433	plasma protein S p
1047	49.5	8.4	1367	2	A41228	hypothetical prote	1120	49.5	8.4	658	2	A86231	hypothetical prote
1048	49.5	8.4	1372	2	T25933	laminin gamma-1 ch	1121	49.5	8.4	663	1	A38283	arachidonase 12-li
1049	49.5	8.4	1607	1	MMMSB2	hypothetical prote	1122	49.5	8.4	682	2	B86336	hypothetical prote
1050	49.5	8.4	1614	2	T29861	WD-40 repeat prote	1123	49.5	8.4	686	2	G87446	potassium-transpor
1051	49.5	8.4	1711	2	AD1842		1124	49.5	8.4				

1125	49	8.3	687	2	T49226	hypothetical prote	1198	48.5	8.2	232	2	A41551	vascular endotheli
1126	49	8.3	699	2	T12170	NADH2 dehydrogenas	1199	48.5	8.2	237	2	S08073	cyclic nucleotide
1127	49	8.3	700	2	T06088	hypothetical prote	1200	48.5	8.2	250	2	S08073	biotin protein lig
1128	49	8.3	725	2	JC2222	major surface glyco	1201	48.5	8.2	250	2	T30124	hypothetical prote
1129	49	8.3	727	2	E84847	probable CCH-type	1202	48.5	8.2	257	2	D71544	hypothetical prote
1130	49	8.3	736	2	A99279	hypothetical prote	1203	48.5	8.2	281	2	T09124	probable aquaporin
1131	49	8.3	739	2	H85245	vfl like protein (1204	48.5	8.2	289	2	JC7279	down syndrome crit
1132	49	8.3	739	2	T05163	hypothetical prote	1205	48.5	8.2	291	2	AF0740	probable cation tr
1133	49	8.3	754	2	AH3004	vgrg protein (impo	1206	48.5	8.2	298	2	T27644	hypothetical prote
1134	49	8.3	786	2	T02729	serine/threonine-s	1207	48.5	8.2	304	2	A33274	insulin-like growt
1135	49	8.3	790	2	H71509	phenylalanine-tRNA	1208	48.5	8.2	305	2	JN0508	insulin-like growt
1136	49	8.3	798	2	E27079	fibronectin recept	1209	48.5	8.2	306	2	E97471	hypothetical prote
1137	49	8.3	814	2	T49207	receptor kinase-11	1210	48.5	8.2	307	2	F71294	hypothetical prote
1138	49	8.3	816	2	E98196	hypothetical prote	1211	48.5	8.2	317	2	A36066	trans-activator of
1139	49	8.3	816	2	AH3090	vgrg protein (impo	1212	48.5	8.2	317	2	D86070	regulator for metE
1140	49	8.3	875	2	F96027	probable maltoolig	1213	48.5	8.2	317	2	F91223	regulator for metE
1141	49	8.3	879	1	QRRTLD	LDL receptor precu	1214	48.5	8.2	320	2	S22450	3-oxoacyl-[acyl-ca
1142	49	8.3	910	2	A34721	androgen receptor	1215	48.5	8.2	320	2	A53119	cell adhesion glyco
1143	49	8.3	911	2	E34721	androgen receptor	1216	48.5	8.2	332	2	S03415	hypothetical prote
1144	49	8.3	925	2	JC2033	G protein-coupled	1217	48.5	8.2	346	2	T34129	hypothetical prote
1145	49	8.3	973	2	T01862	hypothetical prote	1218	48.5	8.2	350	2	S06758	glycerol-3-phospha
1146	49	8.3	976	2	A36355	protein-tyrosine k	1219	48.5	8.2	351	2	S72817	probable glycoprot
1147	49	8.3	1019	2	T13039	tyrosine kinase re	1220	48.5	8.2	352	2	JU0023	glycerol-3-phospha
1148	49	8.3	1042	2	T26644	hypothetical prote	1221	48.5	8.2	353	2	S06760	glycerol-3-phospha
1149	49	8.3	1081	2	T15692	hypothetical prote	1222	48.5	8.2	353	2	S31790	glycerol-3-phospha
1150	49	8.3	1115	2	S40241	G protein-coupled	1223	48.5	8.2	354	1	S04243	proteoglycan link
1151	49	8.3	1176	2	C26427	period clock prote	1224	48.5	8.2	355	1	LKCH	proteoglycan link
1152	49	8.3	1176	2	S40899	vps8 protein - yea	1225	48.5	8.2	357	2	S09267	ig alpha chain C r
1153	49	8.3	1260	1	TVRINU	protein-tyrosine k	1226	48.5	8.2	360	1	S06759	glycerol-3-phospha
1154	49	8.3	1343	2	T20718	hypothetical prote	1227	48.5	8.2	362	2	S21963	glycerol-3-phospha
1155	49	8.3	1353	1	JQ2168	E2 glycoprotein pr	1228	48.5	8.2	362	2	C71281	conserved hypothet
1156	49	8.3	1361	2	S29998	surface protein -	1229	48.5	8.2	363	2	S23137	glycerol-3-phospha
1157	49	8.3	1362	2	A37474	surface glycoprote	1230	48.5	8.2	369	2	T48612	hypothetical prote
1158	49	8.3	1363	1	VGIHQV	E2 glycoprotein pr	1231	48.5	8.2	372	2	S01028	lignin peroxidase
1159	49	8.3	1363	1	VGIHVA	E2 glycoprotein pr	1232	48.5	8.2	372	2	JT0402	lignin peroxidase
1160	49	8.3	1363	1	VGIHFL	E2 glycoprotein pr	1233	48.5	8.2	372	2	A32322	lignin peroxidase
1161	49	8.3	1363	1	VGIHLY	E2 glycoprotein pr	1234	48.5	8.2	375	1	S62638	alcohol dehydrogen
1162	49	8.3	1363	1	VGIHNM	E2 glycoprotein pr	1235	48.5	8.2	396	1	WZBE8	dutp diphosphatase
1163	49	8.3	1363	2	S44241	surface protein -	1236	48.5	8.2	397	2	D83311	conserved hypothet
1164	49	8.3	1363	2	S44240	surface protein -	1237	48.5	8.2	400	2	T46383	hypothetical prote
1165	49	8.3	1425	2	T30811	hepatocyte growth	1238	48.5	8.2	404	2	S75529	beta ketoacyl-acyl
1166	49	8.3	1516	2	T01055	hypothetical prote	1239	48.5	8.2	433	1	JN0560	u-plasminogen acti
1167	49	8.3	1526	2	T19473	hypothetical prote	1240	48.5	8.2	433	2	B82965	hypothetical prote
1168	49	8.3	1645	2	T31339	carbamoyl-phosphat	1241	48.5	8.2	448	2	S41725	integrase - Saccha
1169	49	8.3	1770	2	S56221	hypothetical prote	1242	48.5	8.2	455	2	S33033	hypothetical prote
1170	49	8.3	2019	1	JQ1322	tenascin precursor	1243	48.5	8.2	464	2	G83370	hydrogen cyanide s
1171	49	8.3	2155	2	T30197	alpha tectorin - m	1244	48.5	8.2	470	2	A12188	hypothetical prote
1172	49	8.3	2588	2	T14342	NSD1 protein - mou	1245	48.5	8.2	476	2	S57963	methyl Cpg binding
1173	49	8.3	3938	2	T42761	Bassoon protein -	1246	48.5	8.2	489	2	T06715	probable cytochrom
1174	49	8.3	4302	2	A38971	polycystic kidney	1247	48.5	8.2	498	2	H82679	two-component syst
1175	48.5	8.2	54	1	S23075	protein PMP-D1 - m	1248	48.5	8.2	504	2	T27914	hypothetical prote
1176	48.5	8.2	79	2	T06381	proteinase inhibit	1249	48.5	8.2	506	2	S37583	ret finger protei
1177	48.5	8.2	112	2	S54832	gip1 protein - gar	1250	48.5	8.2	513	1	TVHURF	polycycomb - Africa
1178	48.5	8.2	118	1	PSKFT2	phospholipase A2 (1251	48.5	8.2	521	2	I51693	hypothetical prote
1179	48.5	8.2	119	2	T14396	lipid transfer pro	1252	48.5	8.2	524	2	T23907	phytoene dehydroge
1180	48.5	8.2	120	2	PH1650	lg heavy chain V r	1253	48.5	8.2	543	2	G87635	hypothetical prote
1181	48.5	8.2	127	2	S24689	lg heavy chain V6	1254	48.5	8.2	577	2	T33227	hypothetical prote
1182	48.5	8.2	134	2	AH1877	hypothetical prote	1255	48.5	8.2	586	2	F85857	probable ATP-depen
1183	48.5	8.2	135	2	G83671	hypothetical prote	1256	48.5	8.2	586	2	D91013	probable ATP-depen
1184	48.5	8.2	144	2	C71252	hypothetical prote	1257	48.5	8.2	586	2	G64987	yejH protein - Esc
1185	48.5	8.2	150	2	T46301	hypothetical prote	1258	48.5	8.2	605	2	H69581	transcription acti
1186	48.5	8.2	151	2	T25047	hypothetical prote	1259	48.5	8.2	614	2	S42526	finger protein unk
1187	48.5	8.2	165	2	I39626	nicotine dehydroge	1260	48.5	8.2	634	1	S35574	transcription fact
1188	48.5	8.2	169	1	S18946	ultra high-sulfur	1261	48.5	8.2	640	2	T13346	hypothetical prote
1189	48.5	8.2	172	2	AD0570	fimbria-like prote	1262	48.5	8.2	642	2	S53434	plasma protein S p
1190	48.5	8.2	174	2	T15176	hypothetical prote	1263	48.5	8.2	668	1	Q0BEW1	UL52 protein - hum
1191	48.5	8.2	177	1	CYDFAA	alpha-crystallin c	1264	48.5	8.2	675	1	KXBOS	plasma protein S p
1192	48.5	8.2	188	2	F97428	hypothetical prote	1265	48.5	8.2	702	2	E72775	probable helicase
1193	48.5	8.2	190	2	S52130	vascular endotheli	1266	48.5	8.2	726	2	H82774	phage-related DNA
1194	48.5	8.2	203	2	S54800	nitrite hydratase	1267	48.5	8.2	772	2	T02805	chloride channel p
1195	48.5	8.2	203	2	S19714	nitrite hydratase	1268	48.5	8.2	786	2	AG2375	WD-40 repeat-prote
1196	48.5	8.2	207	2	C70856	hypothetical prote	1269	48.5	8.2	810	2	B30848	plasmid (EC 3.4.21
1197	48.5	8.2	207	2	B83523	hypothetical prote	1270	48.5	8.2	860	2	T39502	hypothetical prote

1271	48.5	8.2	932	2	T45894	hypothetical prote	1344	48	8.1	431	2	S56228	alpha-factor recep
1272	48.5	8.2	958	2	H84783	probable PRD-type	1345	48	8.1	442	2	S50062	cell wall glycopro
1273	48.5	8.2	982	2	B83021	Glutamate-ammonia-	1346	48	8.1	455	2	T32189	zinc finger protei
1274	48.5	8.2	1019	2	A38738	coagulation factor	1347	48	8.1	457	2	S20662	glycine receptor a
1275	48.5	8.2	1021	2	T05108	hypothetical prote	1348	48	8.1	482	2	G83490	probable outer mem
1276	48.5	8.2	1074	2	JC5928	semaphorin F precu	1349	48	8.1	487	1	LQBP34	DNA ligase (ATP) (
1277	48.5	8.2	1163	1	RWHU17	cell surface glyco	1350	48	8.1	487	2	S06464	DNA ligase (ATP) (
1278	48.5	8.2	1222	2	S40377	hypothetical prote	1351	48	8.1	487	2	C47080	copper resistance
1279	48.5	8.2	1490	2	S72351	nonstructural poly	1352	48	8.1	495	2	S32179	tniQ protein homol
1280	48.5	8.2	1506	2	T30886	integumentary muc	1353	48	8.1	506	2	S31720	coat protein - ara
1281	48.5	8.2	1508	2	E87696	glutamate synthase	1354	48	8.1	513	2	S28358	prespore vesicle p
1282	48.5	8.2	1895	2	T15881	hypothetical prote	1355	48	8.1	523	1	S61713	carboxypeptidase C
1283	48.5	8.2	1965	2	T33216	hypothetical prote	1356	48	8.1	537	2	A54424	acrosomal protein
1284	48.5	8.2	2182	2	T14320	calcineurin inhibi	1357	48	8.1	552	2	E70731	probable pitB prot
1285	48.5	8.2	2643	2	T29149	hypothetical prote	1358	48	8.1	561	2	E70610	hypothetical prote
1286	48.5	8.2	3005	1	GNVSTV	genome polyprotein	1359	48	8.1	575	2	S58647	vacuolar transport
1287	48	8.1	61	2	B23889	metallothionein 2	1360	48	8.1	580	2	D84772	probable sugar tra
1288	48	8.1	61	2	S00811	metallothionein II	1361	48	8.1	594	1	A46758	glutamate decarbox
1289	48	8.1	66	2	S59621	metallothionein is	1362	48	8.1	594	2	JC4065	glutamate decarbox
1290	48	8.1	67	2	B69830	hypothetical prote	1363	48	8.1	596	2	T04506	hypothetical prote
1291	48	8.1	68	2	S25775	testis-specific pr	1364	48	8.1	606	2	D85443	probable PPR-repea
1292	48	8.1	74	2	AF3436	hypothetical prote	1365	48	8.1	615	1	KFH012	coagulation factor
1293	48	8.1	107	1	WMBEL2	latency-related pr	1366	48	8.1	616	2	T32131	hypothetical prote
1294	48	8.1	108	2	T51146	ring-box protein 1	1367	48	8.1	621	2	I38467	low density lipopr
1295	48	8.1	117	2	T07645	pEAR1.1 protein h	1368	48	8.1	634	2	T02594	hypothetical prote
1296	48	8.1	131	1	ZYSMN	metalloproteinase	1369	48	8.1	648	2	T21467	hypothetical prote
1297	48	8.1	133	2	T20467	hypothetical prote	1370	48	8.1	651	2	A39372	potassium channel
1298	48	8.1	134	1	WTBO	seminal fluid prot	1371	48	8.1	652	2	T02001	hypothetical prote
1299	48	8.1	142	2	JC4272	pleiotrophic facto	1372	48	8.1	661	2	B96596	hypothetical prote
1300	48	8.1	147	2	T30616	hypothetical prote	1373	48	8.1	662	2	T32371	hypothetical prote
1301	48	8.1	147	2	JC7263	receptor activity	1374	48	8.1	690	2	G84638	hypothetical prote
1302	48	8.1	151	2	S12246	anther-specific pr	1375	48	8.1	698	2	T23469	hypothetical prote
1303	48	8.1	170	2	A64347	conserved hypothet	1376	48	8.1	706	2	T49899	zinc finger transc
1304	48	8.1	191	2	I46412	keratin KAP5.4 - s	1377	48	8.1	713	2	A35502	major surface-labe
1305	48	8.1	192	2	AF2851	hypothetical prote	1378	48	8.1	724	2	B71404	hypothetical prote
1306	48	8.1	192	2	T15218	hypothetical prote	1379	48	8.1	729	2	F97634	anthranilate synth
1307	48	8.1	201	2	T31492	hypothetical prote	1380	48	8.1	729	2	AH2857	anthranilate synth
1308	48	8.1	204	2	S63145	probable membrane	1381	48	8.1	739	2	T21431	hypothetical prote
1309	48	8.1	209	2	F95366	probable aldehyde	1382	48	8.1	748	2	S41050	fibroblast growth
1310	48	8.1	217	2	H85358	hypothetical prote	1383	48	8.1	750	2	S41051	chloride channel p
1311	48	8.1	229	2	D97628	ubiquinol-cytochro	1384	48	8.1	764	2	T07608	HF-1 regulatory el
1312	48	8.1	237	2	I47031	insulin-like growt	1385	48	8.1	780	2	A48143	phenylalanine-tRNA
1313	48	8.1	250	2	S30157	osmotin precursor	1386	48	8.1	786	2	A35466	progesterone recep
1314	48	8.1	251	2	B71298	hypothetical prote	1387	48	8.1	790	2	D81668	phenylalanine-tRNA
1315	48	8.1	260	2	T47391	hypothetical prote	1388	48	8.1	818	2	T32154	hypothetical prote
1316	48	8.1	268	2	B42424	chitinase (EC 3.2.	1389	48	8.1	822	2	T25866	hypothetical prote
1317	48	8.1	271	2	S12783	OX40 antigen precu	1390	48	8.1	824	2	T23923	hypothetical prote
1318	48	8.1	301	2	A81066	transcription regu	1391	48	8.1	834	2	S13442	hemocyanin type A
1319	48	8.1	302	2	T39146	hypothetical prote	1392	48	8.1	840	2	AG0526	penicillin-binding
1320	48	8.1	303	2	T46715	hypothetical prote	1393	48	8.1	860	1	ORHULD	LDL receptor precu
1321	48	8.1	321	1	LNH0ER	IgE Fc receptor II	1394	48	8.1	892	2	F87325	hypothetical prote
1322	48	8.1	332	2	T19150	hypothetical prote	1395	48	8.1	907	2	B75182	DNA-directed RNA p
1323	48	8.1	335	2	H75518	probable cytochrom	1396	48	8.1	923	2	A39596	progesterone recep
1324	48	8.1	336	2	B71366	probable phosphate	1397	48	8.1	923	2	I53280	progesterone recep
1325	48	8.1	338	2	T46981	hypothetical prote	1398	48	8.1	930	2	A25923	progesterone recep
1326	48	8.1	338	2	AD0241	probable dehydroge	1399	48	8.1	933	1	QRHUP	sensor protein Rcs
1327	48	8.1	338	2	AB1816	hypothetical prote	1400	48	8.1	948	2	AD0790	potassium channel
1328	48	8.1	342	2	T09355	hypothetical prote	1401	48	8.1	962	2	I53197	hypothetical prote
1329	48	8.1	344	2	I57698	follicstatin - rat	1402	48	8.1	965	2	S62935	potassium channel
1330	48	8.1	348	2	T28467	major envelope ant	1403	48	8.1	989	2	I48912	receptor-type prot
1331	48	8.1	348	2	C72154	ES1 protein - vari	1404	48	8.1	1013	2	I50615	hypothetical prote
1332	48	8.1	348	2	A34705	collagen - Caenorh	1405	48	8.1	1014	2	T24412	pol protein homolo
1333	48	8.1	356	2	C70398	hypothetical prote	1406	48	8.1	1068	2	T04112	hypothetical prote
1334	48	8.1	363	2	G82070	3-isopropylmalate	1407	48	8.1	1076	2	F96831	probable trehalose
1335	48	8.1	365	2	T33499	hypothetical prote	1408	48	8.1	1100	2	G83376	collagen, cornea-s
1336	48	8.1	367	2	T29752	hypothetical prote	1409	48	8.1	1146	2	A38587	E2 glycoprotein pr
1337	48	8.1	368	1	S74797	GTP-binding protei	1410	48	8.1	1173	1	VGIHHC	Ca2+-transporting
1338	48	8.1	369	2	S41971	3beta-hydroxy-Delt	1411	48	8.1	1173	2	S48877	hypothetical prote
1339	48	8.1	373	2	D71094	probable cofactor	1412	48	8.1	1352	2	G84473	serum albumin - se
1340	48	8.1	374	2	A95960	probable cytochrom	1413	48	8.1	1423	1	S27941	bullous pemphigoid
1341	48	8.1	390	2	S52036	probable alcohol d	1414	48	8.1	1433	2	A46053	collagen alpha 1(X
1342	48	8.1	414	2	AE0239	succinylornithine	1415	48	8.1	1532	2	A61262	hypothetical prote
1343	48	8.1	414	2	T46998	hypothetical prote	1416	48	8.1	1571	2	T00062	hypothetical prote

Db 488 CTAGRC---WM-----TCLPMWGGGTWPRPLMTP-----SRTACLPPTCCSRWLR 533
QY 90 -----PDGRYRCSM 98
Db 534 RWCGWAPGGRWRCSL 549
RESULT 3
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16840
R:Geisler, C.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.
A:Reference number: Z18588
A:Accession: T16840
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1101 <GEI>
A:Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:g1049339; PIDN:AAA52054.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 717/3
Query Match 14.1%; Score 83; DB 2; Length 1101;
Best Local Similarity 24.4%; Pred. No. 1.3;
Matches 32; Conservative 9; Mismatches 40; Indels 50; Gaps 6;
QY 13 LTVSPDCAVTGACRDVQCGAGTCCCAISLWLRG-----
Db 749 LMSVQRCAMGIG-CPGNGQCENGVCPPMPCSSGSIASSVCGMANSCTPIGYICEGRGCCL 807
QY 47 --LRMCTPLGR-----EGEGCHPG-----SHKVPPFRKRKHTCTCPCLNLLCS 87
Db 808 EPLFLCPNGGRASMRVCYRGACFPYGCCTPLGCGCLLSMEFVCPTRSNVAVQCSPNNVC- 866
QY 88 RPPDGRYRCSM 98
Db 867 --PSGA-SCTM 874
RESULT 4
T09059
notch4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09059
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Schmitt, J.
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09059
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1964 <ROW>
A:Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:g2564945;
C:Genetics:
A:Gene: notch4
A:Map position: 17
A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 671/3; 1729/1; 1761/3
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: receptor; signal transduction
F:514-545/Domain: EGF homology <EGF>
Query Match 13.8%; Score 81; DB 2; Length 1964;
Best Local Similarity 30.4%; Pred. No. 3.4;
Matches 24; Conservative 7; Mismatches 22; Indels 26; Gaps 5;

QY 26 CERDVQ-----CGAGTCCCAISLWLRGRLMC-TPLGREGECHPGSHKVPFRKRKHH 76
Db 188 CERDINECFLEPGCPQGTSCHTNL---GSYQCLCPVGQEGPQC-----KIRKG 233
QY 77 TCP---CLPNLLCSRFPDQ 92
Db 234 ACPPGSCLINGTCQLVPEG 252
RESULT 5
XLHU
collipase precursor [validated] - human
N:Alternate names: procollipase
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C:Accession: A42568; A33949; A03163
R:Sims, H.F.; Lowe, M.E.
Biochemistry 31, 7120-7125, 1992
A:Title: The human colipase gene: isolation, chromosomal location, and tissue-specific
A:Reference number: A42568; MUID:92353041; PMID:1643046
A:Accession: A42568
A:Molecule type: DNA
A:Residues: 1-112 <Sims>
A:Cross-references: UNIPROT:P04118; UNIPARC:UPI0000127E78; GB:M95529; NID:g180842; PIDN:AAA52054.1
A:Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBIN:110580)
R:Lowe, M.E.; Rosenblum, J.L.; McEwen, P.; Strauss, A.W.
Biochemistry 29, 823-828, 1990
A:Title: Cloning and characterization of the human colipase cDNA.
A:Reference number: A33949; MUID:90248429; PMID:2337598
A:Accession: A33949
A:Molecule type: mRNA
A:Residues: 1-112 <LOW>
A:Cross-references: UNIPARC:UPI0000127E78; GB:J02883; NID:g180885; PIDN:AAA52054.1; PIDN:AAA52054.1
A:Note: evidence of partial N-glycosylation, possibly at Asn-43
R:Sternby, B.; Engstrom, A.; Hellman, U.; Viher, A.M.; Sternby, N.H.; Borgstrom, B.
Biochim. Biophys. Acta 784, 75-80, 1984
A:Title: The primary sequence of human pancreatic colipase.
A:Reference number: A90652; MUID:84104937; PMID:6691986
A:Accession: A03163
A:Molecule type: protein
A:Residues: 23-108 <STE>
A:Cross-references: UNIPARC:UPI0000174141
A:Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 stoichiometric complex with the lipase, which are known to have an inhibitory effect on the enzyme activity.
C:Genetics:
A:Gene: GDB:CLPS
A:Cross-references: GDB:127277; OMIM:120105
A:Map position: 6pter-6p21.1
A:Introns: 28/3; 69/3
C:Superfamily: colipase
C:Keywords: lipid digestion; lipid hydrolysis; pancreas
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-22/Domain: amino-terminal propeptide #status predicted <APP>
F:23-108/Product: colipase #status experimental <MAT>
F:109-112/Domain: carboxyl-terminal propeptide #status predicted <CPP>
F:134-104,40-56,44-80,45-78,66-86/Disulfide bonds: #status predicted
F:69,72,75,76/Binding site: micellar substrate (Lys, Tyr, Tyr, Tyr) #status predicted
Query Match 13.4%; Score 79; DB 1; Length 112;
Best Local Similarity 28.4%; Pred. No. 0.48;
Matches 31; Conservative 9; Mismatches 45; Indels 24; Gaps 6;
QY 9 IMLLVTVSDCAVITG-----ACERDVQCGAGTCCCAISLWLRGRLMCTPLGRE 56
Db 5 LILLVALSVAVAAPGPRGIILNLENGELCMNSAOC-KSNCCQHSAL-GLARCTSMAGE 62
QY 57 GEGCHPGSHKVPFRKRKHTCTCPCLNLLCSRFPDGRYRCMDLKNINF 105
Db 63 NSEC---SVKTLV---GIYKPCBRGLTC-----EGDKTIVGSITNTNF 101
RESULT 6
A56175

adhesive plaque protein Mgf2 precursor - Mediterranean mussel
C:Species: Mytilus galloprovincialis (Mediterranean mussel)
C>Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A56175
R:Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Biol. Chem. 270, 6698-6701, 1995
A:Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth factor family
A:Reference number: A56175; MUID:95204464; PMID:7896812
A:Accession: A56175
A:Molecule type: mRNA
A:Residues: 1-473 <INO>
A:CROSS-references: UNIPROT:Q25464; UNIPARC:UPI000012AB7B; GB:D43794; NID:g602767; PIDN:
C:Keywords: duplication
F:1-17/Domain: signal sequence #status predicted <SIG>
F:137-419/Domain: EGF homology <EGF1>
F:429-460/Domain: EGF homology <EGF>
F:23,36,43,56,75,382,424,455,469,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #
Query Match 13.2%; Score 77.5; DB 2; Length 473;
Best Local Similarity 31.2%; Pred. No. 2.3;
Matches 24; Conservative 11; Mismatches 23; Indels 19; Gaps 7;
Qy 26 CERDVQCGAGTCCALISLWRLGLRMCTPLGREGECH-PSHKVPPFRKRKHHC--PCL 81
Db 117 CEKVV-CSPNCP-----KNGKCSPLGKTGYKTCGGYTGP---RCEVHACKPNPK 165
Qy 82 PNLLCSRPDGR--YRC 96
Db 166 NKGRCC--FPDGKTGYC 180
RESULT 7
A55035
Cysteine-rich protein CRP1 - earthworm (Enchytraeus buchholzi)
C:Species: Enchytraeus buchholzi
C>Date: 14-Nov-1994 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: A55035; S45034
R:Willuhn, J.; Schmitt-Wrede, H.P.; Greven, H.; Wunderlich, F.
J. Biol. Chem. 269, 24688-24691, 1994
A:Title: cDNA cloning of a cadmium-inducible mRNA encoding a novel cysteine-rich, non-me
A:Reference number: A55035; MUID:95014230; PMID:7929141
A:Accession: A55035
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-251 <WTL>
A:CROSS-references: UNIPROT:Q24774; UNIPARC:UPI000007D243; EMBL:X79344; NID:g488802; PID
C:Superfamily: ultra-high-sulfur keratin
Query Match 13.1%; Score 77; DB 2; Length 251;
Best Local Similarity 30.9%; Pred. No. 1.5;
Matches 25; Conservative 7; Mismatches 45; Indels 4; Gaps 3;
Qy 17 SDCAVITGACERDVQCGAGTCCALISLWRLGLRMCTPLGREGECHPGSHKVPFRKRKH 76
Db 77 SQCKCEKGECKKG--CKEG-CCAPKGVAGSCGCKGCKGCKGCKGCKGCKGCKGCKG 133
Qy 77 TCPCPLNLLCSRPDPGRYRCS 97
Db 134 DCPGSPCKCEK-GDCKVNC 153
RESULT 8
T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-33, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: T14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-1574 <NAX>
A:CROSS-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:g3449293;
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6
Query Match 12.8%; Score 75.5; DB 2; Length 1574;
Best Local Similarity 28.6%; Pred. No. 10;
Matches 24; Conservative 6; Mismatches 33; Indels 21; Gaps 4;
Qy 19 CAVITGAC-----ERDVQCGAGTCCALISLWRLGLRMCTPLGREGECHPGSHKVPFRKR 73
Db 755 CHRVTCGLCPGPKGTGDCGAD--CPBGRWGLGQEQICPACGHCASCPN----- 801
Qy 74 KHHTCPCLPNLLCSRPDPGRYRCS 97
Db 802 ETGTCCLCPGVGSRCD---TCS 822
RESULT 9
JC4861
fertilin beta chain - human
C:Species: Homo sapiens (man)
C>Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4861
R:Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A:Title: Molecular cloning of the human fertilin beta subunit.
A:Reference number: JC4861; MUID:96295488; PMID:8702389
A:Accession: JC4861
A:Molecule type: mRNA
A:Residues: 1-734 <GUP>
A:CROSS-references: UNIPROT:Q99965; UNIPARC:UPI0000161BD9; GB:U38805; NID:g4151118; PID
C:Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: glycoprotein; integrin binding; transmembrane protein
F:382-734/Product: fertilin beta chain #status predicted <NAT>
F:382-467/Domain: disintegrin homology <DIS>
F:448-450/Region: integrin binding #status predicted
F:686-708/Domain: transmembrane #status predicted <TM>
F:121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 12.7%; Score 75; DB 2; Length 734;
Best Local Similarity 28.8%; Pred. No. 6;
Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3;
Qy 15 TVSDCAVITGAC-----ERDVQCGAGTCCALISLWRLGLRMCTPLGREGECHPGSHK 66
Db 401 TEQDCALIGTCCDIATCRFKAGSNCAEGPCCECLFMSKERMCRP---SFEEC-----D 452
Qy 67 VPFRKRKHHTCP 79
Db 453 LPEYCNSSASCP 465
RESULT 10
S45306
notch 3 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S45306
R:Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A:Title: The novel Notch homolog mouse Notch 3 lacks specific epidermal growth factor
A:Reference number: S45306; MUID:95001556; PMID:7918097
A:Accession: S45306
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2318 <LAR>
A:CROSS-references: UNIPROT:Q61982; UNIPARC:UPI000002930C; EMBL:X74760; NID:g483580; PI
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:163-195/Domain: EGF homology <EGF1>

F;474-505/Domain: EGF homology <EGF>
F;854-885/Domain: EGF homology <EGF2>
F;1839-1871/Domain: ankyrin repeat homology <AN1>
F;1872-1904/Domain: ankyrin repeat homology <AN2>
F;1906-1938/Domain: ankyrin repeat homology <AN3>
F;1939-1971/Domain: ankyrin repeat homology <AN4>
F;1972-2004/Domain: ankyrin repeat homology <AN5>

Query Match 12.7%; Score 75; DB 2; Length 2318;
Best Local Similarity 28.1%; Pred. No. 16;
Matches 25; Conservative 5; Mismatches 25; Indels 34; Gaps 5;

QY 19 CAVITGACRDVOCGAGTCAISLWRLGRLMCTPLRGEGEC-----60
DB 1287 CERVARSC-RELQCPVGIPCOQT--ARGPRCACPPGLSGPSRVSRASPSGATNASCASA 1343
QY 61 ---HPGS---HKVPPFRKRKHHTCPCPLP 82
DB 1344 PCLHGSCPLVQSPVPPFR-----CVCAP 1366

RESULT 11

T31070
notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Accession: T31070
R;Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
A;Title: Identification and localization of a sea urchin Notch homologue: insights into
A;Reference number: 220966; MUID:97454256; PMID:9310331
A;Accession: T31070
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2531 <SHE>
A;Cross-references: UNIPARC:UPI000007E31C; EMBL:AF000634; NID:g2570350; PID:g2570351; PID:
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 12.7%; Score 75; DB 2; Length 2531;
Best Local Similarity 29.9%; Pred. No. 17;
Matches 23; Conservative 8; Mismatches 32; Indels 14; Gaps 5;

QY 22 ITGACRDVOCGAGTCAI--SLWRLGRLMCTPLRGEGECHPGSHKVPFRKRKHHTCP 79
DB 120 VDNVCKLEBPQCGGTGRLTSLWDYEC-ECTP-ANTGENCTDDNHCV-----SNP 168
QY 80 CLPNLLCSRPFDGGRYC 96
DB 169 CLNGAVCTSSSDG-YSC 184

RESULT 12

I51909
colipase precursor - rat
N;Alternate names: procolipase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I51909; A34623
R;Payne, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.
Am. J. Physiol. 266, G914-G921, 1994
A;Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA e
A;Reference number: I51909; MUID:94262799; PMID:8203536
A;Accession: I51909
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-112 <PAY>
A;Cross-references: UNIPROT:P17084; UNIPARC:UPI00000127E7C; GB:M58370; NID:g203504; PIDN:
R;Wicker, C.; Puigserver, A.
Biochem. Biophys. Res. Commun. 167, 130-136, 1990
A;Title: Rat pancreatic colipase mRNA: nucleotide sequence of a cDNA clone and nutrition
A;Reference number: A34623; MUID:90179738; PMID:2129524
A;Accession: A34623
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-17,'V',19-112 <WIC>
A;Cross-references: UNIPARC:UPI00001708E5; GB:M33333; NID:g203502; PIDN:AAA40943.1; PID:
C;Superfamily: colipase
C;Keywords: lipid digestion; lipid hydrolysis; pancreas
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-112/Product: colipase #status predicted <MAT>

Query Match 12.6%; Score 74; DB 2; Length 112;
Best Local Similarity 25.8%; Pred. No. 1.5;
Matches 24; Conservative 10; Mismatches 39; Indels 20; Gaps 4;

QY 6 RVSIMLLVTVSDCAVITG-----ACERDVOCGAGTCCCAISLWRLGRLMCTPL 53
DB 2 KVLVLLVTLVAVAAPGRGLFNLNLEDGETCVNSMQC-KSRCCQHDITL-GIARCTHK 59
QY 54 GREGECHPGSHKVPFRKRKHHTCPCPLNLLC 86
DB 60 AMENSECSPKTLGIYR-----CPCERGLTC 86

RESULT 13

T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27283
R;Ainscough, R.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20336
A;Accession: T27283
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1620 <WIL>
A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:g1542303; PIDN:CAB54471.1
A;Experimental source: clone Y64G10A
C;Genetics:
A;Gene: CESP:Y64G10A.f
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;

Query Match 12.6%; Score 74; DB 2; Length 1620;
Best Local Similarity 27.5%; Pred. No. 15;
Matches 22; Conservative 4; Mismatches 16; Indels 38; Gaps 4;

QY 16 VSDCAVITGACRDVOCGAG-----TCCAISLWRLGRLMCTPLRGEGECHPGSHKVP 68
DB 1114 VARCDHVTGEC---RCPAGWTGPDCTSC-----PLGRHGECC-----1148
QY 69 PFRKRKHHTCPCPLNLLCSR 88
DB 1149 -----RHSCQCSNGASCDR 1162

RESULT 14

A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.;
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: UNIPROT:P20333; UNIPARC:UPI000002FAEL; GB:M2315; NID:g189185; PIDN:
R;Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A;Reference number: A36475; MUID:91045991; PMID:2172983

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Qy 17 SDCA-----VITGACERD-----VQCAGTCCAIISWLRLRMCTPL-----GREGEE- 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 98 SRCSDDQVETQACTREQNRICTCRPGWYCALSK-QEGCRLCAPLKRCPGFGVARPGTET 156
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 60 -----CHPGSHKVPFRRKRKHTCTCLPNLLCS 87
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 157 SDVVKRCPAGT-----FSNTTSTDICRPHQICN 186
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RESULT 15
S14458
laminin alpha-1 chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S14458; S14663; A34961
R:Haaparanta, T.; Utito, J.; Ruoslahti, E.; Engvall, E.
Matrix 11, 151-160, 1991
A:Title: Molecular cloning of the cDNA encoding human laminin A chain.
A:Reference number: S14458; MUID:91333420; PMID:1714537
A:Accession: S14458
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3075 <HAA>
A:Cross-references: UNIPROT:P25391; UNIPARC:UPI000012E763
R:Nissinen, M.; Vuolteenaho, R.; Boot-Hanford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A:Title: Primary structure of the human laminin A chain. Limited expression in human ti
A:Reference number: S14663; MUID:91264789; PMID:2049067
A:Accession: S14663
A:Molecule type: mRNA
A:Residues: 1-227, 'FE', 230-251, 'MLP', 255-418, 'E', 420-518, 'L', 520-1022, 'V', 1024-1074, 'V',
A:Cross-references: UNIPARC:UPI000016AB84; EMBL:X38531; NID:G34225; PIDN:CAA41418.1; PI
R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 ch
A:Reference number: A34961; MUID:89280632; PMID:2733383
A:Accession: A34961
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'W', 2397-2745, 'L', 2747-3053, 'L', 3055-3072, 'PSP', <OLS>
A:Cross-references: UNIPARC:UPI0000177439
A:Note: the authors translated the codon AGA for residue 2692 as Pro
C:Genetics:
A:Gene: GDB:LAMAI; LAMA
A:Cross-references: GDB:120135; OMIM:150320
A:Map position: 18p11.32-18p11.22
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bo
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F:18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
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F:327-394/Domain: laminin-type EGF-like homology <LE2>
F:397-451/Domain: laminin-type EGF-like homology <LE3>
F:454-500/Domain: laminin-type EGF-like homology <LE4>
F:503-512/Domain: laminin-type EGF-like homology #status atypical <LE5>
F:517-708/Domain: IVb <DOM4>
F:709-1159/Domain: IIB <DOM3B>
F:709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>
F:742-788/Domain: laminin-type EGF-like homology <LE7>
F:791-846/Domain: laminin-type EGF-like homology <LE8>
F:849-899/Domain: laminin-type EGF-like homology <LE9>
F:902-948/Domain: laminin-type EGF-like homology <LE10>
F:951-995/Domain: laminin-type EGF-like homology <LE11>
F:998-1041/Domain: laminin-type EGF-like homology <LE12>
F:1044-1087/Domain: laminin-type EGF-like homology <LE13>
F:1090-1109/Domain: laminin-type EGF-like homology #status atypical <LE14>
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F/1160-1361/Domain: IYA <DO4A>
F/1362-1553/Domain: IIIa <DO3A>

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 14, 2006, 14:32:47 ; Search time 30.2356 Seconds
(without alignments)
336.193 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVISIMLLLVTSVDCAL.....CSRFPDGRYCRSMCLKINIF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 381649 seqs, 96809478 residues

Total number of hits satisfying chosen parameters: 381649

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	589	100.0	105	6	US-10-415-724-2
2	589	100.0	105	6	US-10-549-241-8
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5	589	100.0	105	7	US-11-265-762-64
6	588	99.8	105	7	US-11-304-129-22
7	588	99.8	105	7	US-11-371-354-56695
8	588	99.8	105	7	US-11-371-354-76648
9	521	88.5	105	6	US-10-549-241-10
10	498	84.6	86	6	US-10-415-724-3
11	498	84.6	86	6	US-10-542-664-1
12	498	84.6	86	7	US-11-304-129-21
13	498	84.6	86	7	US-11-048-649-9
14	498	84.6	86	7	US-11-384-222-7
15	498	84.6	87	6	US-10-415-724-18
16	498	84.6	89	6	US-10-415-724-15
17	497	84.4	86	6	US-10-542-664-2
18	497	84.4	86	6	US-11-304-129-20
19	494	83.9	85	6	US-10-415-724-16
20	478	81.2	86	6	US-10-415-724-17
21	455	77.2	86	7	US-11-048-649-10
22	413	70.1	86	6	US-10-415-724-14
23	413	70.1	86	7	US-11-048-649-21
24	376	63.8	81	6	US-10-415-724-13
25	376	63.8	81	7	US-11-048-649-20
26	315	53.5	80	7	US-11-304-129-34

27	315	53.5	80	7	US-11-048-649-13	Sequence 13, Appl
28	310.5	52.7	81	6	US-10-415-724-12	Sequence 12, Appl
29	303	51.4	108	6	US-10-415-724-5	Sequence 5, Appl
30	303	51.4	108	6	US-10-549-241-4	Sequence 4, Appl
31	303	51.4	108	7	US-11-384-222-4	Sequence 4, Appl
32	298	50.6	107	6	US-10-549-241-6	Sequence 6, Appl
33	298	50.6	107	6	US-11-384-222-6	Sequence 6, Appl
34	291	49.4	81	6	US-10-415-724-6	Sequence 6, Appl
35	291	49.4	81	6	US-10-542-664-3	Sequence 3, Appl
36	291	49.4	81	7	US-11-048-649-5	Sequence 5, Appl
37	287.5	48.8	96	6	US-10-415-724-11	Sequence 11, Appl
38	286	48.6	81	7	US-11-048-649-7	Sequence 7, Appl
39	282.5	48.0	129	6	US-10-549-241-2	Sequence 2, Appl
40	282.5	48.0	129	7	US-11-384-222-2	Sequence 2, Appl
41	267.5	45.4	77	7	US-11-048-649-11	Sequence 11, Appl
42	265.5	45.1	102	7	US-11-048-649-8	Sequence 8, Appl
43	251.5	42.7	100	7	US-11-048-649-6	Sequence 6, Appl
44	250.5	42.5	75	7	US-11-048-649-12	Sequence 12, Appl
47	102	17.3	259	7	US-11-090-997-1050	Sequence 1050, App
48	101	17.1	259	7	US-11-090-997-150	Sequence 150, App
49	101	17.1	272	7	US-11-197-665-4	Sequence 4, Appl
50	100.5	17.1	350	6	US-10-970-823-236	Sequence 236, App
51	100.5	17.1	350	7	US-11-101-316-8	Sequence 8, Appl
52	100.5	17.1	350	7	US-11-376-673-8	Sequence 8, Appl
53	100.5	17.1	350	7	US-11-339-733-6	Sequence 6, Appl
54	100.5	17.1	350	7	US-11-371-354-73637	Sequence 73637, A
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62	79	13.4	112	7	US-11-371-354-74885	Sequence 74885, A
63	78.5	13.3	1581	7	US-11-174-3078-906	Sequence 906, App
64	76.5	13.0	2762	7	US-11-174-3078-2676	Sequence 2676, Ap
65	76	12.9	14	6	US-10-415-724-19	Sequence 19, Appl
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67	75	12.7	579	7	US-11-371-354-70301	Sequence 70301, A
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69	75	12.7	734	7	US-11-238-282-19	Sequence 19, Appl
70	75	12.7	734	7	US-11-300-928-11	Sequence 11, Appl
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75	73	12.4	163	7	US-11-357-080-13	Sequence 13, Appl
76	73	12.4	172	6	US-10-449-902-48116	Sequence 48116, A
77	73	12.4	355	6	US-11-320-192-9	Sequence 9, Appl
78	73	12.4	355	6	US-10-504-973-33	Sequence 33, Appl
79	73	12.4	461	6	US-10-511-937-2945	Sequence 2945, Ap
80	73	12.4	461	6	US-10-533-519-730	Sequence 730, App
81	73	12.4	461	7	US-11-183-218-32	Sequence 32, Appl
82	73	12.4	461	7	US-11-416-310-6	Sequence 6, Appl
83	73	12.4	461	7	US-11-429-276-462	Sequence 462, App
84	73	12.4	461	7	US-11-429-276-467	Sequence 467, App
85	73	12.4	461	7	US-11-419-656-6	Sequence 6, Appl
86	73	12.4	461	7	US-11-371-354-67475	Sequence 67475, A
87	73	12.4	461	7	US-11-429-373-467	Sequence 462, App
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89	73	12.4	461	7	US-11-451-450-2	Sequence 246, App
90	73	12.4	844	7	US-11-429-276-246	Sequence 251, App
91	73	12.4	844	7	US-11-429-276-251	Sequence 246, App
92	73	12.4	844	7	US-11-429-373-246	Sequence 251, App
93	73	12.4	844	7	US-11-429-373-251	Sequence 1986, Ap
94	73	12.4	1170	7	US-11-174-3078-1988	Sequence 2004, Ap
95	73	12.4	3204	6	US-11-174-3078-2004	Sequence 2, Appl
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97	72.5	12.3	1391	7	US-11-174-3078-4782	Sequence 390, App
98	72.5	12.3	2871	6	US-10-574-398-390	Sequence 12, Appl
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101	71.5	12.1	683	7	US-11-371-354-55779	Sequence 1018, Ap
102	71.5	12.1	1176	7	US-11-090-997-1018	

103	71	12.1	438	7	US-11-371-354-69341	Sequence 69341, A	176	67	11.4	1379	7	US-11-174-307B-646	Sequence 646, App
104	71	12.1	593	6	US-10-564-751-8	Sequence 8, Appli	177	67	11.4	1418	7	US-11-217-997-38	Sequence 38, Appli
105	71	12.1	789	7	US-11-174-307B-818	Sequence 818, App	178	67	11.4	1450	7	US-11-217-997-6	Sequence 6, Appli
106	71	12.1	789	7	US-11-174-307B-1730	Sequence 1730, Ap	179	67	11.4	1861	7	US-11-174-307B-1744	Sequence 1744, Ap
107	71	12.1	1883	7	US-11-174-307B-708	Sequence 708, App	180	67	11.4	1873	7	US-11-174-307B-846	Sequence 846, App
108	70.5	12.0	2380	7	US-11-174-307B-1698	Sequence 1698, Ap	181	67	11.4	2000	6	US-10-533-519-674	Sequence 674, App
109	70	11.9	841	6	US-10-725-037-5	Sequence 5, Appli	182	67	11.4	2321	6	US-10-518-751-8	Sequence 8, Appli
110	70	11.9	841	6	US-10-725-488-5	Sequence 5, Appli	183	67	11.4	5738	6	US-10-505-928-150	Sequence 150, App
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112	70	11.9	1673	7	US-11-174-307B-1178	Sequence 1178, Ap	185	66.5	11.3	98	7	US-11-377-336-14	Sequence 14, Appli
113	70	11.9	2658	7	US-11-174-307B-2464	Sequence 2464, Ap	186	66.5	11.3	959	7	US-11-174-307B-5346	Sequence 5346, Ap
114	70	11.9	3250	7	US-11-174-307B-2262	Sequence 2262, Ap	187	66.5	11.3	1030	7	US-11-174-307B-2300	Sequence 2300, Ap
115	70	11.9	3682	7	US-11-174-307B-2486	Sequence 2486, Ap	188	66.5	11.3	1232	7	US-11-174-307B-2840	Sequence 2840, Ap
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117	69.5	11.8	1353	7	US-11-174-307B-66	Sequence 66, Appli	190	66.5	11.3	1289	7	US-11-174-307B-434	Sequence 434, App
118	69.5	11.8	4523	6	US-10-669-920-472	Sequence 472, App	191	66.5	11.3	1737	7	US-11-174-307B-2046	Sequence 2046, Ap
119	69	11.7	1131	7	US-11-174-307B-1604	Sequence 1604, Ap	192	66.5	11.3	3319	7	US-11-174-307B-692	Sequence 692, App
120	69	11.7	1189	6	US-10-540-844-4	Sequence 4, Appli	193	66.5	11.3	3398	6	US-10-547-530-47	Sequence 47, Appli
121	69	11.7	1345	6	US-11-174-307B-2248	Sequence 2248, Ap	194	66.5	11.3	5178	6	US-10-700-439-178	Sequence 178, App
122	69	11.7	1506	6	US-10-669-920-1144	Sequence 1144, Ap	195	66.5	11.3	5179	6	US-10-541-749-151	Sequence 151, App
123	69	11.7	1506	6	US-10-669-920-1153	Sequence 1153, Ap	196	66.5	11.3	5179	7	US-10-541-749-151	Sequence 185, App
124	69	11.7	1568	7	US-11-174-307B-2546	Sequence 2546, Ap	197	66	11.2	85	6	US-10-525-126-295	Sequence 295, App
125	69	11.7	1593	7	US-11-174-307B-2100	Sequence 2100, Ap	198	66	11.2	601	7	US-11-441-587-20	Sequence 20, Appli
126	69	11.7	2000	6	US-10-533-519-666	Sequence 666, App	199	66	11.2	1067	7	US-11-054-369A-5	Sequence 5, Appli
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128	69	11.7	2608	6	US-10-669-920-1155	Sequence 1155, Ap	201	66	11.2	1215	7	US-11-174-307B-2800	Sequence 2800, Ap
129	69	11.7	2902	6	US-10-669-920-1150	Sequence 1150, Ap	202	66	11.2	1220	7	US-11-174-307B-1044	Sequence 1044, Ap
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131	69	11.7	2904	6	US-10-669-920-1146	Sequence 1146, Ap	204	66	11.2	1238	7	US-11-071-796A-21	Sequence 21, Appli
132	69	11.7	2904	6	US-10-669-920-1148	Sequence 1148, Ap	205	66	11.2	1238	7	US-11-188-417A-22	Sequence 22, Appli
133	69	11.7	2904	6	US-10-669-920-1157	Sequence 1157, Ap	206	66	11.2	1238	7	US-11-231-494-22	Sequence 22, Appli
134	69	11.7	2904	6	US-10-669-920-1159	Sequence 1159, Ap	207	66	11.2	1263	7	US-11-174-307B-2848	Sequence 2848, Ap
135	68.5	11.6	729	7	US-11-175-714-8	Sequence 8, Appli	208	66	11.2	1269	7	US-11-174-307B-232	Sequence 232, App
136	68.5	11.6	850	7	US-11-330-403-16770	Sequence 16770, A	209	66	11.2	1296	7	US-11-174-307B-750	Sequence 750, App
137	68.5	11.6	909	6	US-10-449-902-44686	Sequence 44686, A	210	66	11.2	1419	7	US-11-174-307B-132	Sequence 132, App
138	68.5	11.6	969	7	US-11-371-354-66101	Sequence 66101, A	211	66	11.2	1489	7	US-11-174-307B-2422	Sequence 2422, Ap
139	68.5	11.6	1081	7	US-11-174-307B-308	Sequence 308, App	212	66	11.2	1490	7	US-11-174-307B-2534	Sequence 2534, Ap
140	68.5	11.6	3392	7	US-11-174-307B-1654	Sequence 1654, Ap	213	66	11.2	1491	7	US-11-174-307B-382	Sequence 382, App
141	68	11.5	159	7	US-11-357-080-16	Sequence 16, Appli	214	66	11.2	1492	7	US-11-174-307B-2094	Sequence 2094, Ap
142	68	11.5	250	7	US-11-320-192-7	Sequence 7, Appli	215	66	11.2	1509	7	US-11-174-307B-1838	Sequence 1838, Ap
143	68	11.5	250	7	US-11-320-192-10	Sequence 10, Appli	216	66	11.2	1510	7	US-11-174-307B-838	Sequence 838, App
144	68	11.5	427	7	US-11-332-680-9	Sequence 9, Appli	217	66	11.2	1511	7	US-11-174-307B-1120	Sequence 1120, Ap
145	68	11.5	427	7	US-11-332-680-12	Sequence 12, Appli	218	66	11.2	1527	7	US-11-174-307B-1326	Sequence 1326, Ap
146	68	11.5	427	7	US-11-416-310-7	Sequence 7, Appli	219	66	11.2	1686	7	US-11-174-307B-866	Sequence 866, App
147	68	11.5	427	7	US-11-365-989-180	Sequence 180, App	220	66	11.2	1713	7	US-11-174-307B-2224	Sequence 2224, Ap
148	68	11.5	427	7	US-11-419-656-7	Sequence 7, Appli	221	65.5	11.1	98	6	US-10-449-902-38997	Sequence 38997, A
149	68	11.5	491	7	US-11-217-997-30	Sequence 30, Appli	222	65.5	11.1	166	6	US-10-953-349-31436	Sequence 31436, A
150	68	11.5	1300	7	US-11-174-307B-112	Sequence 112, App	223	65.5	11.1	166	6	US-11-056-355B-65783	Sequence 65783, A
151	68	11.5	1302	7	US-11-174-307B-2152	Sequence 2152, Ap	224	65.5	11.1	183	6	US-10-953-349-31434	Sequence 31434, A
152	68	11.5	1398	7	US-11-217-997-4	Sequence 4, Appli	225	65.5	11.1	183	7	US-11-056-355B-65781	Sequence 65781, A
153	68	11.5	1403	7	US-11-217-997-12	Sequence 12, Appli	226	65.5	11.1	236	7	US-11-371-354-56873	Sequence 56873, A
154	68	11.5	1404	7	US-11-217-997-2	Sequence 2, Appli	227	65.5	11.1	258	6	US-10-643-589-4	Sequence 4, Appli
155	68	11.5	1547	7	US-11-217-997-22	Sequence 22, Appli	228	65.5	11.1	262	7	US-11-371-354-62711	Sequence 62711, A
156	68	11.5	1577	7	US-11-217-997-16	Sequence 16, Appli	229	65.5	11.1	342	7	US-11-038-753-1	Sequence 1, Appli
157	68	11.5	1577	7	US-11-217-997-20	Sequence 20, Appli	230	65.5	11.1	720	7	US-11-175-714-4	Sequence 4, Appli
158	68	11.5	1594	7	US-11-217-997-18	Sequence 18, Appli	231	65.5	11.1	1271	7	US-11-174-307B-2618	Sequence 2618, App
159	68	11.5	1620	7	US-11-217-997-42	Sequence 42, Appli	232	65.5	11.1	1272	7	US-11-174-307B-422	Sequence 422, App
160	68	11.5	1653	7	US-11-217-997-40	Sequence 40, Appli	233	65.5	11.1	1274	7	US-11-174-307B-1848	Sequence 1848, Ap
161	67.5	11.5	863	7	US-11-056-355B-82720	Sequence 82720, A	234	65.5	11.1	1660	7	US-11-174-307B-2132	Sequence 2132, Ap
162	67.5	11.5	893	7	US-11-056-355B-82719	Sequence 82719, A	235	65.5	11.1	1661	7	US-11-174-307B-1792	Sequence 1792, Ap
163	67.5	11.5	894	7	US-11-174-307B-1892	Sequence 1892, Ap	236	65.5	11.1	1942	7	US-11-174-307B-1296	Sequence 1296, Ap
164	67.5	11.5	895	7	US-11-056-355B-82718	Sequence 82718, A	237	65.5	11.1	2000	6	US-10-533-519-512	Sequence 512, App
165	67.5	11.5	1094	7	US-11-174-307B-1976	Sequence 1976, Ap	238	65.5	11.1	2471	7	US-11-071-796A-23	Sequence 23, Appli
166	67.5	11.5	1641	7	US-11-174-307B-1356	Sequence 1356, Ap	239	65.5	11.1	2556	7	US-11-264-243-6	Sequence 22, Appli
167	67.5	11.5	1641	7	US-11-174-307B-760	Sequence 760, App	240	65.5	11.1	2556	7	US-11-371-354-73975	Sequence 73975, A
168	67	11.4	310	7	US-11-090-997-1042	Sequence 1042, Ap	241	65	11.0	383	7	US-11-071-796A-22	Sequence 22, Appli
169	67	11.4	383	7	US-11-090-997-1040	Sequence 1040, Ap	242	65	11.0	535	6	US-10-553-436-355	Sequence 355, App
170	67	11.4	575	7	US-11-217-997-32	Sequence 32, Appli	243	65	11.0	1054	7	US-11-288-932-47	Sequence 47, Appli
171	67	11.4	984	7	US-11-174-307B-2022	Sequence 2022, Ap	244	65	11.0	1067	7	US-11-054-369A-3	Sequence 3, Appli
172	67	11.4	1068	7	US-11-054-369A-11	Sequence 11, Appli	245	65	11.0	1135	7	US-11-174-307B-2204	Sequence 2204, Ap
173	67	11.4	1172	6	US-10-700-439-110	Sequence 110, App	246	65	11.0	1209	7	US-11-174-307B-1610	Sequence 1610, Ap
174	67	11.4	1218	6	US-10-833-833-121	Sequence 121, App	247	65	11.0	1218	6	US-10-833-833-124	Sequence 124, App
175	67	11.4	1290	7	US-11-174-307B-832	Sequence 832, App	248	65	11.0	1218	7	US-11-178-724-21	Sequence 21, Appli

250	65	11.0	1218	7	US-11-071-796A-20	Sequence 20, Appl	323	63.5	10.8	2087	6	US-10-669-920-911	Sequence 911, App
251	65	11.0	1218	7	US-11-188-417A-21	Sequence 21, Appl	324	63.5	10.8	2087	6	US-10-669-920-913	Sequence 913, App
252	65	11.0	1218	7	US-11-231-494-21	Sequence 21, Appl	325	63.5	10.8	2203	6	US-10-539-228-726	Sequence 726, App
253	65	11.0	1242	7	US-11-174-307B-1968	Sequence 1968, Ap	326	63.5	10.8	2247	7	US-11-174-307B-5510	Sequence 5510, Ap
254	65	11.0	1416	7	US-11-174-307B-1884	Sequence 1684, Ap	327	63.5	10.8	2499	7	US-11-174-307B-138	Sequence 138, App
255	65	11.0	1419	7	US-11-001-346-101	Sequence 101, App	328	63	10.7	64	7	US-11-350-321-8	Sequence 8, Appl
256	65	11.0	1437	7	US-11-174-307B-2302	Sequence 2302, Ap	329	63	10.7	65	7	US-11-377-883-12	Sequence 12, Appl
257	65	11.0	1438	7	US-11-174-307B-1176	Sequence 1176, Ap	330	63	10.7	65	7	US-11-282-519-8	Sequence 8, Appl
258	65	11.0	1596	7	US-11-174-307B-792	Sequence 792, App	331	63	10.7	94	6	US-10-449-902-48319	Sequence 48319, A
259	65	11.0	1604	7	US-11-174-307B-2686	Sequence 2686, Ap	332	63	10.7	250	7	US-11-320-192-11	Sequence 11, Appl
260	65	11.0	1801	7	US-11-174-307B-2660	Sequence 2660, Ap	333	63	10.7	298	7	US-11-056-358B-6149	Sequence 6149, Ap
261	65	11.0	1944	7	US-11-174-307B-2442	Sequence 2442, Ap	334	63	10.7	350	7	US-11-330-403-5544	Sequence 5544, Ap
262	65	11.0	2508	7	US-11-174-307B-1998	Sequence 1998, Ap	335	63	10.7	386	7	US-11-056-358B-6148	Sequence 6148, Ap
263	65	11.0	2628	7	US-11-174-307B-2692	Sequence 2692, Ap	336	63	10.7	562	7	US-11-174-307B-3662	Sequence 3662, Ap
264	65	11.0	4659	7	US-11-174-307B-1816	Sequence 1816, Ap	337	63	10.7	696	6	US-10-449-902-41608	Sequence 41608, A
265	64.5	11.0	98	7	US-11-377-336-13	Sequence 13, Appl	338	63	10.7	738	7	US-11-174-307B-816	Sequence 816, App
266	64.5	11.0	141	6	US-10-953-349-30197	Sequence 30197, A	339	63	10.7	1103	7	US-11-174-307B-2450	Sequence 2450, Ap
267	64.5	11.0	141	7	US-11-056-358B-67485	Sequence 67485, A	340	63	10.7	1144	7	US-11-174-307B-2720	Sequence 2720, Ap
268	64.5	11.0	229	6	US-10-953-349-30195	Sequence 30195, A	341	63	10.7	1280	6	US-10-669-920-1139	Sequence 1139, Ap
269	64.5	11.0	229	7	US-11-056-358B-67483	Sequence 67483, A	342	63	10.7	1471	7	US-11-174-307B-2316	Sequence 2316, Ap
270	64.5	11.0	873	7	US-11-174-307B-1646	Sequence 1646, Ap	343	63	10.7	1753	7	US-11-174-307B-1198	Sequence 1198, Ap
271	64.5	11.0	1042	7	US-11-174-307B-356	Sequence 356, App	344	63	10.7	1964	7	US-11-174-307B-4458	Sequence 4458, Ap
272	64.5	11.0	1060	7	US-11-174-307B-2216	Sequence 2216, Ap	345	63	10.7	2105	7	US-11-174-307B-1354	Sequence 1354, Ap
273	64.5	11.0	1388	7	US-11-174-307B-1842	Sequence 1842, Ap	346	63	10.7	2117	7	US-11-174-307B-2836	Sequence 2836, Ap
274	64.5	11.0	1391	7	US-11-174-307B-566	Sequence 566, App	347	63	10.7	2195	7	US-11-174-307B-5412	Sequence 5412, Ap
275	64.5	11.0	1564	7	US-11-174-307B-2448	Sequence 2448, Ap	348	63	10.7	4243	7	US-11-174-307B-1722	Sequence 1722, Ap
276	64.5	11.0	1617	7	US-11-174-307B-798	Sequence 798, App	349	62.5	10.6	85	7	US-11-384-643-12	Sequence 12, Appl
277	64.5	11.0	1459	7	US-11-174-307B-1436	Sequence 1436, Ap	350	62.5	10.6	179	6	US-10-953-349-30286	Sequence 30286, A
278	64.5	11.0	2000	6	US-10-533-519-732	Sequence 732, App	351	62.5	10.6	179	7	US-11-056-358B-61518	Sequence 61518, A
279	64.5	11.0	2137	7	US-11-174-307B-4852	Sequence 4852, Ap	352	62.5	10.6	211	6	US-10-953-349-30285	Sequence 30285, A
280	64.5	11.0	2214	6	US-10-570-909-25	Sequence 25, Appl	353	62.5	10.6	211	7	US-11-056-358B-61517	Sequence 61517, A
281	64.5	11.0	2214	6	US-10-570-909-52	Sequence 52, Appl	354	62.5	10.6	213	7	US-11-174-307B-3784	Sequence 3784, Ap
282	64.5	11.0	2279	6	US-10-533-519-1728	Sequence 1728, Ap	355	62.5	10.6	347	7	US-11-324-769-2	Sequence 2, Appl
283	64.5	11.0	2344	7	US-11-174-307B-1496	Sequence 1496, Ap	356	62.5	10.6	466	7	US-11-174-307B-1342	Sequence 1342, Ap
284	64.5	11.0	3331	7	US-11-174-307B-1574	Sequence 1574, Ap	357	62.5	10.6	567	7	US-11-371-354-59045	Sequence 59045, A
285	64	10.9	251	7	US-11-371-354-57191	Sequence 57191, A	358	62.5	10.6	1003	7	US-11-174-307B-2592	Sequence 2592, Ap
286	64	10.9	251	7	US-11-320-192-8	Sequence 8, Appl	359	62.5	10.6	1049	7	US-11-174-307B-624	Sequence 624, App
287	64	10.9	426	7	US-11-056-358B-24730	Sequence 24730, A	360	62.5	10.6	1080	7	US-11-216-721-2	Sequence 2, Appl
288	64	10.9	475	7	US-11-371-354-69949	Sequence 69949, A	361	62.5	10.6	1164	7	US-11-174-307B-2218	Sequence 2218, Ap
289	64	10.9	525	7	US-11-174-307B-5446	Sequence 5446, Ap	362	62.5	10.6	1189	7	US-11-174-307B-1964	Sequence 1964, Ap
290	64	10.9	1365	7	US-11-174-307B-2290	Sequence 2290, Ap	363	62.5	10.6	1285	7	US-11-174-307B-1124	Sequence 1124, Ap
291	64	10.9	1375	7	US-11-174-307B-622	Sequence 622, App	364	62.5	10.6	1298	7	US-11-174-307B-826	Sequence 826, App
292	64	10.9	1396	7	US-11-174-307B-466	Sequence 466, App	365	62.5	10.6	1432	7	US-11-174-307B-2846	Sequence 2846, Ap
293	64	10.9	1486	7	US-11-174-307B-2522	Sequence 2522, Ap	366	62.5	10.6	1459	7	US-11-174-307B-1332	Sequence 1332, Ap
294	64	10.9	1754	7	US-11-174-307B-2600	Sequence 2600, Ap	367	62.5	10.6	1493	7	US-11-174-307B-4196	Sequence 4196, Ap
295	64	10.9	1758	7	US-11-174-307B-2310	Sequence 2310, Ap	368	62.5	10.6	1573	7	US-11-174-307B-770	Sequence 770, App
296	64	10.9	1859	7	US-11-174-307B-940	Sequence 940, App	369	62.5	10.6	1576	7	US-11-174-307B-594	Sequence 594, App
297	64	10.9	1865	7	US-11-174-307B-1078	Sequence 1078, Ap	370	62.5	10.6	1600	7	US-11-174-307B-2664	Sequence 2664, Ap
298	64	10.9	1914	7	US-11-174-307B-20	Sequence 20, Appl	371	62.5	10.6	1680	7	US-11-174-307B-712	Sequence 712, App
299	64	10.9	2128	7	US-11-174-307B-1384	Sequence 1384, Ap	372	62.5	10.6	1736	7	US-11-174-307B-2668	Sequence 2668, Ap
300	64	10.9	2451	6	US-10-669-920-908	Sequence 908, App	373	62.5	10.6	1962	7	US-11-174-307B-1446	Sequence 1446, Ap
301	64	10.9	2503	6	US-10-539-228-723	Sequence 723, App	374	62.5	10.6	2052	7	US-11-174-307B-652	Sequence 652, App
302	64	10.9	2568	7	US-11-174-307B-90	Sequence 90, Appl	375	62.5	10.6	2368	7	US-11-174-307B-2844	Sequence 2844, Ap
303	64	10.9	2643	7	US-11-174-307B-58	Sequence 58, Appl	376	62.5	10.6	2391	7	US-11-174-307B-1386	Sequence 1386, Ap
304	64	10.9	3934	7	US-11-165-586-20	Sequence 20, Appl	377	62.5	10.6	2973	7	US-11-174-307B-1754	Sequence 1754, Ap
305	63.5	10.8	139	6	US-10-449-902-30417	Sequence 30417, A	378	62.5	10.6	3018	7	US-11-174-307B-1996	Sequence 1996, Ap
306	63.5	10.8	713	7	US-11-175-714-5	Sequence 5, Appl	379	62.5	10.6	3303	6	US-10-547-530-49	Sequence 49, Appl
307	63.5	10.8	721	7	US-11-175-714-7	Sequence 7, Appl	380	62	10.5	984	7	US-11-174-307B-1592	Sequence 1592, Ap
308	63.5	10.8	1011	7	US-11-174-307B-1528	Sequence 1528, Ap	381	62	10.5	998	7	US-11-259-133-28	Sequence 28, Appl
309	63.5	10.8	1093	6	US-10-449-902-41338	Sequence 41338, A	382	62	10.5	998	7	US-11-365-989-168	Sequence 168, App
310	63.5	10.8	1307	7	US-11-174-307B-4164	Sequence 4164, A	383	62	10.5	998	7	US-11-371-354-67407	Sequence 67407, A
311	63.5	10.8	1611	7	US-11-174-307B-2234	Sequence 2234, Ap	384	62	10.5	1017	7	US-11-174-307B-956	Sequence 956, App
312	63.5	10.8	1611	7	US-11-174-307B-2552	Sequence 2552, Ap	385	62	10.5	1050	7	US-11-265-762-114	Sequence 114, App
313	63.5	10.8	1641	7	US-11-174-307B-1340	Sequence 1340, Ap	386	62	10.5	1113	6	US-10-543-003-3	Sequence 3, Appl
314	63.5	10.8	1685	7	US-11-174-307B-598	Sequence 598, App	387	62	10.5	1152	7	US-11-174-307B-2712	Sequence 2712, Ap
315	63.5	10.8	1691	7	US-11-174-307B-762	Sequence 762, App	388	62	10.5	1192	7	US-11-174-307B-2814	Sequence 2814, Ap
316	63.5	10.8	1708	7	US-11-174-307B-2086	Sequence 2086, Ap	389	62	10.5	1194	7	US-11-174-307B-5030	Sequence 5030, Ap
317	63.5	10.8	1744	7	US-11-174-307B-2750	Sequence 2750, Ap	390	62	10.5	1228	7	US-11-174-307B-980	Sequence 980, App
318	63.5	10.8	1779	7	US-11-174-307B-1438	Sequence 1438, Ap	391	62	10.5	1315	7	US-11-174-307B-610	Sequence 610, App
319	63.5	10.8	1830	7	US-11-174-307B-1478	Sequence 1478, Ap	392	62	10.5	1337	7	US-11-174-307B-2460	Sequence 2460, Ap
320	63.5	10.8	1832	7	US-11-174-307B-2350	Sequence 2350, Ap	393	62	10.5	1377	7	US-11-174-307B-1066	Sequence 1066, Ap
321	63.5	10.8	1845	7	US-11-174-307B-1980	Sequence 1980, Ap	394	62	10.5	1376	7	US-11-174-307B-378	Sequence 378, App
322	63.5	10.8	1870	7	US-11-174-307B-4998	Sequence 4998, Ap	395	62	10.5	1379	7	US-11-174-307B-1738	Sequence 1738, Ap

548	60.5	10.3	1042	7	US-11-174-307B-2500	Sequence 2500, Ap	623	60	10.2	1577	7	US-11-174-307B-396	Sequence 396, App
549	60.5	10.3	1069	7	US-11-174-307B-1228	Sequence 1228, Ap	624	60	10.2	1655	7	US-11-174-307B-3630	Sequence 3630, Ap
550	60.5	10.3	1168	7	US-11-174-307B-1016	Sequence 1016, Ap	625	60	10.2	1656	7	US-11-174-307B-3004	Sequence 3004, Ap
551	60.5	10.3	1169	7	US-11-174-307B-2532	Sequence 2532, Ap	626	60	10.2	1689	7	US-11-174-307B-1196	Sequence 1196, Ap
552	60.5	10.3	1170	7	US-11-174-307B-1300	Sequence 1300, Ap	627	60	10.2	1723	7	US-11-174-307B-908	Sequence 908, App
553	60.5	10.3	1199	7	US-11-174-307B-2390	Sequence 2390, Ap	628	60	10.2	1764	7	US-11-174-307B-2034	Sequence 2034, Ap
554	60.5	10.3	1245	7	US-11-174-307B-1602	Sequence 1602, Ap	629	60	10.2	1768	7	US-11-174-307B-1220	Sequence 1220, Ap
555	60.5	10.3	1299	7	US-11-174-307B-1524	Sequence 1524, Ap	630	60	10.2	1776	6	US-10-933-854-3	Sequence 3, Appl1
556	60.5	10.3	1313	7	US-11-174-307B-2312	Sequence 2312, Ap	631	60	10.2	1782	7	US-11-174-307B-1652	Sequence 1652, Ap
557	60.5	10.3	1378	7	US-11-174-307B-432	Sequence 432, App	632	60	10.2	1784	7	US-11-174-307B-2856	Sequence 2856, Ap
558	60.5	10.3	1424	7	US-11-174-307B-504	Sequence 504, App	633	60	10.2	1825	7	US-11-174-307B-882	Sequence 882, App
559	60.5	10.3	1443	7	US-11-174-307B-2906	Sequence 2906, Ap	634	60	10.2	1825	7	US-11-174-307B-978	Sequence 978, App
560	60.5	10.3	1506	7	US-11-174-307B-1992	Sequence 1992, Ap	635	60	10.2	1945	7	US-11-174-307B-2726	Sequence 2726, Ap
561	60.5	10.3	1507	7	US-11-174-307B-494	Sequence 494, App	636	60	10.2	2045	7	US-11-174-307B-1618	Sequence 1618, Ap
562	60.5	10.3	1549	7	US-11-174-307B-608	Sequence 608, App	637	60	10.2	2433	7	US-11-174-307B-1990	Sequence 1990, Ap
563	60.5	10.3	1565	7	US-11-174-307B-1824	Sequence 1824, Ap	638	60	10.2	2574	7	US-11-174-307B-1414	Sequence 1414, Ap
564	60.5	10.3	1567	7	US-11-174-307B-2116	Sequence 2116, Ap	639	60	10.2	2633	7	US-11-174-307B-1520	Sequence 1520, Ap
565	60.5	10.3	1571	7	US-11-174-307B-2074	Sequence 2074, Ap	640	59.5	10.1	5109	7	US-11-174-307B-1520	Sequence 560, App
566	60.5	10.3	1592	7	US-11-174-307B-5088	Sequence 5088, Ap	641	59.5	10.1	139	7	US-11-050-875-560	Sequence 26, Appl1
567	60.5	10.3	1655	7	US-11-174-307B-962	Sequence 962, App	642	59.5	10.1	173	7	US-11-303-169-26	Sequence 13, Appl1
568	60.5	10.3	1761	7	US-11-174-307B-1526	Sequence 1526, Ap	643	59.5	10.1	432	6	US-10-540-847-13	Sequence 17, Appl1
569	60.5	10.3	1782	7	US-11-174-307B-780	Sequence 780, App	644	59.5	10.1	438	6	US-11-174-307B-2856	Sequence 3800, Ap
570	60.5	10.3	1796	7	US-11-174-307B-910	Sequence 910, App	645	59.5	10.1	521	7	US-11-174-307B-3272	Sequence 3272, Ap
571	60.5	10.3	1811	7	US-11-174-307B-924	Sequence 924, App	646	59.5	10.1	729	7	US-11-174-307B-230	Sequence 230, App
572	60.5	10.3	1867	7	US-11-174-307B-406	Sequence 406, App	647	59.5	10.1	802	7	US-11-174-307B-5486	Sequence 5486, Ap
573	60.5	10.3	1867	7	US-11-174-307B-2604	Sequence 2604, Ap	648	59.5	10.1	821	7	US-11-371-354-67925	Sequence 67925, A
574	60.5	10.3	1884	7	US-11-174-307B-2588	Sequence 2588, Ap	649	59.5	10.1	839	7	US-11-174-307B-2580	Sequence 2580, Ap
575	60.5	10.3	1897	7	US-11-174-307B-2884	Sequence 2884, Ap	650	59.5	10.1	876	7	US-11-174-307B-1072	Sequence 1072, Ap
576	60.5	10.3	1942	7	US-11-174-307B-1096	Sequence 1096, Ap	651	59.5	10.1	876	7	US-11-174-307B-144	Sequence 144, App
577	60.5	10.3	1948	7	US-11-174-307B-2702	Sequence 2702, Ap	652	59.5	10.1	886	6	US-10-533-519-1196	Sequence 1196, Ap
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580	60.5	10.3	2037	7	US-11-174-307B-3360	Sequence 3360, Ap	655	59.5	10.1	1075	7	US-11-174-307B-3060	Sequence 3060, Ap
581	60.5	10.3	2077	7	US-11-174-307B-2340	Sequence 2340, Ap	656	59.5	10.1	1132	7	US-11-174-307B-892	Sequence 892, App
582	60.5	10.3	2079	7	US-11-174-307B-2126	Sequence 2126, Ap	657	59.5	10.1	1136	7	US-11-174-307B-2400	Sequence 2400, Ap
583	60.5	10.3	2079	7	US-11-174-307B-2408	Sequence 2408, Ap	658	59.5	10.1	1146	7	US-11-174-307B-476	Sequence 476, App
584	60.5	10.3	2757	7	US-11-174-307B-1642	Sequence 1642, Ap	659	59.5	10.1	1155	7	US-11-174-307B-644	Sequence 644, App
585	60.5	10.3	3723	7	US-11-174-307B-2802	Sequence 2802, Ap	660	59.5	10.1	1155	7	US-11-174-307B-1546	Sequence 1546, Ap
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587	60	10.2	314	7	US-11-293-697-2665	Sequence 2665, Ap	662	59.5	10.1	1212	7	US-11-174-307B-3094	Sequence 3094, Ap
588	60	10.2	351	7	US-11-455-506-21	Sequence 21, Appl	663	59.5	10.1	1232	7	US-11-174-307B-524	Sequence 524, App
589	60	10.2	375	7	US-11-377-336-53	Sequence 53, Appl	664	59.5	10.1	1270	7	US-11-174-307B-364	Sequence 364, App
590	60	10.2	383	7	US-11-330-403-13153	Sequence 13153, A	665	59.5	10.1	1284	7	US-11-174-307B-1880	Sequence 1880, Ap
591	60	10.2	399	7	US-11-430-226-9	Sequence 9, Appl1	666	59.5	10.1	1298	7	US-11-174-307B-970	Sequence 970, App
592	60	10.2	401	7	US-11-377-336-50	Sequence 50, Appl	667	59.5	10.1	1299	7	US-11-174-307B-1640	Sequence 1640, Ap
593	60	10.2	598	6	US-10-669-920-804	Sequence 804, App	668	59.5	10.1	1316	7	US-11-174-307B-1812	Sequence 1812, Ap
594	60	10.2	623	7	US-11-430-226-2	Sequence 2, Appl1	669	59.5	10.1	1317	7	US-11-174-307B-306	Sequence 306, App
595	60	10.2	623	7	US-11-430-226-5	Sequence 5, Appl1	670	59.5	10.1	1318	7	US-11-174-307B-2184	Sequence 2184, Ap
596	60	10.2	659	7	US-11-174-307B-614	Sequence 614, App	671	59.5	10.1	1323	7	US-11-174-307B-326	Sequence 326, App
597	60	10.2	850	7	US-11-174-307B-534	Sequence 534, App	672	59.5	10.1	1353	7	US-11-174-307B-1502	Sequence 1502, Ap
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599	60	10.2	1053	7	US-11-174-307B-596	Sequence 596, App	674	59.5	10.1	1408	7	US-11-174-307B-2196	Sequence 2196, Ap
600	60	10.2	1077	7	US-11-174-307B-1630	Sequence 1630, Ap	675	59.5	10.1	1449	7	US-11-174-307B-134	Sequence 134, App
601	60	10.2	1192	7	US-11-174-307B-394	Sequence 394, App	676	59.5	10.1	1449	7	US-11-174-307B-336	Sequence 336, App
602	60	10.2	1192	7	US-11-174-307B-1832	Sequence 1832, Ap	677	59.5	10.1	1478	7	US-11-174-307B-710	Sequence 710, App
603	60	10.2	1257	7	US-11-174-307B-24	Sequence 24, Appl	678	59.5	10.1	1495	7	US-11-174-307B-1656	Sequence 1656, Ap
604	60	10.2	1263	7	US-11-174-307B-1290	Sequence 1290, Ap	679	59.5	10.1	1530	7	US-11-174-307B-1862	Sequence 1862, Ap
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606	60	10.2	1326	7	US-11-174-307B-1514	Sequence 1514, Ap	681	59.5	10.1	1587	7	US-11-174-307B-2652	Sequence 2652, Ap
607	60	10.2	1413	7	US-11-174-307B-654	Sequence 654, App	682	59.5	10.1	1595	7	US-11-174-307B-4562	Sequence 4562, Ap
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610	60	10.2	1363	7	US-11-174-307B-2430	Sequence 2430, Ap	685	59.5	10.1	1665	7	US-11-174-307B-1726	Sequence 1726, Ap
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615	60	10.2	1452	7	US-11-174-307B-4154	Sequence 4154, Ap	690	59.5	10.1	1733	7	US-11-174-307B-814	Sequence 814, App
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618	60	10.2	1502	7	US-11-174-307B-1380	Sequence 1380, Ap	693	59.5	10.1	1799	6	US-10-562-469-8	Sequence 8, Appl1
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620	60	10.2	1523	6	US-10-533-365-236	Sequence 236, App	695	59.5	10.1	1828	7	US-11-174-307B-2544	Sequence 2544, Ap
622	60	10.2	1575	7	US-11-174-307B-2648	Sequence 2648, Ap							

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698	59.5	10.1	1868	7	US-11-174-307B-2266	Sequence 2266, Ap	771	59	10.0	1991	7	US-11-174-307B-2144	Sequence 2144, Ap
699	59.5	10.1	1896	7	US-11-174-307B-1376	Sequence 1376, Ap	772	59	10.0	1991	7	US-11-174-307B-2570	Sequence 2570, Ap
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701	59.5	10.1	2061	7	US-11-174-307B-1216	Sequence 1216, Ap	774	59	10.0	2062	7	US-11-174-307B-876	Sequence 876, App
702	59.5	10.1	2325	7	US-11-174-307B-5472	Sequence 5472, Ap	775	59	10.0	2085	7	US-11-174-307B-954	Sequence 954, App
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705	59.5	10.1	2505	6	US-10-669-920-15	Sequence 15, Appl	778	59	10.0	2143	7	US-11-174-307B-2550	Sequence 2550, Ap
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707	59.5	10.1	2841	7	US-11-174-307B-2530	Sequence 2530, Ap	780	59	10.0	2472	7	US-11-174-307B-1716	Sequence 1716, Ap
708	59	10.0	78	7	US-11-372-771-22	Sequence 22, Appl	781	59	10.0	3003	7	US-11-174-307B-228	Sequence 228, App
709	59	10.0	78	7	US-11-372-761-22	Sequence 22, Appl	782	59	10.0	3362	7	US-11-174-307B-2314	Sequence 2314, App
710	59	10.0	159	7	US-11-377-336-45	Sequence 45, Appl	783	58.5	9.9	76	6	US-10-449-902-39281	Sequence 39281, A
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712	59	10.0	314	7	US-11-056-355B-88093	Sequence 88093, A	785	58.5	9.9	92	7	US-11-417-317-79	Sequence 79, Appl
713	59	10.0	315	6	US-10-374-780A-2390	Sequence 2390, Ap	786	58.5	9.9	92	7	US-11-360-450-79	Sequence 79, Appl
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716	59	10.0	516	6	US-10-449-902-44623	Sequence 44623, A	789	58.5	9.9	92	7	US-11-418-410-79	Sequence 79, Appl
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729	59	10.0	1096	7	US-11-174-307B-4668	Sequence 4668, Ap	802	58.5	9.9	322	7	US-11-056-355B-107864	Sequence 107864, A
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732	59	10.0	1220	7	US-11-174-307B-1542	Sequence 1542, Ap	805	58.5	9.9	381	7	US-11-371-354-56279	Sequence 56279, A
733	59	10.0	1221	7	US-11-174-307B-1672	Sequence 1672, Ap	806	58.5	9.9	397	7	US-11-412-325-211	Sequence 211, App
734	59	10.0	1223	7	US-11-174-307B-2472	Sequence 2472, Ap	807	58.5	9.9	430	6	US-10-540-847-15	Sequence 15, Appl
735	59	10.0	1245	7	US-11-174-307B-850	Sequence 850, App	808	58.5	9.9	430	6	US-10-553-520-81	Sequence 81, Appl
736	59	10.0	1259	7	US-11-174-307B-5038	Sequence 5038, App	809	58.5	9.9	455	6	US-10-548-389-22	Sequence 22, Appl
737	59	10.0	1281	7	US-11-174-307B-1826	Sequence 1826, Ap	810	58.5	9.9	455	6	US-11-416-310-5	Sequence 5, Appl
738	59	10.0	1303	7	US-11-174-307B-430	Sequence 430, App	811	58.5	9.9	455	7	US-11-361-415-99	Sequence 99, Appl
739	59	10.0	1310	7	US-11-174-307B-1186	Sequence 1186, Ap	812	58.5	9.9	455	7	US-11-404-081-2	Sequence 2, Appl
740	59	10.0	1310	7	US-11-174-307B-3450	Sequence 3450, Ap	813	58.5	9.9	455	7	US-11-419-656-5	Sequence 5, Appl
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742	59	10.0	1377	7	US-11-174-307B-518	Sequence 518, App	815	58.5	9.9	486	7	US-11-174-307B-82	Sequence 82, Appl
743	59	10.0	1393	7	US-11-174-307B-606	Sequence 606, App	816	58.5	9.9	503	7	US-11-363-402-1	Sequence 1, Appl
744	59	10.0	1425	7	US-11-174-307B-706	Sequence 706, App	817	58.5	9.9	503	7	US-11-090-997-1596	Sequence 1596, Ap
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748	59	10.0	1465	7	US-11-174-307B-1720	Sequence 1720, Ap	821	58.5	9.9	584	6	US-10-540-898-468	Sequence 468, App
749	59	10.0	1479	7	US-11-174-307B-758	Sequence 758, App	822	58.5	9.9	584	6	US-10-540-898-470	Sequence 470, App
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752	59	10.0	1518	7	US-11-174-307B-932	Sequence 932, App	825	58.5	9.9	787	7	US-11-412-325-70	Sequence 70, Appl
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754	59	10.0	1530	7	US-11-174-307B-854	Sequence 854, App	827	58.5	9.9	915	7	US-11-174-307B-702	Sequence 702, App
755	59	10.0	1560	7	US-11-174-307B-1846	Sequence 1846, Ap	828	58.5	9.9	929	7	US-11-174-307B-3988	Sequence 3988, Ap
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757	59	10.0	1703	7	US-11-174-307B-558	Sequence 558, App	830	58.5	9.9	1076	7	US-11-174-307B-3980	Sequence 3980, Ap
758	59	10.0	1705	7	US-11-174-307B-4242	Sequence 4242, Ap	831	58.5	9.9	1146	7	US-11-174-307B-84	Sequence 84, Appl
759	59	10.0	1706	7	US-11-174-307B-2322	Sequence 2322, Ap	832	58.5	9.9	1193	6	US-10-505-928-537	Sequence 537, App
760	59	10.0	1706	7	US-11-174-307B-2342	Sequence 2342, Ap	833	58.5	9.9	1281	7	US-11-174-307B-578	Sequence 578, App
761	59	10.0	1709	7	US-11-174-307B-2342	Sequence 2342, Ap	834	58.5	9.9	1293	7	US-11-174-307B-1080	Sequence 1080, Ap
762	59	10.0	1742	7	US-11-174-307B-2970	Sequence 2970, Ap	835	58.5	9.9	1333	7	US-11-174-307B-1258	Sequence 1258, Ap
763	59	10.0	1773	7	US-11-174-307B-1238	Sequence 1238, Ap	836	58.5	9.9	1335	7	US-11-174-307B-1106	Sequence 1106, Ap
764	59	10.0	1783	7	US-11-174-307B-1710	Sequence 1710, Ap	837	58.5	9.9	1337	7	US-11-174-307B-896	Sequence 896, App
765	59	10.0	1786	7	US-11-174-307B-902	Sequence 902, App	838	58.5	9.9	1367	7	US-11-174-307B-3818	Sequence 3818, Ap
766	59	10.0	1814	7	US-11-174-307B-602	Sequence 602, App	839	58.5	9.9	1368	7	US-11-174-307B-116	Sequence 116, App
767	59	10.0	1814	7	US-11-174-307B-1182	Sequence 1182, Ap	840	58.5	9.9	1368	7	US-11-174-307B-4560	Sequence 4560, Ap
768	59	10.0	1880	7	US-11-174-307B-2102	Sequence 2102, Ap	841	58.5	9.9	1407	7	US-11-174-307B-464	Sequence 464, App

842	58.5	9.9	1408	7	US-11-174-307B-2510	Sequence 2510, Ap	915	58	9.8	1348	7	US-11-174-307B-2452	Sequence 2452, Ap
843	58.5	9.9	1416	7	US-11-174-307B-1480	Sequence 1480, Ap	916	58	9.8	1359	7	US-11-174-307B-1994	Sequence 1994, Ap
844	58.5	9.9	1463	7	US-11-174-307B-1920	Sequence 1920, Ap	917	58	9.8	1391	7	US-11-174-307B-2252	Sequence 2252, Ap
845	58.5	9.9	1471	7	US-11-174-307B-4592	Sequence 4592, Ap	918	58	9.8	1431	7	US-11-174-307B-1112	Sequence 1112, Ap
846	58.5	9.9	1477	7	US-11-174-307B-1160	Sequence 1160, Ap	919	58	9.8	1431	7	US-11-174-307B-1112	Sequence 1112, Ap
847	58.5	9.9	1555	7	US-11-174-307B-1366	Sequence 1366, Ap	920	58	9.8	1449	7	US-11-174-307B-190	Sequence 190, App
848	58.5	9.9	1576	7	US-11-174-307B-856	Sequence 856, App	921	58	9.8	1460	7	US-11-174-307B-5280	Sequence 5280, Ap
849	58.5	9.9	1576	7	US-11-174-307B-2886	Sequence 2886, Ap	922	58	9.8	1464	7	US-11-174-307B-2038	Sequence 2038, Ap
850	58.5	9.9	1600	7	US-11-174-307B-544	Sequence 544, App	923	58	9.8	1467	7	US-11-174-307B-1854	Sequence 1854, Ap
851	58.5	9.9	1628	7	US-11-174-307B-2748	Sequence 2748, Ap	924	58	9.8	1480	7	US-11-174-307B-752	Sequence 752, App
852	58.5	9.9	1652	7	US-11-174-307B-1188	Sequence 1188, Ap	925	58	9.8	1485	7	US-11-174-307B-2306	Sequence 2306, Ap
853	58.5	9.9	1663	7	US-11-174-307B-938	Sequence 938, App	926	58	9.8	1485	7	US-11-174-307B-2306	Sequence 2306, Ap
854	58.5	9.9	1692	7	US-11-174-307B-2858	Sequence 2858, Ap	927	58	9.8	1521	7	US-11-174-307B-36	Sequence 36, Appl
855	58.5	9.9	1693	7	US-11-174-307B-4190	Sequence 4190, Ap	928	58	9.8	1523	7	US-11-174-307B-1098	Sequence 1098, Ap
856	58.5	9.9	1784	7	US-11-174-307B-2728	Sequence 2728, Ap	929	58	9.8	1523	7	US-11-174-307B-786	Sequence 786, App
857	58.5	9.9	1785	7	US-11-174-307B-1774	Sequence 1774, Ap	930	58	9.8	1533	7	US-11-174-307B-2056	Sequence 2056, Ap
858	58.5	9.9	1788	7	US-11-174-307B-2834	Sequence 2834, Ap	931	58	9.8	1533	7	US-11-174-307B-1110	Sequence 1110, Ap
859	58.5	9.9	1845	7	US-11-174-307B-1310	Sequence 1310, Ap	932	58	9.8	1552	7	US-11-174-307B-126	Sequence 126, Ap
860	58.5	9.9	1848	7	US-11-174-307B-1372	Sequence 1372, Ap	933	58	9.8	1572	7	US-11-174-307B-5028	Sequence 5028, Ap
861	58.5	9.9	1907	7	US-11-174-307B-2770	Sequence 2770, Ap	934	58	9.8	1674	7	US-11-174-307B-1328	Sequence 1328, Ap
862	58.5	9.9	1925	7	US-11-174-307B-2362	Sequence 2362, Ap	935	58	9.8	1674	7	US-11-174-307B-1328	Sequence 1328, Ap
863	58.5	9.9	1961	7	US-11-174-307B-1714	Sequence 1714, Ap	936	58	9.8	1696	7	US-11-174-307B-630	Sequence 630, App
864	58.5	9.9	1965	7	US-11-174-307B-1092	Sequence 1092, Ap	937	58	9.8	1730	7	US-11-174-307B-5198	Sequence 5198, Ap
865	58.5	9.9	1994	6	US-10-544-731-2	Sequence 2, Appl	938	58	9.8	1744	7	US-11-174-307B-580	Sequence 580, App
866	58.5	9.9	2010	7	US-11-174-307B-1358	Sequence 1358, Ap	939	58	9.8	1744	7	US-11-174-307B-580	Sequence 580, App
867	58.5	9.9	2052	7	US-11-174-307B-516	Sequence 516, App	940	58	9.8	1826	7	US-11-174-307B-1322	Sequence 1322, Ap
868	58.5	9.9	2064	7	US-11-174-307B-2494	Sequence 2494, Ap	941	58	9.8	1917	7	US-11-174-307B-2172	Sequence 2172, Ap
869	58.5	9.9	2411	7	US-11-174-307B-4618	Sequence 4618, Ap	942	58	9.8	1929	7	US-11-174-307B-2462	Sequence 2462, Ap
870	58.5	9.9	2445	7	US-11-174-307B-2052	Sequence 2052, Ap	943	58	9.8	2097	7	US-11-174-307B-148	Sequence 148, App
871	58.5	9.9	4391	7	US-11-183-325-56	Sequence 56, Appl	944	58	9.8	2149	7	US-11-174-307B-3214	Sequence 3214, Ap
872	58.5	9.9	4709	7	US-11-174-307B-2292	Sequence 2292, Ap	945	58	9.8	2240	6	US-10-544-731-4	Sequence 4, Appl
873	58	9.8	77	6	US-10-953-349-15269	Sequence 15269, A	946	58	9.8	2258	6	US-10-544-731-3	Sequence 3, Appl
874	58	9.8	77	6	US-10-953-349-15269	Sequence 15269, A	945	58	9.8	2258	6	US-10-544-731-3	Sequence 3, Appl
875	58	9.8	106	6	US-10-953-349-15268	Sequence 15268, A	947	58	9.8	2366	7	US-11-174-307B-804	Sequence 804, App
876	58	9.8	106	6	US-10-953-349-15268	Sequence 15268, A	948	58	9.8	2366	7	US-11-174-307B-1488	Sequence 1488, Ap
877	58	9.8	121	6	US-10-449-902-29150	Sequence 29150, A	949	58	9.8	2643	7	US-11-174-307B-1864	Sequence 1864, Ap
878	58	9.8	121	6	US-10-449-902-29150	Sequence 29150, A	950	58	9.8	2643	7	US-11-174-307B-1864	Sequence 1864, Ap
879	58	9.8	121	6	US-10-449-902-29150	Sequence 29150, A	951	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
880	58	9.8	121	6	US-10-449-902-29150	Sequence 29150, A	952	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
881	58	9.8	197	7	US-11-293-697-3943	Sequence 3943, Ap	953	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
882	58	9.8	239	6	US-10-374-780A-535	Sequence 535, App	954	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
883	58	9.8	239	6	US-10-374-780A-535	Sequence 535, App	955	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
884	58	9.8	310	6	US-10-570-909-7	Sequence 537, App	956	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
885	58	9.8	310	6	US-10-570-909-7	Sequence 537, App	957	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
886	58	9.8	383	6	US-10-570-909-118	Sequence 118, App	958	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
887	58	9.8	515	7	US-11-174-307B-3284	Sequence 3284, Ap	959	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
888	58	9.8	523	7	US-11-056-355B-76541	Sequence 76541, A	960	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
889	58	9.8	523	7	US-11-174-307B-2320	Sequence 2320, Ap	961	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
890	58	9.8	539	7	US-11-056-355B-76540	Sequence 76540, A	962	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
891	58	9.8	540	7	US-11-447-913-1	Sequence 1, Appl	963	57.5	9.8	3291	7	US-11-174-307B-2666	Sequence 2666, Ap
892	58	9.8	854	7	US-11-090-997-1584	Sequence 1584, Ap	964	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
893	58	9.8	854	7	US-11-090-997-1584	Sequence 1584, Ap	965	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
894	58	9.8	944	7	US-11-174-307B-2280	Sequence 2280, Ap	966	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
895	58	9.8	950	7	US-11-174-307B-2002	Sequence 2002, Ap	967	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
896	58	9.8	1023	7	US-11-174-307B-1554	Sequence 1554, Ap	968	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
897	58	9.8	1050	7	US-11-174-307B-2020	Sequence 2020, Ap	969	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
898	58	9.8	1092	7	US-11-174-307B-912	Sequence 912, App	970	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
899	58	9.8	1092	7	US-11-174-307B-2066	Sequence 2066, Ap	971	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
900	58	9.8	1123	7	US-11-330-403-3085	Sequence 3085, App	972	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
901	58	9.8	1179	7	US-11-174-307B-508	Sequence 508, App	973	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
902	58	9.8	1187	7	US-11-174-307B-2092	Sequence 2092, Ap	974	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
903	58	9.8	1187	7	US-11-174-307B-2394	Sequence 2394, Ap	975	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
904	58	9.8	1194	7	US-11-045-540-2	Sequence 2, Appl	976	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
905	58	9.8	1205	7	US-11-045-540-3	Sequence 3, Appl	977	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
906	58	9.8	1205	7	US-11-371-354-69641	Sequence 69641, A	978	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
907	58	9.8	1214	7	US-11-174-307B-986	Sequence 986, App	979	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
908	58	9.8	1217	6	US-10-537-102-28	Sequence 28, Appl	980	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
909	58	9.8	1220	7	US-11-174-307B-1048	Sequence 1048, Ap	981	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
910	58	9.8	1234	7	US-11-174-307B-656	Sequence 656, App	982	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
911	58	9.8	1237	7	US-11-045-540-4	Sequence 4, Appl	983	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
912	58	9.8	1248	7	US-11-174-307B-98	Sequence 98, Appl	984	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
913	58	9.8	1285	7	US-11-045-540-5	Sequence 5, Appl	985	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
914	58	9.8	1331	7	US-11-174-307B-2396	Sequence 2396, Ap	986	57.5	9.8	3291	7	US-11-056-355B-9511	Sequence 9511, Ap
						Sequence 2766, Ap	987	57.5	9.8	3291	7	US-11-174-307B-1408	Sequence 1408, Ap
							988	57.5	9.8	3291	7	US-11-174-307B-1408	Sequence 1408, Ap
							989	57.5	9.8	3291	7	US-11-174-307B-1408	Sequence 1408, Ap
							990	57.5	9.8	3291	7	US-11-174-307B-1408	Sequence 1408, Ap

991	57.5	9.8	986	7	US-11-174-307B-2680	Sequence 2680, Ap	1064	57	9.7	303	6	US-10-953-349-19821	Sequence 19821, A
992	57.5	9.8	1058	7	US-11-174-307B-420	Sequence 420, App	1065	57	9.7	303	7	US-11-056-355B-55599	Sequence 55599, A
993	57.5	9.8	1058	7	US-11-174-307B-1586	Sequence 1586, Ap	1066	57	9.7	309	6	US-10-953-349-19820	Sequence 19820, A
994	57.5	9.8	1125	7	US-11-174-307B-650	Sequence 650, App	1067	57	9.7	309	7	US-11-056-355B-55598	Sequence 55598, A
995	57.5	9.8	1146	7	US-11-174-307B-2352	Sequence 2504, Ap	1068	57	9.7	347	7	US-11-330-403-9458	Sequence 9458, Ap
996	57.5	9.8	1167	7	US-11-174-307B-2372	Sequence 2372, Ap	1070	57	9.7	443	7	US-11-371-354-75247	Sequence 75247, A
997	57.5	9.8	1175	7	US-11-174-307B-2734	Sequence 2734, Ap	1071	57	9.7	443	7	US-11-371-354-76113	Sequence 76113, A
998	57.5	9.8	1175	7	US-11-174-307B-2734	Sequence 2734, Ap	1072	57	9.7	468	7	US-11-371-354-62463	Sequence 62463, A
999	57.5	9.8	1188	7	US-11-174-307B-1544	Sequence 1544, Ap	1073	57	9.7	468	7	US-11-265-762-116	Sequence 116, App
1000	57.5	9.8	1231	7	US-11-174-307B-1962	Sequence 1962, Ap	1074	57	9.7	573	6	US-10-449-902-44264	Sequence 44264, A
1001	57.5	9.8	1252	7	US-11-174-307B-536	Sequence 536, App	1075	57	9.7	582	7	US-11-293-697-3683	Sequence 3683, Ap
1002	57.5	9.8	1263	7	US-11-174-307B-1510	Sequence 1510, Ap	1076	57	9.7	598	6	US-10-540-898-465	Sequence 465, App
1003	57.5	9.8	1269	7	US-11-174-307B-164	Sequence 164, App	1077	57	9.7	619	7	US-11-174-307B-194	Sequence 194, App
1004	57.5	9.8	1275	7	US-11-174-307B-1886	Sequence 1886, Ap	1078	57	9.7	655	6	US-10-505-928-843	Sequence 843, App
1005	57.5	9.8	1292	7	US-11-174-307B-364	Sequence 364, App	1078	57	9.7	655	6	US-10-505-928-843	Sequence 843, App
1006	57.5	9.8	1296	7	US-11-174-307B-2482	Sequence 2482, Ap	1081	57	9.7	712	6	US-10-533-519-18993	Sequence 1893, Ap
1007	57.5	9.8	1323	7	US-11-174-307B-1734	Sequence 1734, Ap	1082	57	9.7	712	6	US-11-259-133-16	Sequence 16, Appl
1008	57.5	9.8	1325	7	US-11-174-307B-450	Sequence 450, App	1083	57	9.7	722	7	US-11-371-354-69529	Sequence 69529, A
1009	57.5	9.8	1329	7	US-11-174-307B-2050	Sequence 2050, Ap	1084	57	9.7	753	6	US-10-449-902-47701	Sequence 47701, A
1010	57.5	9.8	1356	6	US-10-508-580-18	Sequence 2050, Ap	1085	57	9.7	838	7	US-11-174-307B-808	Sequence 808, App
1011	57.5	9.8	1356	7	US-11-174-307B-64	Sequence 18, Appl	1086	57	9.7	856	7	US-11-174-307B-5482	Sequence 5482, Ap
1012	57.5	9.8	1356	7	US-11-365-989-144	Sequence 64, Appl	1087	57	9.7	856	7	US-11-174-307B-1942	Sequence 1942, Ap
1013	57.5	9.8	1356	7	US-11-401-340-4	Sequence 144, App	1088	57	9.7	903	7	US-11-174-307B-574	Sequence 574, App
1014	57.5	9.8	1356	7	US-11-404-555-2	Sequence 2, Appl	1089	57	9.7	904	7	US-11-174-307B-2616	Sequence 2616, Ap
1015	57.5	9.8	1370	7	US-11-174-307B-2124	Sequence 2124, Ap	1090	57	9.7	906	7	US-11-174-307B-2610	Sequence 2610, Ap
1016	57.5	9.8	1395	7	US-11-174-307B-1130	Sequence 1130, Ap	1091	57	9.7	909	7	US-11-174-307B-1506	Sequence 1506, Ap
1017	57.5	9.8	1463	7	US-11-174-307B-1308	Sequence 1308, Ap	1092	57	9.7	910	7	US-11-174-307B-2232	Sequence 2232, Ap
1018	57.5	9.8	1469	7	US-11-174-307B-1890	Sequence 1890, Ap	1093	57	9.7	914	7	US-11-174-307B-2084	Sequence 2084, Ap
1019	57.5	9.8	1470	7	US-11-174-307B-1280	Sequence 1280, Ap	1094	57	9.7	917	7	US-11-419-672-4	Sequence 4, Appl
1020	57.5	9.8	1483	7	US-11-174-307B-5082	Sequence 5082, Ap	1095	57	9.7	975	7	US-11-174-307B-2030	Sequence 2030, Ap
1021	57.5	9.8	1486	7	US-11-174-307B-684	Sequence 684, App	1096	57	9.7	994	7	US-11-174-307B-918	Sequence 918, App
1022	57.5	9.8	1494	7	US-11-174-307B-820	Sequence 820, App	1097	57	9.7	1020	7	US-11-174-307B-1624	Sequence 1624, Ap
1023	57.5	9.8	1527	7	US-11-174-307B-2694	Sequence 2694, Ap	1098	57	9.7	1027	7	US-11-174-307B-4296	Sequence 4296, Ap
1024	57.5	9.8	1534	7	US-11-174-307B-2156	Sequence 2156, Ap	1099	57	9.7	1036	7	US-11-299-791-21	Sequence 21, Appl
1025	57.5	9.8	1537	7	US-11-174-307B-716	Sequence 716, App	1100	57	9.7	1050	7	US-11-174-307B-1948	Sequence 1948, Ap
1026	57.5	9.8	1557	7	US-11-174-307B-1244	Sequence 1244, Ap	1101	57	9.7	1055	7	US-11-174-307B-2854	Sequence 2854, Ap
1027	57.5	9.8	1591	7	US-11-174-307B-576	Sequence 576, App	1102	57	9.7	1130	7	US-11-312-958-52	Sequence 52, Appl
1028	57.5	9.8	1592	7	US-11-174-307B-1172	Sequence 1172, Ap	1103	57	9.7	1130	7	US-11-429-599-36	Sequence 36, Appl
1029	57.5	9.8	1600	7	US-11-174-307B-636	Sequence 636, App	1104	57	9.7	1130	7	US-11-174-307B-1918	Sequence 1918, Ap
1030	57.5	9.8	1652	7	US-11-174-307B-1450	Sequence 1450, App	1105	57	9.7	1143	7	US-11-174-307B-756	Sequence 756, App
1031	57.5	9.8	1662	7	US-11-174-307B-1966	Sequence 1966, Ap	1106	57	9.7	1156	7	US-11-174-307B-316	Sequence 316, App
1032	57.5	9.8	1673	7	US-11-174-307B-812	Sequence 812, App	1107	57	9.7	1168	7	US-11-174-307B-2684	Sequence 2684, Ap
1033	57.5	9.8	1713	7	US-11-174-307B-4894	Sequence 4894, Ap	1108	57	9.7	1181	7	US-11-174-307B-1844	Sequence 1844, Ap
1034	57.5	9.8	1722	7	US-11-174-307B-2838	Sequence 2838, Ap	1109	57	9.7	1224	7	US-11-174-307B-1844	Sequence 1844, Ap
1035	57.5	9.8	1737	7	US-11-174-307B-674	Sequence 674, App	1110	57	9.7	1227	7	US-11-174-307B-486	Sequence 486, App
1036	57.5	9.8	1740	7	US-11-174-307B-1390	Sequence 1390, Ap	1111	57	9.7	1233	7	US-11-174-307B-1468	Sequence 1468, Ap
1037	57.5	9.8	1753	7	US-11-174-307B-802	Sequence 802, App	1112	57	9.7	1242	7	US-11-174-307B-1678	Sequence 1678, Ap
1038	57.5	9.8	1765	7	US-11-174-307B-2382	Sequence 2382, Ap	1113	57	9.7	1259	7	US-11-174-307B-1126	Sequence 1126, Ap
1039	57.5	9.8	1800	7	US-11-174-307B-1392	Sequence 1392, Ap	1114	57	9.7	1260	7	US-11-174-307B-1794	Sequence 1794, Ap
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1041	57.5	9.8	1847	7	US-11-174-307B-2852	Sequence 2852, Ap	1116	57	9.7	1277	7	US-11-174-307B-888	Sequence 888, App
1042	57.5	9.8	1933	7	US-11-174-307B-2226	Sequence 2226, Ap	1117	57	9.7	1296	7	US-11-174-307B-2080	Sequence 2080, Ap
1043	57.5	9.8	1962	7	US-11-174-307B-998	Sequence 998, App	1118	57	9.7	1314	7	US-11-174-307B-736	Sequence 736, App
1044	57.5	9.8	2046	7	US-11-174-307B-3456	Sequence 3456, App	1119	57	9.7	1319	7	US-11-174-307B-774	Sequence 774, App
1045	57.5	9.8	2119	7	US-11-174-307B-4798	Sequence 4798, Ap	1120	57	9.7	1322	7	US-11-174-307B-592	Sequence 592, App
1046	57.5	9.8	2124	7	US-11-174-307B-3446	Sequence 3446, Ap	1121	57	9.7	1325	7	US-11-174-307B-454	Sequence 454, App
1047	57.5	9.8	2250	7	US-11-174-307B-1394	Sequence 1394, Ap	1122	57	9.7	1330	7	US-11-174-307B-304	Sequence 304, App
1048	57.5	9.8	2265	6	US-10-562-469-11	Sequence 11, Appl	1123	57	9.7	1337	7	US-11-174-307B-2412	Sequence 2412, Ap
1049	57.5	9.8	2274	7	US-11-174-307B-56	Sequence 56, App	1124	57	9.7	1352	7	US-11-174-307B-1090	Sequence 1090, Ap
1050	57.5	9.8	2355	6	US-10-530-187-212	Sequence 272, App	1125	57	9.7	1357	7	US-11-174-307B-1426	Sequence 1426, Ap
1051	57.5	9.8	2355	6	US-10-700-439-135	Sequence 135, App	1126	57	9.7	1358	7	US-11-174-307B-320	Sequence 320, App
1052	57.5	9.8	2355	6	US-11-105-233-158	Sequence 158, App	1127	57	9.7	1358	7	US-11-174-307B-2628	Sequence 2628, Ap
1053	57.5	9.8	2386	6	US-10-530-187-271	Sequence 271, App	1128	57	9.7	1358	7	US-11-174-307B-2640	Sequence 2640, Ap
1054	57.5	9.8	2394	7	US-11-174-307B-2722	Sequence 2722, Ap	1129	57	9.7	1369	7	US-11-174-307B-2492	Sequence 2492, Ap
1055	57.5	9.8	2616	7	US-11-174-307B-1680	Sequence 1680, Ap	1130	57	9.7	1371	7	US-11-174-307B-384	Sequence 384, App
1056	57.5	9.8	2740	7	US-11-174-307B-1234	Sequence 1234, Ap	1131	57	9.7	1395	7	US-11-174-307B-2624	Sequence 2624, Ap
1057	57.5	9.8	4393	6	US-10-525-573-366	Sequence 366, App	1132	57	9.7	1395	7	US-11-174-307B-366	Sequence 366, App
1058	57.5	9.8	4393	7	US-11-450-360-1	Sequence 1, Appl	1133	57	9.7	1410	7	US-11-174-307B-964	Sequence 964, App
1059	57	9.7	35	7	US-11-155-989-122	Sequence 1, Appl	1134	57	9.7	1412	7	US-11-174-307B-3072	Sequence 3072, Ap
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1061	57	9.7	157	7	US-11-056-355B-58091	Sequence 58091, A	1136	57	9.7	1416	7	US-11-174-307B-2646	Sequence 2646, Ap
1062	57	9.7	291	6	US-10-953-349-19822	Sequence 19822, A	1137	57	9.7	1418	7	US-11-174-307B-950	Sequence 950, App
1063	57	9.7	291	7	US-11-056-355B-55600	Sequence 55600, A	1138	57	9.7	1439	7	US-11-174-307B-604	Sequence 604, App
							1139	57	9.7	1482	7	US-11-174-307B-880	Sequence 880, App

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1142	57	9.7	1535	7	US-11-174-307B-94	Sequence 94, App	1216	56.5	9.6	1276	7	US-11-174-307B-1764	Sequence 1764, Ap
1143	57	9.7	1536	7	US-11-174-307B-1218	Sequence 1218, Ap	1217	56.5	9.6	1277	7	US-11-174-307B-440	Sequence 440, App
1144	57	9.7	1540	7	US-11-174-307B-2418	Sequence 2418, Ap	1218	56.5	9.6	1280	7	US-11-174-307B-2512	Sequence 2512, Ap
1145	57	9.7	1569	7	US-11-174-307B-2258	Sequence 2258, Ap	1219	56.5	9.6	1292	7	US-11-174-307B-514	Sequence 514, App
1146	57	9.7	1597	7	US-11-174-307B-618	Sequence 618, App	1220	56.5	9.6	1304	7	US-11-174-307B-2586	Sequence 2586, Ap
1147	57	9.7	1605	7	US-11-174-307B-1410	Sequence 1410, Ap	1221	56.5	9.6	1305	7	US-11-174-307B-2140	Sequence 2140, Ap
1148	57	9.7	1633	7	US-11-174-307B-2704	Sequence 2704, Ap	1222	56.5	9.6	1349	7	US-11-174-307B-2466	Sequence 2466, Ap
1149	57	9.7	1637	7	US-11-174-307B-2178	Sequence 2178, Ap	1223	56.5	9.6	1365	7	US-11-174-307B-482	Sequence 482, App
1150	57	9.7	1637	7	US-11-174-307B-2562	Sequence 2562, Ap	1224	56.5	9.6	1376	7	US-11-174-307B-836	Sequence 836, App
1151	57	9.7	1649	7	US-11-174-307B-860	Sequence 860, App	1225	56.5	9.6	1381	7	US-11-174-307B-3378	Sequence 3378, Ap
1152	57	9.7	1698	7	US-11-174-307B-718	Sequence 718, App	1226	56.5	9.6	1394	7	US-11-174-307B-640	Sequence 640, App
1153	57	9.7	1721	7	US-11-174-307B-968	Sequence 968, App	1227	56.5	9.6	1449	7	US-11-174-307B-1362	Sequence 1362, Ap
1154	57	9.7	1735	7	US-11-174-307B-2246	Sequence 2246, Ap	1228	56.5	9.6	1459	7	US-11-174-307B-1396	Sequence 1396, Ap
1155	57	9.7	1738	7	US-11-174-307B-864	Sequence 864, App	1229	56.5	9.6	1462	7	US-11-174-307B-1412	Sequence 1412, Ap
1156	57	9.7	1766	7	US-11-174-307B-5194	Sequence 5194, Ap	1230	56.5	9.6	1463	7	US-11-436-904-16	Sequence 16, Appl
1157	57	9.7	1775	7	US-11-174-307B-526	Sequence 526, App	1231	56.5	9.6	1486	7	US-11-174-307B-772	Sequence 772, App
1158	57	9.7	1822	6	US-10-505-928-700	Sequence 700, App	1232	56.5	9.6	1487	7	US-11-174-307B-696	Sequence 696, App
1159	57	9.7	1872	7	US-11-174-307B-1664	Sequence 1664, Ap	1233	56.5	9.6	1487	7	US-11-174-307B-2972	Sequence 2972, Ap
1160	57	9.7	1910	7	US-11-174-307B-2256	Sequence 2256, Ap	1234	56.5	9.6	1488	7	US-11-174-307B-4372	Sequence 4372, Ap
1161	57	9.7	1951	7	US-11-174-307B-3118	Sequence 3118, Ap	1235	56.5	9.6	1502	7	US-11-174-307B-632	Sequence 632, App
1162	57	9.7	1968	7	US-11-174-307B-730	Sequence 730, App	1236	56.5	9.6	1517	7	US-11-174-307B-1368	Sequence 1368, Ap
1163	57	9.7	2017	7	US-11-174-307B-2682	Sequence 2682, Ap	1237	56.5	9.6	1518	7	US-11-436-904-2	Sequence 2, Appl
1164	57	9.7	2180	7	US-11-174-307B-530	Sequence 530, App	1238	56.5	9.6	1518	7	US-11-436-904-18	Sequence 18, Appl
1165	56.5	9.6	80	7	US-11-412-325-205	Sequence 205, App	1239	56.5	9.6	1521	7	US-11-174-307B-1956	Sequence 1956, Ap
1166	56.5	9.6	156	7	US-11-050-875-561	Sequence 561, App	1240	56.5	9.6	1531	7	US-11-174-307B-170	Sequence 170, App
1167	56.5	9.6	214	7	US-11-293-697-3355	Sequence 3355, Ap	1241	56.5	9.6	1545	7	US-11-174-307B-1584	Sequence 1584, Ap
1168	56.5	9.6	229	7	US-11-293-697-4810	Sequence 4810, Ap	1242	56.5	9.6	1546	7	US-11-174-307B-1896	Sequence 1896, Ap
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1171	56.5	9.6	294	6	US-10-953-349-7532	Sequence 7532, Ap	1245	56.5	9.6	1573	7	US-11-436-904-20	Sequence 20, Appl
1172	56.5	9.6	316	6	US-10-953-349-7531	Sequence 7531, Ap	1246	56.5	9.6	1577	7	US-11-174-307B-1118	Sequence 1118, Ap
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1174	56.5	9.6	353	7	US-11-371-354-52368	Sequence 12268, A	1248	56.5	9.6	1610	7	US-11-174-307B-1472	Sequence 1472, Ap
1175	56.5	9.6	353	7	US-11-371-354-55201	Sequence 55201, A	1249	56.5	9.6	1610	7	US-11-174-307B-1688	Sequence 1688, Ap
1176	56.5	9.6	353	7	US-11-371-354-76042	Sequence 76042, A	1250	56.5	9.6	1657	7	US-11-174-307B-1212	Sequence 1212, Ap
1177	56.5	9.6	381	7	US-11-197-712-255	Sequence 255, App	1251	56.5	9.6	1660	7	US-11-174-307B-2908	Sequence 2908, Ap
1178	56.5	9.6	401	7	US-11-303-169-4	Sequence 4, Appl	1252	56.5	9.6	1711	7	US-11-174-307B-2190	Sequence 2190, Ap
1179	56.5	9.6	404	6	US-10-540-847-3	Sequence 3, Appl	1253	56.5	9.6	1713	7	US-11-174-307B-1752	Sequence 1752, Ap
1180	56.5	9.6	419	7	US-11-366-965-13	Sequence 13, Appl	1254	56.5	9.6	1720	7	US-11-174-307B-3676	Sequence 3676, Ap
1181	56.5	9.6	463	6	US-10-540-847-16	Sequence 16, Appl	1255	56.5	9.6	1739	7	US-11-174-307B-318	Sequence 318, App
1182	56.5	9.6	439	7	US-11-056-355B-6832	Sequence 6832, Ap	1256	56.5	9.6	1780	7	US-11-174-307B-1970	Sequence 1970, Ap
1183	56.5	9.6	459	6	US-10-540-847-8	Sequence 8, Appl	1257	56.5	9.6	1808	7	US-11-174-307B-1788	Sequence 1788, Ap
1184	56.5	9.6	459	6	US-10-540-847-9	Sequence 9, Appl	1258	56.5	9.6	1826	7	US-11-174-307B-1400	Sequence 1400, Ap
1185	56.5	9.6	462	7	US-11-056-355B-6831	Sequence 6831, Ap	1259	56.5	9.6	1882	7	US-11-174-307B-1388	Sequence 1388, Ap
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1187	56.5	9.6	468	6	US-10-449-902-53196	Sequence 53196, A	1261	56.5	9.6	1955	7	US-11-174-307B-1590	Sequence 1590, Ap
1188	56.5	9.6	480	7	US-11-056-355B-6830	Sequence 6830, Ap	1262	56.5	9.6	1970	7	US-11-174-307B-1984	Sequence 1984, Ap
1189	56.5	9.6	500	7	US-11-293-697-4684	Sequence 4684, Ap	1263	56.5	9.6	1980	7	US-11-174-307B-1298	Sequence 1298, Ap
1190	56.5	9.6	518	7	US-11-174-307B-3402	Sequence 3402, Ap	1264	56.5	9.6	2133	7	US-11-174-307B-894	Sequence 894, App
1191	56.5	9.6	647	7	US-11-174-307B-714	Sequence 714, App	1265	56.5	9.6	2202	6	US-10-544-731-8	Sequence 8, Appl
1192	56.5	9.6	741	6	US-10-526-324-2142	Sequence 2142, Ap	1266	56.5	9.6	2227	6	US-10-544-731-7	Sequence 7, Appl
1193	56.5	9.6	764	6	US-10-574-398-54	Sequence 54, Appl	1267	56.5	9.6	2233	6	US-10-544-731-9	Sequence 9, Appl
1194	56.5	9.6	764	6	US-10-533-519-2239	Sequence 2239, Ap	1268	56	9.5	16	7	US-11-304-129-11	Sequence 11, Appl
1195	56.5	9.6	764	7	US-11-223-738-6	Sequence 6, Appl	1269	56	9.5	124	7	US-11-056-355B-17338	Sequence 17338, A
1196	56.5	9.6	788	7	US-11-188-417B-30	Sequence 30, Appl	1270	56	9.5	132	7	US-11-056-355B-85497	Sequence 85497, A
1197	56.5	9.6	794	6	US-10-533-519-920	Sequence 920, App	1271	56	9.5	132	7	US-11-056-355B-96353	Sequence 96353, A
1198	56.5	9.6	830	7	US-11-443-904-33	Sequence 33, Appl	1272	56	9.5	152	6	US-10-953-349-38062	Sequence 38062, A
1199	56.5	9.6	870	7	US-11-090-997-1592	Sequence 1592, Ap	1273	56	9.5	156	7	US-11-404-843-122	Sequence 122, App
1200	56.5	9.6	891	7	US-11-330-123-91	Sequence 91, Appl	1274	56	9.5	163	7	US-11-056-355B-85496	Sequence 85496, A
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1206	56.5	9.6	1094	7	US-11-174-307B-438	Sequence 438, App	1279	56	9.5	264	7	US-11-056-355B-106290	Sequence 106290, A
1207	56.5	9.6	1095	7	US-11-174-307B-240	Sequence 240, App	1280	56	9.5	265	7	US-11-056-355B-117529	Sequence 117529, A
1208	56.5	9.6	1125	7	US-11-056-355B-86061	Sequence 86061, A	1281	56	9.5	265	7	US-11-056-355B-106289	Sequence 106289, A
1209	56.5	9.6	1150	7	US-11-056-355B-86060	Sequence 86060, A	1282	56	9.5	270	7	US-11-056-355B-117528	Sequence 117528, A
1210	56.5	9.6	1170	7	US-11-174-307B-2404	Sequence 2404, Ap	1283	56	9.5	276	7	US-11-330-403-4917	Sequence 4917, Ap
1211	56.5	9.6	1220	7	US-11-174-307B-362	Sequence 362, App	1284	56	9.5	376	7	US-11-119-526A-41	Sequence 41, Appl
1212	56.5	9.6	1221	7	US-11-174-307B-2644	Sequence 2644, Ap	1285	56	9.5	388	7	US-11-119-526A-41	Sequence 41, Appl
1213	56.5	9.6	1227	7	US-11-174-307B-2644	Sequence 2644, Ap	1286	56	9.5	393	7	US-11-330-403-14853	Sequence 14853, A

1287	56	9.5	408	7	US-11-119-526A-6	Sequence 6, Appli	1360	56	9.5	1721	7	US-11-174-307B-1148	Sequence 1148, Ap
1288	56	9.5	457	7	US-11-174-307B-188	Sequence 188, App	1363	56	9.5	1747	7	US-11-174-307B-2700	Sequence 2700, Ap
1289	56	9.5	465	7	US-11-392-436-6	Sequence 6, Appli	1364	56	9.5	1761	7	US-11-174-307B-3708	Sequence 3708, Ap
1290	56	9.5	490	6	US-10-449-902-38615	Sequence 38615, A	1365	56	9.5	1764	7	US-11-174-307B-900	Sequence 900, App
1291	56	9.5	503	7	US-11-174-307B-86	Sequence 86, Appl	1366	56	9.5	1786	6	US-10-519-328-2	Sequence 2, Appl1
1292	56	9.5	528	7	US-11-392-436-22	Sequence 22, Appl	1367	56	9.5	1792	6	US-11-174-307B-1192	Sequence 1192, Ap
1293	56	9.5	533	7	US-11-174-307B-190	Sequence 190, App	1368	56	9.5	1816	7	US-11-174-307B-590	Sequence 590, App
1294	56	9.5	565	6	US-10-669-920-663	Sequence 663, App	1369	56	9.5	1821	6	US-10-505-928-451	Sequence 451, App
1295	56	9.5	572	7	US-11-174-307B-5524	Sequence 5524, Ap	1370	56	9.5	1821	6	US-10-519-328-1	Sequence 1, Appl1
1296	56	9.5	612	6	US-10-449-902-41558	Sequence 41558, A	1371	56	9.5	1863	7	US-11-174-307B-1830	Sequence 1830, Ap
1297	56	9.5	628	7	US-11-174-307B-3552	Sequence 3552, Ap	1372	56	9.5	1869	7	US-11-174-307B-746	Sequence 746, App
1298	56	9.5	637	6	US-10-449-902-53555	Sequence 53555, A	1373	56	9.5	1884	7	US-11-174-307B-234	Sequence 234, App
1299	56	9.5	648	6	US-10-669-920-807	Sequence 807, App	1374	56	9.5	1919	7	US-11-174-307B-4028	Sequence 4028, Ap
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1301	56	9.5	746	6	US-10-669-920-665	Sequence 665, App	1376	56	9.5	1937	7	US-11-174-307B-3074	Sequence 3074, Ap
1302	56	9.5	746	6	US-11-371-354-12063	Sequence 12063, A	1377	56	9.5	2062	7	US-11-174-307B-1454	Sequence 1454, Ap
1303	56	9.5	746	7	US-11-371-354-72055	Sequence 72055, A	1378	56	9.5	2068	7	US-11-174-307B-2662	Sequence 2662, Ap
1304	56	9.5	746	7	US-11-371-354-75761	Sequence 75761, A	1379	56	9.5	2077	7	US-11-174-307B-324	Sequence 324, App
1305	56	9.5	754	7	US-11-056-3558-81272	Sequence 81272, A	1380	56	9.5	2101	7	US-11-174-307B-778	Sequence 778, App
1306	56	9.5	763	6	US-10-982-908-28	Sequence 28, Appl	1381	56	9.5	2110	7	US-11-174-307B-2010	Sequence 2010, Ap
1307	56	9.5	820	6	US-10-982-908-26	Sequence 26, Appl	1382	56	9.5	2127	7	US-11-174-307B-748	Sequence 748, App
1308	56	9.5	826	7	US-11-056-3558-81271	Sequence 81271, A	1383	56	9.5	2205	7	US-11-174-307B-1504	Sequence 1504, Ap
1309	56	9.5	849	7	US-11-056-3558-81270	Sequence 81270, A	1384	56	9.5	2235	7	US-11-174-307B-2036	Sequence 2036, Ap
1310	56	9.5	921	7	US-11-174-307B-2044	Sequence 2044, Ap	1385	56	9.5	2280	7	US-11-174-307B-1878	Sequence 1878, Ap
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1313	56	9.5	967	7	US-11-174-307B-412	Sequence 412, App	1388	56	9.5	2416	7	US-11-174-307B-1564	Sequence 1564, Ap
1314	56	9.5	997	7	US-11-174-307B-4404	Sequence 4404, Ap	1389	56	9.5	2435	7	US-11-174-307B-1790	Sequence 1790, Ap
1315	56	9.5	1059	7	US-11-174-307B-1950	Sequence 1950, Ap	1390	56	9.5	2459	7	US-11-174-307B-1578	Sequence 1578, Ap
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1317	56	9.5	1187	7	US-11-174-307B-1728	Sequence 1728, Ap	1392	56	9.5	2782	7	US-11-174-307B-722	Sequence 722, App
1318	56	9.5	1209	7	US-11-174-307B-360	Sequence 360, App	1393	56	9.5	2973	7	US-11-174-307B-1566	Sequence 1566, Ap
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1322	56	9.5	1248	7	US-11-174-307B-1482	Sequence 1482, Ap	1397	55.5	9.4	147	7	US-11-344-932-482	Sequence 482, App
1323	56	9.5	1250	7	US-11-174-307B-1868	Sequence 1868, Ap	1398	55.5	9.4	143	6	US-10-612-783-5816	Sequence 5816, Ap
1324	56	9.5	1251	7	US-11-174-307B-426	Sequence 426, App	1399	55.5	9.4	159	7	US-11-377-336-42	Sequence 42, Appl
1325	56	9.5	1266	7	US-11-174-307B-478	Sequence 478, App	1400	55.5	9.4	168	7	US-11-056-3558-91545	Sequence 91545, A
1326	56	9.5	1266	7	US-11-174-307B-678	Sequence 678, App	1401	55.5	9.4	168	7	US-11-056-3558-95301	Sequence 95301, A
1327	56	9.5	1283	7	US-11-174-307B-678	Sequence 678, App	1402	55.5	9.4	173	6	US-11-303-169-31	Sequence 31, Appl
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1331	56	9.5	1324	7	US-11-174-307B-1210	Sequence 1210, Ap	1406	55.5	9.4	323	7	US-11-330-403-4957	Sequence 4957, Ap
1332	56	9.5	1337	7	US-11-174-307B-1360	Sequence 1360, Ap	1407	55.5	9.4	332	7	US-11-330-403-4960	Sequence 4960, Ap
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1343	56	9.5	1475	7	US-11-174-307B-898	Sequence 898, App	1418	55.5	9.4	393	7	US-11-330-403-14331	Sequence 14331, A
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1354	56	9.5	1653	7	US-11-174-307B-626	Sequence 626, App	1429	55.5	9.4	526	7	US-11-024-544A-14	Sequence 14, Appl
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1435	55.5	9.4	536	7	US-11-265-761-95	Sequence 95, Appl
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1443	55.5	9.4	685	7	US-11-175-714-32	Sequence 32, Appl
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1468	55.5	9.4	1098	7	US-11-174-307B-2414	Sequence 2414, Ap
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1470	55.5	9.4	1122	7	US-11-174-307B-2524	Sequence 2524, Ap
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1484	55.5	9.4	1192	7	US-11-174-307B-2334	Sequence 2334, Ap
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Job time : 39.2356 secs

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OM protein - protein search, using sw model

Run on: December 14, 2006, 14:05:27 ; Search time 214.398 Seconds
(without alignments)
453.020 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

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Scoring table: BLOSUM62

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Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	589	100.0	105	PROK1_HUMAN	P58294 homo sapien
2	589	100.0	105	Q5VWD4_HUMAN	Q5vwd4 homo sapien
3	588	99.8	105	Q8TC69_HUMAN	Q8tc69 homo sapien
4	545	92.5	105	PROK1_RAT	Q8r414 rattus norv
5	432	73.3	81	Q8K457_MOUSE	Q8k457 mus musculu
6	417	70.8	81	Q2ZF12_BOVIN	Q2zf12 bos taurus
7	368	62.5	104	Q2XXR8_VARVA	Q2xxr8 varanus var
8	363	61.6	104	Q2XXR7_VARVA	Q2xxr7 varanus var
9	321	54.5	106	Q4RVU3_TETNG	Q4rvu3 tetraodon n
10	318	54.0	108	Q863H4_BOVIN	Q863h4 bos taurus
11	315	53.5	81	VPRA_DENPO	P25687 dendroaspis
12	303	51.4	108	Q6ISR0_HUMAN	Q6isr0 homo sapien
13	298.5	50.7	96	Q8JFQ0_BOMMX	Q8jfq0 bombina max
14	298	50.6	102	Q4SR12_TETNG	Q4sr12 tetraodon n
15	298	50.6	107	PROK2_RAT	Q8r413 rattus norv
16	298	50.6	107	Q50E37_MURI	Q50e37 arvicanthis
17	298	50.6	107	Q50E38_MURI	Q50e38 arvicanthis
18	298	50.6	128	Q863H5_BOVIN	Q863h5 bos taurus
19	293.5	49.8	96	Q5W280_BOMOR	Q5w280 bombina ori
20	287.5	48.8	96	BVB_BOMVA	Q9pw66 bombina var
21	282.5	48.0	129	PROK2_HUMAN	Q9hc23 homo sapien
22	282.5	48.0	129	Q53Z79_HUMAN	Q53z79 homo sapien
23	277.5	47.1	128	PROK2_MOUSE	Q9qxu7 mus musculu
24	277.5	47.1	128	Q50E33_MURI	Q50e33 arvicanthis
25	277.5	47.1	128	Q50E34_MURI	Q50e34 arvicanthis
26	277.5	47.1	128	Q6V8J7_RAT	Q6v8j7 rattus norv
27	274.5	46.6	96	Q8JF86_BOMMX	Q8jfe6 bombina max
28	273.5	46.4	96	Q8JFX8_BOMMX	Q8jfx8 bombina max
29	273.5	46.4	96	Q8JFY1_BOMMX	Q8jfy1 bombina max
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32	266.5	45.2	96	Q8JFY2_BOMMX	Q8jfy2 bombina max
33	203	34.5	82	Q2TBS7_BOVIN	Q2tbs7 bos taurus
34	200	34.0	86	Q50E35_MURI	Q50e35 arvicanthis
35	200	34.0	86	Q50E36_MURI	Q50e36 arvicanthis
36	193	32.8	39	Q50E61_MURI	Q50e61 arvicanthis
37	126.5	21.5	124	Q56R10_PENMO	Q56r10 penaeus mon
38	112	19.0	96	Q8UUX3_CHICK	Q8uux3 gallus gall
39	109	18.5	104	Q56R11_PACLE	Q56r11 pacifastacu
40	108.5	18.4	221	DKK4_MOUSE	Q8vej3 mus musculu
41	107.5	18.3	224	DKK4_HUMAN	Q8ubt3 homo sapien
42	107.5	18.3	224	Q3KXK0_HUMAN	Q3kxk0 homo sapien
43	107.5	18.3	350	DKK3_CHICK	Q90839 gallus gall
44	104	17.7	255	Q9DDA4_XENLA	Q9dd44 xenopus lae
45	102	17.3	180	Q4RJF1_TETNG	Q4rjfi tetraodon n
46	102	17.3	259	DKK2_HUMAN	Q9ubt2 homo sapien
47	101.5	17.2	256	Q5BHU6_GECJA	Q5ehu6 gecko japon
48	101	17.1	259	DKK2_MOUSE	Q9qy28 mus musculu
49	101	17.1	259	Q8BFW0_MOUSE	Q8bfw0 m 10, 11 da
50	101	17.1	272	DKK1_MOUSE	Q54908 mus musculu
51	101	17.1	272	Q80UL5_MOUSE	Q80ul5 m dickkopf
52	100.5	17.1	171	Q43532_HUMAN	Q43532 homo sapien
53	100.5	17.1	215	Q8N294_HUMAN	Q8n294 homo sapien
54	100.5	17.1	341	Q5R8T0_PONPY	Q5r8t0 pongo pygma
55	100.5	17.1	350	DKK3_HUMAN	Q9ubp4 homo sapien
56	100.5	17.1	350	Q4R4I7_MACFA	Q4r4i7 macaca fasc
57	100.5	17.1	350	Q5R4Q2_PONPY	Q5r4q2 pongo pygma
58	99.5	16.9	277	Q9ES33_RAT	Q9es33 rattus norv
59	99.5	16.9	348	Q5RKL1_RAT	Q5rkl1 rattus norv
60	98.5	16.7	349	DKK3_MOUSE	Q9quu9 mus musculu
61	97	16.5	266	DKK1_HUMAN	Q94907 homo sapien
62	96.5	16.4	268	Q6PVU5_RABIT	Q6pvu5 oryctolagus
63	95.5	16.2	259	Q57464_XENLA	Q57464 xenopus lae
64	95	16.1	177	Q4SL69_TETNG	Q4sl69 tetraodon n
65	94.5	16.0	350	Q6P081_HUMAN	Q6p081 homo sapien
66	94	16.0	240	Q9PH33_BRARE	Q9ph33 brachydanio
67	94	16.0	418	Q4T860_TETNG	Q4t860 tetraodon n
68	93.5	15.9	1233	Q4S163_TETNG	Q4s163 tetraodon n
69	93	15.8	88	Q5D229_HADSP	Q5d229 hadronyche
70	92	15.6	88	Q5D228_HADSP	Q5d228 hadronyche
71	90.5	15.4	400	Q3U1Z8_MOUSE	Q3u1z8 mus musculu
72	90.5	15.4	425	CN130_MOUSE	Q8bu44 mus musculu
73	90.5	15.4	425	Q52KC0_MOUSE	Q52kc0 m hypotheti
74	90.5	15.4	425	Q642A8_RAT	Q642a8 rattus norv
75	89	15.1	88	Q5D230_HADSP	Q5d230 hadronyche
76	88.5	15.0	640	Q96397_CHLRE	Q96397 chlamydomon
77	86	14.6	241	Q9W6D9_BRARE	Q9w6d9 brachydanio
78	85	14.4	107	COL_RABIT	F42890 oryctolagus
79	84.5	14.3	102	Q3UW21_MOUSE	Q3uw21 mus musculu
80	84	14.3	1331	Q4S572_TETNG	Q4s572 tetraodon n
81	83.5	14.2	110	Q4PML0_IXOSC	Q4pml0 ixodes scap
82	83	14.1	708	P87363_CHICK	P87363 gallus gall
83	83	14.1	966	Q22378_CABEL	Q22378 caenorhabdi
84	82.5	14.0	274	Q5RCC3_PONPY	Q5rc33 pongo pygma
85	82.5	14.0	425	CN130_HUMAN	Q8n806 homo sapien
86	82	13.9	1165	Q5BKFS_XENTR	Q5bkfs xenopus tro
87	81.5	13.8	446	Q8NB03_HUMAN	Q8nb03 homo sapien
88	81	13.8	1964	NOTC4_MOUSE	P31695 mus musculu
89	80.5	13.7	113	Q9D2R7_MOUSE	Q9d2r7 mus musculu
90	80.5	13.7	386	Q32NM5_XENLA	Q32nm5 xenopus lae
91	80.5	13.7	388	Q6BY16_XENLA	Q6by16 xenopus lae
92	80.5	13.7	388	Q6JA22_XENLA	Q6ja22 xenopus lae
93	80.5	13.7	729	Q8BNH3_MOUSE	Q8bnh3 mus musculu
94	80.5	13.7	787	Q8K061_MOUSE	Q8k061 mus musculu
95	80.5	13.7	1193	Q4S758_TETNG	Q4s758 tetraodon n
96	80	13.6	412	Q86HY9_DICDI	Q86hy9 dictyosteli
97	79.5	13.5	191	Q6ZQW6_HUMAN	Q6zqw6 homo sapien
98	79.5	13.5	404	Q6ZQW7_HUMAN	Q6zqw7 homo sapien
99	79.5	13.5	446	Q8NIN5_HUMAN	Q8nin5 homo sapien
100	79.5	13.5	704	FBLN1_CHICK	Q73775 gallus gall
101	79.5	13.5	870	Q8IQG6_DRONE	Q8iqg6 drosophila
102	79.5	13.5	1353	Q4UGZ9_THRAE	Q4ugz9 theileria a
103	79	13.4	109	Q5U809_HUMAN	Q5u809 homo sapien
104	79	13.4	112	COL_HUMAN	P04118 homo sapien

105	79	13.4	112	2	Q5T9G7_HUMAN	Q5t9g7	homo sapien	178	74	12.6	1171	2	Q4RLR5_TETNG	Q4rlr5	tetraodon n
106	79	13.4	224	2	Q4H3Q2_CIOIN	Q4h3q2	ciona intes	179	74	12.6	1216	2	Q5TZK7_BRARE	Q5tzk7	brachydanio
107	79	13.4	225	2	Q4H3Q3_CIOIN	Q4h3q3	ciona intes	180	74	12.6	1216	2	Q9OY55_BRARE	Q9oy55	brachydanio
108	79	13.4	919	2	Q61V24_CAEBR	Q61v24	caenorhabdi	181	74	12.6	1254	2	Q5TZK8_BRARE	Q5tzk8	brachydanio
109	79	13.4	1651	2	Q9T9Q2_CAEBL	Q9t9q2	caenorhabdi	182	74	12.6	1254	2	Q9OY56_BRARE	Q9oy56	brachydanio
110	79	13.4	2447	2	Q13149_FUGRU	Q13149	fugu rubrip	183	74	12.6	1254	2	Q9YHU2_BRARE	Q9yhu2	brachydanio
111	79	13.4	5533	2	Q5RIP6_BRARE	Q5rip6	brachydanio	184	74	12.6	4680	2	Q7PV66_ANOGA	Q7pv66	anopheles g
112	78.5	13.3	162	2	Q5JHV8_PYRKO	Q5jnv8	pyrococcus	185	73.5	12.5	701	2	Q8AVE8_XENLA	Q8ave8	xenopus lae
113	78.5	13.3	593	2	Q5R5T2_PONPY	Q5r5t2	pongo pygma	186	73.5	12.5	2146	2	Q4T7A2_TETNG	Q4t7a2	tetraodon n
114	78	13.2	70	1	QXIX_CONBE	Qxix33	conus betul	187	73.5	12.5	2715	1	MLL4_HUMAN	Q8um6	homo sapien
115	78	13.2	425	2	Q53RA0_HUMAN	Q53ra0	homo sapien	188	73	12.4	64	1	TX16_PHORI	P83893	phoeutria
116	78	13.2	1408	2	Q4RX38_TETNG	Q4rx38	tetraodon n	189	73	12.4	172	2	Q8RU50_ORYSA	Q8ru50	oryza sativ
117	78	13.2	4599	1	LRP1B_HUMAN	Q9nr2	homo sapien	190	73	12.4	417	2	TNR16_MOUSE	Q920w1	mus musculu
118	77.5	13.2	350	2	Q54EN7_DICDI	Q54en7	dictyosteli	191	73	12.4	417	2	Q8BYI1_MOUSE	Q8byi1	mus musculu
119	77.5	13.2	473	1	FP2_MYTGA	Q25464	mytilus gal	192	73	12.4	418	2	Q5ZMN4_CHICK	Q5zmn4	gallus gall
120	77.5	13.2	911	2	Q7Z2T0_BRARE	Q7z2t0	brachydanio	193	73	12.4	427	2	Q8CFT3_MOUSE	Q8cft3	mus musculu
121	77.5	13.2	2559	1	STAB2_MOUSE	Q8r4u0	mus musculu	194	73	12.4	457	2	Q8IVS6_HUMAN	Q8ivs6	homo sapien
122	77	13.1	21	2	Q24774_ENCHU	Q24774	enchytraeus	195	73	12.4	461	1	TNR1B_HUMAN	P20333	h tumor nec
123	77	13.1	231	2	Q70LQ4_ENCBU	Q70lq4	enchytraeus	196	73	12.4	461	2	Q5THJ6_HUMAN	Q5thj6	homo sapien
124	77	13.1	693	2	Q50SM8_XENLA	Q50sm8	xenopus lae	197	73	12.4	732	2	Q9RH03_AZOIR	Q9rh03	azospirillum
125	77	13.1	762	2	Q8ML23_DROME	Q8ml23	drosophila	198	73	12.4	835	2	Q69ZY6_MOUSE	Q69zy6	mus musculu
126	77	13.1	1961	2	Q6MG89_RAT	Q6mg89	rattus norv	199	73	12.4	1123	2	Q4H346_CIOIN	Q4h346	ciona intes
127	77	13.1	3570	2	Q7Q737_ANOGA	Q7q737	anopheles g	200	73	12.4	2871	1	FBN1_PIG	Q9tv36	sus scrofa
128	76.5	13.0	81	2	Q54HF8_DICDI	Q54hf8	dictyosteli	201	73	12.4	3075	1	LAM1_HUMAN	P25391	homo sapien
129	76.5	13.0	425	2	Q4R222_MACFA	Q4r222	macaca fasc	202	73	12.4	3857	1	O88840_MOUSE	O88840	mus musculu
130	76.5	13.0	1637	2	Q9XSV8_BOVIN	Q9xsv8	bos taurus	203	72.5	12.3	103	2	Q6Z331_ORYSA	O6z331	oryza sativ
131	76.5	13.0	5146	2	Q8SPM4_BOVIN	Q8spm4	bos taurus	204	72.5	12.3	517	2	Q9NFO1_HUMAN	Q9np01	homo sapien
132	76	12.9	264	2	Q5H2W5_RAT	Q5hw5	rattus norv	205	72.5	12.3	615	2	Q22886_CAEBL	Q22886	caenorhabdi
133	76	12.9	496	2	Q54L19_DICDI	Q54l19	dictyosteli	206	72.5	12.3	1365	2	Q75N88_HUMAN	Q75n88	homo sapien
134	76	12.9	496	2	Q6TWJ0_DICDI	Q6twj0	dictyosteli	207	72.5	12.3	1365	1	FBN1_HUMAN	P98133	bos taurus
135	76	12.9	1299	2	Q385C6_9TRYP	Q385c6	trypanosoma	208	72.5	12.3	2871	1	FBN1_BOVIN	P35555	homo sapien
136	75.5	12.8	1099	2	Q86CP7_HUMAN	Q86cp7	homo sapien	209	72.5	12.3	3277	2	Q6VU67_HUMAN	Q6vu67	homo sapien
137	75.5	12.8	1099	2	Q6OV58_CAEBR	Q6ov58	caenorhabdi	210	72.5	12.3	3333	2	Q76E14_HUMAN	Q76e14	homo sapien
138	75.5	12.8	1574	1	EGFL3_RAT	Q88281	rattus norv	211	72.5	12.3	3333	2	Q6VU68_HUMAN	Q6vu68	homo sapien
139	75.5	12.8	1761	2	Q86XN2_HUMAN	Q86xn2	homo sapien	212	72	12.2	101	2	Q65313_9ROSI	Q65313	lavatera th
140	75	12.7	130	2	Q4PMW2_IXOSC	Q4pmw2	ixodes scap	213	72	12.2	146	2	Q5K4F7_SCHGR	Q5k4f7	schistocerc
141	75	12.7	303	2	Q3TTU9_MOUSE	Q3ttu9	mus musculu	214	72	12.2	269	2	Q4I3B1_GIBZE	Q4i3b1	gibbetella
142	75	12.7	490	1	TPMS2_MOUSE	Q9j1q8	mus musculu	215	72	12.2	348	2	Q54KB6_DICDI	Q54kb6	dictyosteli
143	75	12.7	490	2	Q3URE3_MOUSE	Q3uke3	mus musculu	216	72	12.2	576	2	Q6YID6_PENMO	Q6yid6	penaeus mon
144	75	12.7	490	2	Q7TN04_MOUSE	Q7tn04	mus musculu	217	72	12.2	1361	2	Q9NGV2_DROME	Q9ngv2	drosophila
145	75	12.7	579	2	Q6P2G0_HUMAN	Q6p2g0	homo sapien	218	72	12.2	1361	2	Q9V714_DROME	Q9v714	drosophila
146	75	12.7	647	2	Q6P3V5_HUMAN	Q6p3v5	homo sapien	219	72	12.2	1639	1	LAMC1_DROME	P15215	drosophila
147	75	12.7	735	1	ADAM2_HUMAN	Q99655	homo sapien	220	72	12.2	1639	2	Q5BI30_DROME	Q5bi30	drosophila
148	75	12.7	1051	2	Q5U4U1_XENLA	Q5u4u1	xenopus lae	221	71.5	12.1	450	2	Q5ZVJ3_CIOIN	Q5zvj3	ciona intes
149	75	12.7	1214	2	Q90YD2_XENLA	Q90yd2	xenopus lae	222	71.5	12.1	173	2	Q64767_ADEG1	Q64767	avian adeno
150	75	12.7	1581	1	LAMC3_MOUSE	Q9r0b6	mus musculu	223	71.5	12.1	591	1	GRN_CAVPO	P28797	cavia porce
151	75	12.7	1581	2	Q4VA13_MOUSE	Q4va13	mus musculu	224	71.5	12.1	638	2	Q8NBH6_HUMAN	Q8nbh6	homo sapien
152	75	12.7	1957	2	Q4SU28_TETNG	Q4su28	tetraodon n	225	71.5	12.1	703	1	FBLN1_HUMAN	P23142	homo sapien
153	75	12.7	2003	1	NOTC4_HUMAN	Q99466	homo sapien	226	71.5	12.1	1170	1	TSP2_BOVIN	Q95116	bos taurus
154	75	12.7	2003	2	Q5SPL1_HUMAN	Q5spl1	homo sapien	227	71.5	12.1	1178	1	TSP2_CHICK	P35440	gallus gall
155	75	12.7	2003	2	Q5SSY7_HUMAN	Q5ssy7	homo sapien	228	71.5	12.1	1285	1	CRUM2_HUMAN	Q51j48	homo sapien
156	75	12.7	2005	2	Q5STG5_HUMAN	Q5stg5	homo sapien	229	71.5	12.1	1519	2	Q8WPN0_9UROC	Q8wpn0	oikopleura
157	75	12.7	2318	1	NOTC3_MOUSE	Q61982	mus musculu	230	71.5	12.1	1744	2	Q8CH1_MOUSE	Q8chh1	mus musculu
158	75	12.7	2319	1	NOTC3_RAT	Q9r172	rattus norv	231	71.5	12.1	1809	1	FYV1_DROME	Q96838	drosophila
159	75	12.7	2531	2	Q16004_LYTVA	Q16004	lytechinus	232	71.5	12.1	2013	2	Q6PHU4_MOUSE	Q6phu4	mus musculu
160	75	12.7	2884	2	Q4SHN1_TETNG	Q4shn1	tetraodon n	233	71.5	12.1	2713	2	Q5NU09_MOUSE	Q5nu09	mus musculu
161	74.5	12.6	104	2	Q7XZ46_GRIJA	Q7xz46	griffithsia	234	71	12.1	286	2	Q7JMU0_MELIC	Q7jmu0	meiodogyne
162	74.5	12.6	113	1	COL_MOUSE	Q9cgc2	mus musculu	235	71	12.1	288	2	Q5RIP8_BRARE	Q5rip8	brachydanio
163	74.5	12.6	190	2	Q4T7E9_TETNG	Q4t7e9	tetraodon n	236	71	12.1	305	2	Q25467_MELIC	Q25467	meiodogyne
164	74.5	12.6	194	2	Q4SIA7_TETNG	Q4sia7	tetraodon n	237	71	12.1	438	2	Q53Y88_HUMAN	Q53y88	homo sapien
165	74.5	12.6	286	2	Q7R5C8_GIALA	Q7r5c8	giardia lam	238	71	12.1	442	2	Q55GL3_DICDI	Q55gl3	dictyosteli
166	74.5	12.6	387	2	Q4KLX7_XENLA	Q4klx7	xenopus lae	239	71	12.1	457	2	Q8TEC5_HUMAN	Q8tec5	homo sapien
167	74.5	12.6	387	2	Q9PVD4_XENLA	Q9pvd4	xenopus lae	240	71	12.1	593	1	GRN_HUMAN	P28799	h grandulis
168	74.5	12.6	392	2	Q6NUF1_XENLA	Q6nuf1	xenopus lae	241	71	12.1	593	2	Q53HQ8_HUMAN	Q53hq8	homo sapien
169	74.5	12.6	720	2	Q2U318_ASPOR	Q2u318	aspergillus	242	71	12.1	593	2	Q540U8_HUMAN	Q540u8	homo sapien
170	74.5	12.6	1426	2	Q4RTA6_TETNG	Q4rta6	tetraodon n	243	71	12.1	1379	2	Q59H72_HUMAN	Q59h72	homo sapien
171	74.5	12.6	2327	2	Q9IBG7_XENLA	Q9ibg7	xenopus lae	244	71	12.1	1568	1	Q5VUP0_HUMAN	Q5vup0	homo sapien
172	74	12.6	92	2	Q615U9_ORYSA	Q615u9	oryza sativ	245	71	12.1	1587	2	LAMC3_HUMAN	Q5vup1	homo sapien
173	74	12.6	111	1	COL_SPEPR	Q9ix17	spermophilu	246	71	12.1	2359	2	Q5VUPI_HUMAN	Q5vupi	homo sapien
174	74	12.6	112	1	COL_RAT	P17084	rattus norv	247	71	12.1	287	2	Q59FG2_HUMAN	Q59fg2	homo sapien
175	74	12.6	239	2	Q3FKI4_9BURK	Q3fki4	rhodofera	248	70.5	12.0	444	2	Q75212_BRARE	Q75212	brachydanio
176	74	12.6	623	2	Q4PBA3_USTWA	Q4pba3	ustilago ma	249	70.5	12.0	444	2	Q6QW08_AZOB	Q6qw08	azospirillum
177	74	12.6	1168	2	Q60XC0_CAEBR	Q60xc0	caenorhabdi	250	70.5	12.0	490	2	Q6P7D7_RAT	Q6p7d7	rattus norv

251	70.5	12.0	555	2	Q4RN57_TETNG	Q4rn57 tetraodon n	324	68.5	11.6	931	2	Q61PT4_CABBR	Q61ft4 caenorhabdi
252	70.5	12.0	701	2	Q4T4W9_TETNG	Q4t4w9 tetraodon n	325	68.5	11.6	960	2	Q8MM07_CABEL	Q8mm07 caenorhabdi
253	70.5	12.0	1063	2	Q7QU10_GIALA	Q7qu10 giardia lam	326	68.5	11.6	969	2	Q8IV28_HUMAN	Q8iv28 homo sapien
254	70.5	12.0	1212	2	Q42347_CHICK	Q42347 gallus gall	327	68.5	11.6	1172	1	TSP2_MOUSE	Q03350 mus musculu
255	70.5	12.0	1847	2	Q76952_AEDAE	Q76952 aedes aegyp	328	68.5	11.6	1172	2	Q7TMT3_MOUSE	Q7tmt3 mus musculu
256	70.5	12.0	2871	1	FBN1_MOUSE	Q61554 mus musculu	329	68.5	11.6	1172	2	Q8CG21_MOUSE	Q8cgt1 mus musculu
257	70.5	12.0	2872	2	Q9WUH8_RAT	Q9wuh8 rattus norv	330	68.5	11.6	1180	2	Q5CZ12_HUMAN	Q5cz12 homo sapien
258	70	11.9	68	1	TX16_PHONI	P83997 phonetria	331	68.5	11.6	1375	1	NID2_HUMAN	Q14112 homo sapien
259	70	11.9	92	2	Q2MCN5_HYDMA	Q2mcn5 hydra magni	332	68.5	11.6	1801	2	Q8WSJ2_BOMMO	Q8wsj2 bombyx mori
260	70	11.9	315	2	Q56J31_CANFA	Q56j31 canis famli	333	68.5	11.6	1827	2	Q8JHV6_BRARE	Q8jhw6 brachydanio
261	70	11.9	426	2	Q6TMJ6_DICDI	Q6tmj6 dictyosteli	334	68.5	11.6	1952	2	Q95SN5_DROME	Q95sn5 drosophila
262	70	11.9	460	2	Q5SV22_HUMAN	Q5sv22 homo sapien	335	68.5	11.6	4547	2	Q9W343_DROME	Q9w343 drosophila
263	70	11.9	490	2	Q920K3_RAT	Q920k3 rattus norv	336	68	11.5	112	1	COL_CANFA	F19090 canis famli
264	70	11.9	706	2	Q4H3Q7_CIOIN	Q4h3q7 ciona intes	337	68	11.5	113	2	Q5T9G1_HUMAN	Q5t9g1 homo sapien
265	70	11.9	729	2	Q7T3M4_BRARE	Q7t3m4 brachydanio	338	68	11.5	314	2	Q5XTR8_MACMU	Q5xt8 macaca mula
266	70	11.9	729	2	Q4V9K5_BRARE	Q4v9k5 brachydanio	339	68	11.5	345	2	Q7JKP2_CABEL	Q7jpk2 caenorhabdi
267	70	11.9	750	2	Q4RQ92_TETNG	Q4rq92 tetraodon n	340	68	11.5	358	2	Q9U362_CABEL	Q9u362 caenorhabdi
268	70	11.9	841	1	TSIR1_HUMAN	Q7rt1 homo sapien	341	68	11.5	427	1	TNR16_HUMAN	P08138 homo sapien
269	70	11.9	947	2	Q8BKK7_MOUSE	Q8bkk7 mus musculu	342	68	11.5	489	1	MA2A1_RAT	P28434 rattus norv
270	70	11.9	950	2	Q802C1_XENLA	Q802c1 xenopus lae	343	68	11.5	497	2	Q4AQC1_9CHLB	Q4aqc1 chlorobium
271	70	11.9	1140	2	Q80T91_MOUSE	Q80t91 mus musculu	344	68	11.5	586	1	UL84_HCMVA	P16727 human cytom
272	70	11.9	1790	2	Q55F41_DICDI	Q55f41 dictyosteli	345	68	11.5	586	2	Q6RFX3_HCMV	Q6rfx3 human cytom
273	70	11.9	2428	2	Q816X6_BOOMI	Q8i6x6 boophilus m	346	68	11.5	587	2	Q6SW58_HCMV	Q6sw58 human cytom
274	69.5	11.8	89	2	Q5D232_HADSP	Q5d232 hadronyche	347	68	11.5	593	2	Q4R529_MACFA	Q4r529 macaca fasc
275	69.5	11.8	111	2	Q4PN79_IXOSC	Q4pn79 ixodes scap	348	68	11.5	677	2	Q4T3P3_TETNG	Q4t3p3 tetraodon n
276	69.5	11.8	113	2	Q8MKJ5_DROME	Q8mkj5 drosophila	349	68	11.5	729	2	Q6GPT6_XENLA	Q6gpt6 xenopus lae
277	69.5	11.8	123	2	Q3XNW9_PROT	Q3xnw9 magnetococc	350	68	11.5	794	2	Q8T4P0_LYTVA	Q8t4p0 lytechinus
278	69.5	11.8	413	2	Q9H81_HUMAN	Q9h81 homo sapien	351	68	11.5	893	2	Q9Y1Y3_9METZ	Q9y1y3 ephydatia f
279	69.5	11.8	540	2	Q4CXJ4_TRYCR	Q4cxj4 trypanosoma	352	68	11.5	944	2	Q4SLY2_TETNG	Q4sly2 tetraodon n
280	69.5	11.8	551	2	Q61MD2_CABBR	Q61md2 caenorhabdi	353	68	11.5	964	2	Q4STC1_TETNG	Q4stc1 tetraodon n
281	69.5	11.8	587	2	Q61T62_CABBR	Q61t62 caenorhabdi	354	68	11.5	1090	2	Q5SPG5_BRARE	Q5spg5 brachydanio
282	69.5	11.8	802	2	Q7JL02_CABEL	Q7jl02 caenorhabdi	355	68	11.5	1119	2	Q18034_CABEL	Q18034 caenorhabdi
283	69.5	11.8	818	2	Q4V7B3_RAT	Q4v7b3 rattus norv	356	68	11.5	1150	1	MA2A1_MOUSE	P27046 mus musculu
284	69.5	11.8	847	2	Q90W12_ONCMV	Q90w12 oncorhynch	357	68	11.5	1984	1	YL_DROME	P98163 drosophila
285	69.5	11.8	949	2	P90956_CABEL	P90956 caenorhabdi	358	68	11.5	2906	2	Q9WUH9_RAT	Q9wuh9 rattus norv
286	69.5	11.8	1147	2	Q3TLU3_MOUSE	Q3tlu3 mus musculu	359	68	11.5	5147	1	FAT_DROME	P33450 drosophila
287	69.5	11.8	2352	2	Q61240_HALRO	Q61240 halocynthia	360	67.5	11.5	110	2	Q5TA82_HUMAN	Q5ta82 homo sapien
288	69.5	11.8	2653	2	Q2S253_LUCCU	Q2s253 lucilia cup	361	67.5	11.5	200	2	Q7PWE6_ANOGA	Q7pwe6 anopheles g
289	69.5	11.8	4545	2	Q61291_MOUSE	Q61291 mus musculu	362	67.5	11.5	269	2	Q583F5_9TRYP	Q583f5 trypanosoma
290	69.5	11.8	4545	2	Q912X7_MOUSE	Q912x7 mus musculu	363	67.5	11.5	358	2	Q941Y3_ORYSA	Q941y3 oryza sativ
291	69.5	11.8	4545	2	Q920Y4_MOUSE	Q920y4 mus musculu	364	67.5	11.5	395	2	Q5TV39_ANOGA	Q5tv39 anopheles g
292	69	11.7	106	2	Q33AQ5_ORYSA	Q33aq5 oryza sativ	365	67.5	11.5	413	2	Q6ZP14_HUMAN	Q6ztp14 homo sapien
293	69	11.7	217	2	Q7X234_GRIJA	Q7x234 griffithsia	366	67.5	11.5	442	2	Q569T8_XENLA	Q569t8 xenopus lae
294	69	11.7	220	1	UPAS_RAT	P51573 rattus norv	367	67.5	11.5	443	2	Q2TAU8_XENLA	Q2tau8 xenopus lae
295	69	11.7	294	2	Q8IRV4_DROME	Q8irv4 drosophila	368	67.5	11.5	509	2	Q4SU37_TETNG	Q4su37 tetraodon n
296	69	11.7	328	1	UPAR_RAT	P49616 rattus norv	369	67.5	11.5	576	2	Q9Y3V7_HUMAN	Q9y3v7 homo sapien
297	69	11.7	388	2	Q66JK7_XENTR	Q66jk7 xenopus tro	370	67.5	11.5	608	2	Q627A0_CABBR	Q627a0 caenorhabdi
298	69	11.7	403	2	Q4R3X4_MACFA	Q4r3x4 macaca fasc	371	67.5	11.5	884	2	Q7QT01_GIALA	Q7qt01 giardia lam
299	69	11.7	611	2	Q4S228_TETNG	Q4s228 tetraodon n	372	67.5	11.5	895	2	Q9LX29_ARATH	Q9lx29 arabidopsis
300	69	11.7	949	2	Q3V7A7_9PRIM	Q3v7a7 macaca fusc	373	67.5	11.5	1068	2	Q6QHS4_STRPU	Q6qhs4 strongyloce
301	69	11.7	1599	2	Q616G7_CABBR	Q616g7 caenorhabdi	374	67.5	11.5	1184	1	FBLN2_HUMAN	P98095 homo sapien
302	69	11.7	1976	2	Q59ES6_HUMAN	Q59es6 homo sapien	375	67.5	11.5	1184	2	Q86V58_HUMAN	Q86v58 homo sapien
303	69	11.7	2360	2	Q7Y2P0_EIMMA	Q7y2p0 eimeria max	376	67.5	11.5	1231	2	Q8UIU0_HUMAN	Q8uiu0 homo sapien
304	69	11.7	2911	1	FBN2_HUMAN	P35556 homo sapien	377	67.5	11.5	1231	2	Q8UIU1_HUMAN	Q8uiu1 homo sapien
305	69	11.7	3133	1	HMCT_BOMMO	P98092 bombyx mori	378	67.5	11.5	1356	2	Q8C622_MOUSE	Q8c622 mus musculu
306	69	11.7	3712	1	LAMA_DROME	Q00174 drosophila	379	67.5	11.5	1356	2	Q4N8M7_THRPA	Q4n8m7 theileria p
307	68.5	11.6	143	2	Q330K6_TRIMU	Q330k6 trimeresuru	380	67.5	11.5	1403	1	NID2_MOUSE	Q88322 mus musculu
308	68.5	11.6	182	2	Q307E7_SHEEP	Q307e7 ovis aries	381	67.5	11.5	1403	2	Q3TFN0_MOUSE	Q3tpn0 mus musculu
309	68.5	11.6	295	2	Q9NEG2_DROSOPH	Q9neg2 drosophila	382	67.5	11.5	1403	2	Q3US45_MOUSE	Q3ue45 mus musculu
310	68.5	11.6	328	2	Q8MQG3_CABBR	Q8mqg3 caenorhabdi	383	67.5	11.5	1403	2	Q7TQF0_MOUSE	Q7tqf0 mus musculu
311	68.5	11.6	333	2	Q3HTT8_CANFA	Q3htt8 canis famli	384	67.5	11.5	1403	2	Q8CFA3_MOUSE	Q8cf3 mus musculu
312	68.5	11.6	369	2	Q565V9_9BACT	Q565v9 uncultured	385	67.5	11.5	1403	2	Q8RSG0_MOUSE	Q8rsg0 mus musculu
313	68.5	11.6	469	2	Q5BLB3_BRARE	Q5blb3 brachydanio	386	67.5	11.5	1504	1	SLIT_DROME	P24014 drosophila
314	68.5	11.6	587	2	Q3VQV5_PROAB	Q3qv5 prosthecoch	387	67.5	11.5	1687	2	Q61204_MOUSE	Q61204 mus musculu
315	68.5	11.6	598	1	FBLN1_CERAE	Q8mjf9 cercopithec	388	67.5	11.5	1751	2	Q4SK18_TETNG	Q4sk18 tetraodon n
316	68.5	11.6	671	2	Q6BET7_CABEL	Q6bet7 caenorhabdi	389	67.5	11.5	4699	2	Q9V383_DROME	Q9v383 drosophila
317	68.5	11.6	708	2	Q7F803_ORYSA	Q7f803 oryza sativ	390	67.5	11.5	23015	2	Q8IQ18_DROME	Q8iq18 drosophila
318	68.5	11.6	726	2	Q8AW87_CVNPY	Q8aw87 cynops pyrr	391	67	11.4	237	1	ALG14_YEAST	P38242 saccharomyc
319	68.5	11.6	728	2	Q90656_CHICK	Q90656 gallus gall	392	67	11.4	328	2	Q35771_RAT	Q35771 rattus norv
320	68.5	11.6	850	2	Q04384_BRAOL	Q04384 brassica ol	393	67	11.4	371	2	Q5U215_RAT	Q5u215 rattus norv
321	68.5	11.6	894	2	Q17429_CABEL	Q17429 caenorhabdi	394	67	11.4	463	2	Q68QF3_LITFO	Q68qf3 lithobius f
322	68.5	11.6	898	2	Q8MQG2_CABEL	Q8mqg2 caenorhabdi	395	67	11.4	473	2	Q3T572_MOUSE	Q3t572 mus musculu
323	68.5	11.6	909	2	Q5ZEL8_ORYSA	Q5zel8 oryza sativ	396	67	11.4	495	2	Q54QC5_DICDI	Q54qc5 dictyosteli

397	67	11.4	724	2	Q4ZJ75_XENLA	Q4zj75 xenopus lae	470	66	11.2	1057	2	Q4N4P8_THEPA	Q4n4p8 theileria p
398	67	11.4	885	2	Q7RLC5_GIALA	Q7rlc5 giardia lam	471	66	11.2	1062	2	Q3UG73_MOUSE	Q3ug73 mus musculus
399	67	11.4	993	1	EPHB3_MOUSE	P54754 mus musculus	472	66	11.2	1095	2	Q90XG4_CHICK	Q90xg4 gallus gall
400	67	11.4	993	1	EPHB3_MOUSE	Q91y89 mus musculus	473	66	11.2	1140	2	Q68DE5_HUMAN	Q68de5 homo sapien
401	67	11.4	1050	2	Q71G60_RSIV	P19660 red sea bre	474	66	11.2	1140	2	Q66K67_HUMAN	Q66kg7 homo sapien
402	67	11.4	1172	1	TSP2_HUMAN	P31442 homo sapien	475	66	11.2	1147	2	Q6DIB5_MOUSE	Q6dib5 mus musculus
403	67	11.4	1172	2	Q5RI52_HUMAN	Q5ri52 homo sapien	476	66	11.2	1238	1	JAG2_HUMAN	Q9y219 homo sapien
404	67	11.4	1193	2	Q5RI52_HUMAN	Q5ri52 homo sapien	477	66	11.2	1327	1	Y2006_MYCTU	Q10850 mycobacteri
405	67	11.4	1218	1	JAG1_MOUSE	Q90819 gallus gall	478	66	11.2	1327	2	Q7T261_MYCBO	Q7t261 mycobacteri
406	67	11.4	1218	1	Q3UVN4_MOUSE	Q9qxx0 mus musculus	479	66	11.2	1416	2	Q39WC4_GROMG	Q39wc4 geobacter m
407	67	11.4	1219	1	JAG1_RAT	Q3uvn4 mus musculus	480	66	11.2	1523	1	SLIT3_MOUSE	Q9wvb4 mus musculus
408	67	11.4	1229	1	EGFL3_HUMAN	Q63722 rattus norv	481	66	11.2	1523	2	Q3UHN1_MOUSE	Q3uhn1 mus musculus
409	67	11.4	1289	1	Q59FL3_HUMAN	Q59f95 homo sapien	482	66	11.2	1523	2	Q5SS56_MOUSE	Q5se56 mus musculus
410	67	11.4	1640	2	Q4AC86_HUMAN	Q59f13 homo sapien	483	66	11.2	1743	2	Q9XWX5_CABEL	Q9xwx5 caenorhabdi
411	67	11.4	1722	2	Q19350_CABEL	Q4ac86 homo sapien	484	66	11.2	1914	2	Q499U7_RAT	Q499u7 rattus norv
412	67	11.4	2225	2	Q571J3_MOUSE	Q19350 caenorhabdi	485	66	11.2	2289	2	Q4S3T6_TETNG	Q4s3t6 tetraodon n
413	67	11.4	2321	1	NOTC3_HUMAN	Q571j3 mus musculus	486	66	11.2	2378	2	Q4RW31_TETNG	Q4rw31 tetraodon n
414	67	11.4	2437	1	NOTC3_BRARE	Q9um47 homo sapien	487	66	11.2	2809	1	FBN3_HUMAN	Q75n90 homo sapien
415	67	11.4	2825	2	Q70465_MOUSE	P46530 brachydanio	488	66	11.2	5374	2	Q99ND0_MOUSE	Q99nd0 mus musculus
416	67	11.4	2907	1	FBN2_MOUSE	Q70465 mus musculus	489	65.5	11.1	99	2	Q9CPW1_MOUSE	Q9cpw1 m adult mal
417	66.5	11.3	84	2	Q5D231_HADSP	Q61555 mus musculus	490	65.5	11.1	99	2	Q9D7P0_MOUSE	Q9d7p0 mus musculus
418	66.5	11.3	98	1	KRA33_HUMAN	Q5d231 hadronyche	491	65.5	11.1	110	1	LCE2B_HUMAN	Q14633 homo sapien
419	66.5	11.3	98	1	Q52LP0_HUMAN	Q9byr6 homo sapien	492	65.5	11.1	110	2	Q5TA80_HUMAN	Q5ta80 homo sapien
420	66.5	11.3	98	2	Q6NTD4_HUMAN	Q52lp0 homo sapien	493	65.5	11.1	110	2	Q5TA81_HUMAN	Q5ta81 homo sapien
421	66.5	11.3	287	2	Q81PJ1_DROME	Q6ntd4 homo sapien	494	65.5	11.1	110	2	Q4PMX5_IXOSC	Q4pmx5 ixodes scap
422	66.5	11.3	382	2	Q72B35_DESVH	Q81pj1 drosophila	495	65.5	11.1	113	2	Q8H3W3_ORYSA	Q8h3w9 oryza sativ
423	66.5	11.3	462	2	Q3UDD6_MOUSE	Q72b35 desulfovibr	496	65.5	11.1	176	2	Q4V4J0_DROME	Q4v4j0 drosophila
424	66.5	11.3	480	2	Q34XA1_9GAMM	Q3ud6 mus musculus	497	65.5	11.1	208	2	Q4CWR8_TRYCR	Q4cwr8 trypanosoma
425	66.5	11.3	511	2	Q6IN42_RAT	Q34xa1 alkalilimn	498	65.5	11.1	230	2	Q5VTG9_HUMAN	Q5vtg9 homo sapien
426	66.5	11.3	588	1	GRN_RAT	Q6in42 rattus norv	499	65.5	11.1	236	2	Q7Z3S9_HUMAN	Q7z3s9 homo sapien
427	66.5	11.3	589	1	GRN_MOUSE	P23785 r granulina	500	65.5	11.1	236	2	Q8WUQ3_HUMAN	Q8wuq9 homo sapien
428	66.5	11.3	589	2	Q3TVQ3_MOUSE	P28798 mus musculus	501	65.5	11.1	244	2	Q2Y7J9_NITMU	Q2y7j9 nitrosospir
429	66.5	11.3	589	2	Q3TVQ3_MOUSE	Q3tvq3 mus musculus	502	65.5	11.1	249	2	Q5BKT8_HUMAN	Q5bkt8 homo sapien
430	66.5	11.3	589	2	Q3UC19_MOUSE	Q3tvq6 mus musculus	503	65.5	11.1	254	2	Q5UCC6_HUMAN	Q5ucc6 homo sapien
431	66.5	11.3	589	2	Q544Y8_MOUSE	Q3uc19 mus musculus	504	65.5	11.1	256	1	FSTL3_MOUSE	Q5qec7 mus musculus
432	66.5	11.3	593	2	Q3U9K2_MOUSE	Q544y8 m adult mal	505	65.5	11.1	256	2	Q542M9_MOUSE	Q542m9 mus musculus
433	66.5	11.3	597	2	Q54X44_DICDI	Q3u9k2 mus musculus	506	65.5	11.1	262	2	Q5UCC4_HUMAN	Q5ucc4 homo sapien
434	66.5	11.3	602	2	Q3TW77_MOUSE	Q54x44 dictyosteli	507	65.5	11.1	262	2	Q8N541_HUMAN	Q8n541 homo sapien
435	66.5	11.3	602	2	Q3U5Q6_MOUSE	Q3tw77 mus musculus	508	65.5	11.1	266	2	Q86Y14_HUMAN	Q86y14 homo sapien
436	66.5	11.3	602	2	Q3U8W3_MOUSE	Q3u5q6 mus musculus	509	65.5	11.1	269	2	Q6UWP3_HUMAN	Q6uwp3 homo sapien
437	66.5	11.3	602	2	Q3U9N4_MOUSE	Q3u8q3 mus musculus	510	65.5	11.1	269	2	Q8NC23_HUMAN	Q8nc23 homo sapien
438	66.5	11.3	602	2	Q9D2V3_MOUSE	Q3u9n4 m bone marr	511	65.5	11.1	323	2	Q4Q266_LEIMA	Q4q266 leishmania
439	66.5	11.3	674	2	Q8TAN9_STRPU	Q9d2v3 mus musculus	512	65.5	11.1	337	2	Q8NHD3_HUMAN	Q8nhd3 homo sapien
440	66.5	11.3	714	1	DLLI_RAT	Q8tan9 strongyloce	513	65.5	11.1	342	2	Q6F193_HUMAN	Q6f192 homo sapien
441	66.5	11.3	907	2	Q4R1B4_LEUMA	P97677 rattus norv	514	65.5	11.1	342	2	Q8NHD5_HUMAN	Q8nhd5 homo sapien
442	66.5	11.3	949	1	PCDAB_PANTR	Q4r1b4 leucophaea	515	65.5	11.1	343	2	Q5XG84_HUMAN	Q5xg84 homo sapien
443	66.5	11.3	1045	2	Q8T3A6_CABEL	Q5drtf3 pan.trogloed	516	65.5	11.1	343	2	Q42607_XENLA	Q42607 xenopus lae
444	66.5	11.3	1070	2	Q8T3A7_GIALA	Q8t3a6 caenorhabdi	517	65.5	11.1	356	2	Q96FY1_HUMAN	Q96fy1 homo sapien
445	66.5	11.3	1070	2	Q8T3A7_CABEL	Q7r2w4 giardia lam	518	65.5	11.1	363	2	Q4AL35_9CHLB	Q4al35 chlorobium
446	66.5	11.3	1111	2	Q9XWD6_CABEL	Q8t3a7 caenorhabdi	519	65.5	11.1	409	2	Q3TV46_MOUSE	Q3tv46 mus musculus
447	66.5	11.3	1174	2	Q3TGL4_MOUSE	Q9xwd6 caenorhabdi	520	65.5	11.1	433	2	Q7ZX39_XENLA	Q7zx39 xenopus lae
448	66.5	11.3	1174	2	Q99K58_MOUSE	Q3tgl4 mus musculus	521	65.5	11.1	438	2	Q6INJ1_XENLA	Q6inj1 xenopus lae
449	66.5	11.3	1221	1	FBLN2_MOUSE	Q99k58 mus musculus	522	65.5	11.1	459	2	Q62327_MOUSE	Q62327 mus musculus
450	66.5	11.3	1444	2	Q6A051_MOUSE	P37889 mus musculus	523	65.5	11.1	474	2	Q3U2A9_MOUSE	Q3u2a9 mus musculus
451	66.5	11.3	1713	2	Q5RH37_BRARE	Q6a051 mus musculus	524	65.5	11.1	479	2	Q84WPA_ARATH	Q84wp4 arabidopsis
452	66.5	11.3	1945	2	Q4RVQ6_TETNG	Q5rh37 brachydanio	525	65.5	11.1	516	2	Q60SB3_CABER	Q60se4 caenorhabdi
453	66.5	11.3	3224	2	Q4RVQ6_TETNG	Q4rvq6 tetraodon n	526	65.5	11.1	546	2	Q3UWY9_MOUSE	Q3uw9y mus musculus
454	66.5	11.3	5179	1	MUC2_HUMAN	Q4rvq6 tetraodon n	527	65.5	11.1	589	2	Q8NHD4_HUMAN	Q8nhd4 homo sapien
455	66	11.2	64	1	CX13_CONIM	Q02817 homo sapien	528	65.5	11.1	602	2	Q3UWJ3_MOUSE	Q3uwj3 mus musculus
456	66	11.2	64	2	Q59A89_CONIM	P69497 conus imper	529	65.5	11.1	602	2	Q3UD85_MOUSE	Q3ud85 mus musculus
457	66	11.2	85	1	HEPC_MORCS	Q59aa9 conus imper	530	65.5	11.1	656	1	EGFL3_MOUSE	Q60u70 mus musculus
458	66	11.2	149	2	Q8GA35_ECOLI	P82951 morone chry	531	65.5	11.1	722	1	DLLI_MOUSE	Q81483 mus musculus
459	66	11.2	174	2	Q9N2N0_BOMMO	Q8ga35 escherichia	532	65.5	11.1	744	2	Q8NHD2_HUMAN	Q8nhd2 mus musculus
460	66	11.2	208	2	Q6KGH7_ORYSA	Q9n2n0 bombyx mori	533	65.5	11.1	768	2	Q36581_9RETR	Q36581 multiple sc
461	66	11.2	234	2	Q7QGV2_ANOGA	Q6k6h7 oryza sativ	535	65.5	11.1	804	2	Q3UK95_MOUSE	Q3uk95 mus musculus
462	66	11.2	258	2	Q9Z548_TORAC	Q7qgv2 anopheles g	536	65.5	11.1	818	2	Q8CC59_MOUSE	Q8cc59 mus musculus
463	66	11.2	274	2	Q7Q953_ANOGA	Q9z548 nicotiana t	537	65.5	11.1	830	1	SREC_HUMAN	Q14162 homo sapien
464	66	11.2	350	2	Q6NCID6_RHOPA	Q7q953 anopheles g	538	65.5	11.1	887	2	Q3UMW1_MOUSE	Q3umw1 mus musculus
465	66	11.2	722	2	Q7R168_GIALA	Q6ncid6 rhodopseudo	539	65.5	11.1	1062	2	Q9C5X4_ARATH	Q9c5x4 arabidopsis
466	66	11.2	724	2	Q32NV6_XENLA	Q7r168 giardia lam	540	65.5	11.1				
467	66	11.2	728	2	Q54DV5_DICDI	Q32nv6 xenopus lae	541	65.5	11.1				
468	66	11.2	792	2	Q90243_CHICK	Q54dv5 dictyosteli	542	65.5	11.1				
469	66	11.2	898	2	Q60UE2_CABER	Q90243 gallus gall							
						Q60ue2 caenorhabdi							

543	65.5	11.1	1110	2	Q614U4_CAEBR	Q614U4 caenorhabdi	616	64.5	11.0	705	2	Q2ILJ6_9DELT	Q2ilj6 anaeromyxob
544	65.5	11.1	1114	2	Q3U2A7_MOUSE	Q3u2a7 mus musculus	617	64.5	11.0	727	2	Q8ROX1_MOUSE	Q8rox1 mus musculus
545	65.5	11.1	1114	2	Q9JKW7_MOUSE	Q9jkw7 mus musculus	618	64.5	11.0	744	2	Q7Q8A1_ANOGA	Q7q8a1 anopheles g
546	65.5	11.1	1235	2	Q6IO50_HUMAN	Q6io50 homo sapien	619	64.5	11.0	772	2	Q4QBY8_LEINA	Q4qby8 leishmania
547	65.5	11.1	1465	2	QARN50_TETNG	Qarn50 tetradodon n	620	64.5	11.0	804	2	Q7TFT4_MOUSE	Q7tft4 mus musculus
548	65.5	11.1	2067	2	Q59ED8_HUMAN	Q59ed8 homo sapien	621	64.5	11.0	822	2	Q62287_MOUSE	Q62287 mus musculus
549	65.5	11.1	2213	1	SORL_RABIT	Q59209 o sortilin-	622	64.5	11.0	841	2	Q4YVB8_PLABE	Q4yvb8 plasmodium
550	65.5	11.1	2471	1	NOTC2_HUMAN	Q95271 homo sapien	623	64.5	11.0	853	2	Q8I719_PLAF7	Q8i719 plasmodium
551	65.5	11.1	2471	2	QSVT00_HUMAN	Q5vtd0 homo sapien	624	64.5	11.0	853	2	Q8MMZ4_PLAFA	Q8mmz4 plasmodium
552	65.5	11.1	2555	2	Q5SXK3_HUMAN	Q5sxk3 homo sapien	625	64.5	11.0	873	2	Q8QGN9_BRARE	Q8qgn9 brachydanio
553	65.5	11.1	2556	1	NOTCH_HUMAN	P46531 homo sapien	626	64.5	11.0	914	2	Q2R2A2_ORYSA	Q2r2a2 oryza sativ
554	65.5	11.1	3718	1	LAMAS_MOUSE	Q61001 mus musculus	627	64.5	11.0	969	2	Q96KG6_HUMAN	Q96kg6 homo sapien
555	65	11.0	78	2	Q9MB66_TOBAC	Q9mb66 nicotiana t	628	64.5	11.0	987	2	Q6XLI8_CALJA	Q6xli8 callithrix
556	65	11.0	90	2	Q5D233_HADIN	Q5d233 hadronyche	629	64.5	11.0	1021	2	Q3UGU1_MOUSE	Q3ugu1 mus musculus
557	65	11.0	95	2	Q9RJN7_STRCO	Q9rjn7 streptomyce	630	64.5	11.0	1026	2	Q8SWV0_DROME	Q8swv0 drosophila
558	65	11.0	131	1	CHHB1_BOMMO	P05688 bombyx mori	631	64.5	11.0	1162	2	Q2Q422_CANFA	Q2q422 canis famil
559	65	11.0	147	2	Q6QXV5_ORYSA	Q6qxv5 oryza sativ	632	64.5	11.0	1211	2	Q383K6_9TRYP	Q383k6 trypanosoma
560	65	11.0	181	2	Q4FAF9_9CHLB	Q4faf9 chlorobium	633	64.5	11.0	1296	2	Q6AWM6_DROME	Q6awm6 drosophila
561	65	11.0	212	2	Q45KX0_HUMAN	Q45kx0 homo sapien	634	64.5	11.0	1308	2	Q3GPM8_CAEER	Q3gpm8 caenorhabdi
562	65	11.0	263	2	Q99740_HUMAN	Q99740 homo sapien	635	64.5	11.0	1378	2	Q3UHB0_MOUSE	Q3uhb0 mus musculus
563	65	11.0	302	1	CH14_SOLTU	P52406 solanum tub	636	64.5	11.0	1378	2	Q68HV2_MOUSE	Q68hv2 mus musculus
564	65	11.0	306	2	Q2KJ78_BOVIN	Q2kj78 bos taurus	637	64.5	11.0	1505	2	Q5S3N1_SALSA	Q5s3n1 salmo salar
565	65	11.0	315	2	Q4U3E1_HUMAN	Q4u3el homo sapien	638	64.5	11.0	1557	2	Q75412_HUMAN	Q75412 homo sapien
566	65	11.0	320	2	Q9PUK3_CHICK	Q9puk3 gallus gall	639	64.5	11.0	1587	2	Q00508_HUMAN	Q00508 homo sapien
567	65	11.0	329	2	Q81144_SOLTU	Q81144 solanum tub	640	64.5	11.0	1624	2	Q75413_HUMAN	Q75413 homo sapien
568	65	11.0	329	2	Q81145_SOLTU	Q81145 solanum tub	641	64.5	11.0	1633	2	Q61GZ2_CAEER	Q61gz2 caenorhabdi
569	65	11.0	362	2	Q9PVN4_CHICK	Q9pvn4 gallus gall	642	64.5	11.0	1717	2	Q7PXF5_ANOGA	Q7pxf5 anopheles g
570	65	11.0	379	2	Q7SXV0_BRARE	Q7sxv0 brachydanio	643	64.5	11.0	1790	1	LAMB1_DROME	l1046 drosophila
571	65	11.0	383	2	Q669Y6_HUMAN	Q669y6 homo sapien	644	64.5	11.0	1793	2	Q69ZV8_MOUSE	Q69zv8 mus musculus
572	65	11.0	420	2	Q8I499_CUPSA	Q8i499 cupiennius	645	64.5	11.0	1946	2	Q4S290_TETNG	Q4s290 tetradodon n
573	65	11.0	426	2	Q3V346_MOUSE	Q3v346 mus musculus	646	64.5	11.0	2214	1	SORL_HUMAN	Q92673 h sortilin-
574	65	11.0	433	2	Q912M6_RAT	Q912m6 rattus norv	647	64.5	11.0	2771	2	Q9WTS7_MOUSE	Q9wts7 mus musculus
575	65	11.0	448	2	Q4UW87_XANCP	Q4uw87 xanthomonas	648	64.5	11.0	2796	2	Q3UHK6_MOUSE	Q3uhk6 mus musculus
576	65	11.0	448	2	Q8PW72_XANCP	Q8pw72 xanthomonas	649	64.5	11.0	2833	2	Q3UHS2_MOUSE	Q3uhs2 mus musculus
577	65	11.0	461	2	Q6VAU8_RAT	Q6vau8 rattus norv	650	64.5	11.0	3664	2	Q2Q1W5_BRARE	Q2q1w5 brachydanio
578	65	11.0	474	1	TNR1B_RAT	Q80WY6 rattus norv	651	64.5	11.0	3695	1	LAMAS_HUMAN	Q15230 homo sapien
579	65	11.0	474	2	Q5YLP0_RAT	Q5ylp0 rattus norv	652	64.5	11.0	3695	1	Q8TDF8_HUMAN	Q8tdf8 homo sapien
580	65	11.0	481	2	Q2WV02_GLOBE	Q2wv02 clostridium	653	64	10.9	112	1	COL_PIG	Q1566 aus scrofa
581	65	11.0	531	1	PK1L1_MOUSE	Q8r526 mus musculus	654	64	10.9	112	2	Q315G6_PIG	Q315g6 aus scrofa
582	65	11.0	773	2	Q53TL0_HUMAN	Q53tl0 homo sapien	655	64	10.9	115	2	Q38CZ2_9TRYP	Q38cz2 trypanosoma
583	65	11.0	787	2	Q80V13_MOUSE	Q80v13 mus musculus	656	64	10.9	116	2	Q5Q981_IXOSC	Q5q981 ixodes scap
584	65	11.0	823	2	Q61GU3_CAEBR	Q61gu3 caenorhabdi	657	64	10.9	117	2	Q9YD41_AERPE	Q9yda1 aeropyrum p
585	65	11.0	1218	1	JAG1_HUMAN	P78504 homo sapien	658	64	10.9	130	1	KRA3A_SHEEP	P02443 ovis aries
586	65	11.0	1295	1	GLP1_CAEEL	P13508 caenorhabdi	659	64	10.9	146	1	TXVE_TRIFL	P67862 trimeresuru
587	65	11.0	2146	1	CRB_DROME	P10040 drosophila	660	64	10.9	148	2	Q71RP9_TRIST	Q71rp9 trimeresuru
588	65	11.0	2524	2	Q9GPA5_BRAFL	Q9gpa5 branchiosto	661	64	10.9	163	2	Q4SF04_TETNG	Q4sfu4 tetradodon n
589	65	11.0	3447	2	Q4DUJAE_TRYCR	Q4dujac trypanosoma	662	64	10.9	178	1	CHHE2_BOMMO	P20730 bombyx mori
590	65	11.0	3467	2	Q4D2A9_TRYCR	Q4d2a9 trypanosoma	663	64	10.9	199	2	Q9H557_HUMAN	Q9h557 homo sapien
591	65	11.0	3481	2	Q4DJK2_TRYCR	Q4dj2k trypanosoma	664	64	10.9	217	2	Q85613_ECOLI	Q85613 escherichia
592	65	11.0	3481	2	Q4DNC0_TRYCR	Q4dnc0 trypanosoma	665	64	10.9	217	2	Q7A9R9_ECOS7	Q7a9r9 escherichia
593	65	11.0	4599	1	LAP1B_MOUSE	Q4dnc0 trypanosoma	666	64	10.9	225	2	Q8XCA3_ECOS7	Q8xca3 escherichia
594	65	11.0	4655	1	LRP2_HUMAN	Q9ji18 mus musculus	667	64	10.9	285	2	Q868R9_ANOGA	Q868r9 anopheles g
595	65	11.0	4655	2	Q7Z5C0_HUMAN	P98164 homo sapien	668	64	10.9	286	2	Q5CAG9_ORYSA	Q5cag9 oryza sativ
596	65	11.0	4655	2	Q7Z5C1_HUMAN	Q7z5c0 homo sapien	669	64	10.9	309	2	Q74ZS4_ASHGO	Q74zs4 ashbya goss
597	64.5	11.0	90	2	Q5T9G3_HUMAN	Q5t9g3 homo sapien	670	64	10.9	315	2	Q616A1_CAEER	Q616a1 caenorhabdi
598	64.5	11.0	98	1	KEA32_HUMAN	Q3byr7 homo sapien	671	64	10.9	322	2	Q65113_ORYSA	Q65113 oryza sativ
599	64.5	11.0	102	1	TXCA_CAEEX	Q8mcx1 caerostris	672	64	10.9	325	1	VT2_SFVKA	P25943 shope fibro
600	64.5	11.0	134	2	Q6ZR78_HUMAN	Q6zr78 homo sapien	673	64	10.9	325	2	Q77PB3_9POXV	Q77pb3 rabbit fibr
601	64.5	11.0	153	2	Q52VJ2_CIOIN	Q52vj2 ciona intes	674	64	10.9	370	2	Q6DSV5_ERWCT	Q6dsv5 erwinia car
602	64.5	11.0	170	2	Q52VK0_CIOIN	Q52vk0 ciona intes	675	64	10.9	389	2	Q8R226_MOUSE	Q8r226 mus musculus
603	64.5	11.0	191	1	Y064_TREPA	Q83103 treponema p	676	64	10.9	425	1	TNR16_RAT	P07174 rattus norv
604	64.5	11.0	197	2	Q8WQ21_LOCMI	Q8wq21 locusta nig	677	64	10.9	426	2	Q8LAF6_ARATH	Q8laf6 arabidopsis
605	64.5	11.0	245	2	Q6ZT26_HUMAN	Q6zt26 homo sapien	678	64	10.9	426	2	Q93XX5_ARATH	Q93xx5 arabidopsis
606	64.5	11.0	325	2	Q614Z3_CAEER	Q614z3 caenorhabdi	679	64	10.9	475	1	U3IP2_HUMAN	Q43818 homo sapien
607	64.5	11.0	369	2	Q83KX8_SHIFL	Q83kx8 shigella fl	680	64	10.9	479	2	Q3G7J0_9DELT	Q3g7j0 pelobacter
608	64.5	11.0	375	2	Q7PR44_ANOGA	Q7pr44 anopheles g	681	64	10.9	554	2	Q3X1B9_9ACTN	Q3x1b9 rubrobacter
609	64.5	11.0	397	2	Q52VK2_CIOIN	Q52vk2 ciona intes	682	64	10.9	578	1	TRBM_CANFA	Q5w798 canis famil
610	64.5	11.0	405	2	Q8BK34_MOUSE	Q8bks4 mus musculus	683	64	10.9	581	2	Q5LU50_SILPO	Q5lu50 silicibacte
611	64.5	11.0	420	2	Q3FPH1_9EURK	Q3fph1 burkholderi	684	64	10.9	587	1	UL84_HCMVT	P29839 human cytom
612	64.5	11.0	450	2	Q53FZ7_HUMAN	Q53fz7 homo sapien	685	64	10.9	588	2	Q43FM5_9CHLB	Q43fm5 chlorobium
613	64.5	11.0	456	2	Q54IG3_DICTDI	Q54ig3 dictyosteli	686	64	10.9	590	2	Q8C088_MOUSE	Q8c088 mus musculus
614	64.5	11.0	500	1	LRP11_HUMAN	Q86vz4 homo sapien	687	64	10.9	657	2	Q4PIC7_USTWA	Q4pic7 ustilago ma
615	64.5	11.0	626	2	Q8NDJ1_HUMAN	Q8nd91 homo sapien	688	64	10.9	682	2	Q3A3T0_PELCD	Q3a3t0 pelobacter

689	64	10.9	723	2	Q9QW16_9MURI	Q9qwl6 rattus sp.	762	63.5	10.8	3004	2	Q9VYN8_DROME	Q9vyn8 drosophila
690	64	10.9	737	2	Q8JZM4_MOUSE	Q8jzm4 mus musculus	763	63.5	10.8	3689	2	Q7PPF9_ANOGA	Q7ppf9 anopheles g
691	64	10.9	737	2	Q8VD97_MOUSE	Q8vd97 mus musculus	764	63.5	10.8	3707	1	PGEM_MOUSE	Q05793 mus musculus
692	64	10.9	983	2	Q4T849_TETNG	Q4t849 tetraodon n	765	63.5	10.8	4260	2	Q4T3T2_TETNG	Q4t3t2 tetraodon n
693	64	10.9	990	2	Q6BTQ2_DEBHA	Q6btq2 debaryomyces	766	63.5	10.8	4981	2	Q2PZL6_MOUSE	Q2pzl6 mus musculus
694	64	10.9	1032	2	Q75WG1_PENJP	Q75wg1 penaeus jap	767	63.5	10.8	5376	1	ZAN_MOUSE	Q88799 mus musculus
695	64	10.9	1037	2	Q3UV32_MOUSE	Q3uv32 mus musculus	768	63	10.7	65	2	Q4GWW4_CRAGI	Q4gww4 crassostrea
696	64	10.9	1114	2	Q75WG2_PENJP	Q75wg2 penaeus jap	769	63	10.7	92	2	Q2MCN6_HYDAT	Q2mcn6 hydra atten
697	64	10.9	1143	2	Q21010_CAEBL	Q21010 caenorhabdi	770	63	10.7	93	2	Q313L8_HYDMA	Q313l8 hydra magni
698	64	10.9	1144	1	MAZAL_HUMAN	Q16706 homo sapien	771	63	10.7	94	2	Q75150_ORYSA	Q75150 oryza sativ
699	64	10.9	1145	2	Q2PJ74_CAEBL	Q2pj74 caenorhabdi	772	63	10.7	128	2	Q52VH7_COIN	Q52vh7 ciona intes
700	64	10.9	1180	2	Q3BP15_XANC5	Q3bp15 xanthomonas	773	63	10.7	148	2	Q71RP8_TRIST	Q71rp8 trimeresaur
701	64	10.9	1364	2	Q4R003_TETNG	Q4r003 tetraodon n	774	63	10.7	173	2	Q9RJ35_STRCO	Q9rj35 streptomyces
702	64	10.9	1437	2	Q4DUD8_TRYCR	Q4dud8 trypanosoma	775	63	10.7	204	1	TNR26_MOUSE	P83626 mus musculus
703	64	10.9	1515	2	Q9DE37_BRARE	Q9de37 brachydanio	776	63	10.7	204	1	Q3U3N2_MOUSE	Q3u3n2 mus musculus
704	64	10.9	1818	2	Q2Y144_BLAGL	Q2y144 blattella g	777	63	10.7	215	2	Q80W51_MOUSE	Q80w51 mus musculus
705	64	10.9	2030	2	Q2WBY6_PLADU	Q2wby6 platynereis	778	63	10.7	300	2	Q84BD4_MYXXA	Q84bd4 myxococcus
706	64	10.9	2192	2	Q804R1_BRARE	Q804r1 brachydanio	779	63	10.7	319	2	Q4T826_TETNG	Q4t826 tetraodon n
707	64	10.9	2215	1	SORL_MOUSE	Q88307 m sortilin-	780	63	10.7	349	1	XRC3_MOUSE	Q9cxk6 mus musculus
708	64	10.9	2215	2	Q3UHM3_MOUSE	Q3uhm3 mus musculus	781	63	10.7	350	2	O14189_SCHPO	O14189 schizosacch
709	64	10.9	2523	2	Q61211_CAEBR	Q61211 caenorhabdi	782	63	10.7	351	2	Q37HL4_RHOPA	Q37hl4 rhodopseudo
710	64	10.9	2532	2	Q629H6_CAEBR	Q629h6 caenorhabdi	783	63	10.7	368	2	Q861M1_DICDI	Q861m1 dictyosteli
711	64	10.9	2602	2	Q7PSV8_ANOGA	Q7psv8 anopheles g	784	63	10.7	369	1	YDHH_ECOLI	P77570 escherichia
712	64	10.9	2824	2	Q9W7R3_BRARE	Q9w7r3 brachydanio	785	63	10.7	369	2	Q320Z7_SHIDS	Q320z7 shigella bo
713	64	10.9	3019	2	Q4RU98_TETNG	Q4ru98 tetraodon n	786	63	10.7	369	2	Q32FD3_SHIDS	Q32fd3 shigella dy
714	64	10.9	3225	2	Q61PT2_CAEBR	Q61ft2 caenorhabdi	787	63	10.7	369	2	Q3Z1Z6_SHISS	Q3z1z6 shigella so
715	64	10.9	3487	2	Q4D378_TRYCR	Q4d378 trypanosoma	788	63	10.7	369	2	Q8X644_ECO57	Q8x644 escherichia
716	63.5	10.8	131	2	Q9YXZ8_9FLAV	Q9yxz8 gb virus c.	789	63	10.7	369	2	Q8FH85_ECOL6	Q8fh85 escherichia
717	63.5	10.8	147	2	Q353G9_9GANM	Q353g9 alkalilimni	790	63	10.7	394	2	Q9NGP9_POLPA	Q9ngp9 polysphondy
718	63.5	10.8	156	2	Q21VF9_RHOPA	Q21vf9 rhodopseudo	791	63	10.7	395	2	Q559Z3_DICDI	Q559z3 dictyosteli
719	63.5	10.8	156	2	Q6N0U5_RHOPA	Q6n0u5 rhodopseudo	792	63	10.7	421	2	Q9DEV1_CYPCA	Q9dev1 cyprinus ca
720	63.5	10.8	159	2	Q5LXG8_SILPO	Q5lxg8 silicibacte	793	63	10.7	450	2	Q869J7_9MYRI	Q869j7 glomeris ma
721	63.5	10.8	168	2	Q8LT29_TRYCR	Q8lt29 trypanosoma	794	63	10.7	456	2	Q3WTR3_9RHIZ	Q3wtr3 mesorhizobi
722	63.5	10.8	215	2	Q851P4_ORYSA	Q851p4 oryza sativ	795	63	10.7	469	2	Q52V41_COIN	Q52v41 ciona intes
723	63.5	10.8	225	2	Q626R3_CAEBR	Q626r3 caenorhabdi	796	63	10.7	528	2	Q9CXD8_MOUSE	Q9cxd8 mus musculus
724	63.5	10.8	240	1	KCP3_RAT	Q497b3 rattus norv	797	63	10.7	583	2	Q3TSU5_MOUSE	Q3tsu5 mus musculus
725	63.5	10.8	261	2	Q39TH1_GEOMG	Q39th1 geobacter m	798	63	10.7	601	2	Q52KT2_XENLA	Q52kt2 xenopus lae
726	63.5	10.8	286	2	Q4TT93_CAEBL	Q4tt93 caenorhabdi	799	63	10.7	608	2	Q8S1M4_ORYSA	Q8s1m4 oryza sativ
727	63.5	10.8	309	2	Q4RKX9_TETNG	Q4rkx9 tetraodon n	800	63	10.7	648	2	Q9VJU4_DROME	Q9vj4 drosophila
728	63.5	10.8	349	2	Q40HQ7_9ROB	Q40hq7 jannaschia	801	63	10.7	669	2	Q4V526_DROME	Q4v526 drosophila
729	63.5	10.8	358	2	Q54KB3_DICDI	Q54kb3 dictyosteli	802	63	10.7	694	2	Q53QB9_ORYSA	Q53qb9 oryza sativ
730	63.5	10.8	360	2	Q86AK7_DICDI	Q86ak7 dictyosteli	803	63	10.7	701	2	Q86BL2_DROME	Q86bl2 drosophila
731	63.5	10.8	372	2	Q7Y1J2_ORYSA	Q7y1j2 oryza sativ	804	63	10.7	712	2	Q50JF9_CAEBL	Q50jf9 caenorhabdi
732	63.5	10.8	380	2	Q61ES5_ORYSA	Q61es5 oryza sativ	805	63	10.7	735	1	ADAM2_MACFA	Q28478 macaca fasc
733	63.5	10.8	383	2	Q70534_RAT	Q70534 rattus norv	806	63	10.7	735	2	Q4R6R5_MACFA	Q4r6r5 macaca fasc
734	63.5	10.8	383	2	Q62779_RAT	Q62779 rattus norv	807	63	10.7	740	2	Q528V2_ORYSA	Q528v2 oryza sativ
735	63.5	10.8	407	2	Q3K7E8_PSEPF	Q3k7e8 pseudomonas	808	63	10.7	780	2	Q3U2X9_MOUSE	Q3u2x9 mus musculus
736	63.5	10.8	507	2	Q56BV3_9CAUD	Q56bv3 enterobacte	809	63	10.7	782	2	Q9WU23_MOUSE	Q9wu23 mus musculus
737	63.5	10.8	521	2	Q39NV6_BURS3	Q39nv6 burkholderi	810	63	10.7	827	2	Q8BRK9_MOUSE	Q8brk9 mus musculus
738	63.5	10.8	536	2	Q5RG03_BRARE	Q5rg03 brachydanio	811	63	10.7	909	2	Q6DIG4_XENTR	Q6dig4 xenopus tro
739	63.5	10.8	562	2	Q10709_9FLAV	Q10709 gb virus c.	812	63	10.7	917	1	LRP8_CHICK	Q98931 gallus gall
740	63.5	10.8	682	2	Q26630_METHH	Q26630 methanobact	813	63	10.7	949	1	PCDAB_HUMAN	Q9y311 homo sapien
741	63.5	10.8	721	2	Q91902_XENLA	Q91902 xenopus lae	814	63	10.7	987	2	Q616G9_CAEBR	Q616g9 caenorhabdi
742	63.5	10.8	747	2	Q4DFR4_TRYCR	Q4dfr4 trypanosoma	815	63	10.7	1037	2	Q5VY43_HUMAN	Q5vy43 homo sapien
743	63.5	10.8	747	2	Q8VHF4_MOUSE	Q8vhf4 mus musculus	816	63	10.7	1107	2	Q4S977_TETNG	Q4s977 tetraodon n
744	63.5	10.8	767	2	Q9DGR2_XENLA	Q9dgr2 xenopus lae	817	63	10.7	1139	1	MA2A2_HUMAN	P49641 homo sapien
745	63.5	10.8	778	2	Q91BG4_XENLA	Q91bg4 xenopus lae	818	63	10.7	1150	2	Q6GQ11_XENLA	Q6gq11 xenopus lae
746	63.5	10.8	847	2	Q8JBV9_9VIRU	Q8jbv9 penicillium	819	63	10.7	1152	2	Q4S7D3_TETNG	Q4s7d3 tetraodon n
747	63.5	10.8	871	2	Q626H3_CAEBR	Q626h3 caenorhabdi	820	63	10.7	1249	2	Q8VI66_RAT	Q8vi66 rattus norv
748	63.5	10.8	898	2	Q3URX7_MOUSE	Q3urx7 mus musculus	821	63	10.7	1278	2	Q9U350_CAEBL	Q9u350 caenorhabdi
749	63.5	10.8	905	2	Q18260_CAEBL	Q18260 caenorhabdi	822	63	10.7	1280	2	Q6QHS1_LYTVV	Q6qhs1 lytechinus
750	63.5	10.8	909	2	Q7SEF5_NEUCK	Q7sef5 neurospora	823	63	10.7	1356	1	SPIKE_CVNNL	Q6qls2 human coron
751	63.5	10.8	949	2	Q4S2B5_TETNG	Q4s2b5 tetraodon n	824	63	10.7	1367	2	Q61QY1_CAEBR	Q61qy1 caenorhabdi
752	63.5	10.8	1004	2	Q8CGA7_MOUSE	Q8cga7 mus musculus	825	63	10.7	1418	2	Q4CR51_TRYCR	Q4cr51 trypanosoma
753	63.5	10.8	1034	2	Q8VHL7_MOUSE	Q8vhl7 mus musculus	826	63	10.7	1441	2	Q867Q2_CAEBR	Q867q2 caenorhabdi
754	63.5	10.8	1034	2	Q8VHK5_MOUSE	Q8vhk5 mus musculus	827	63	10.7	2468	2	Q800E4_BRARE	Q800e4 brachydanio
755	63.5	10.8	1776	2	Q5BG13_EMENI	Q5bg13 aspergillus	828	63	10.7	2528	2	Q8AXP0_CYNPY	Q8axp0 cynops pyrr
756	63.5	10.8	1935	2	Q6QHS3_LYTVV	Q6qhs3 lytechinus	829	63	10.7	2660	2	Q7QL19_ANOGA	Q7ql19 anopheles g
757	63.5	10.8	2019	2	Q68FE0_MOUSE	Q68fe0 mus musculus	830	63	10.7	3301	1	CELR3_MOUSE	Q91i10 mus musculus
758	63.5	10.8	2030	2	Q4RHF2_TETNG	Q4rhf2 tetraodon n	831	63	10.7	3444	2	Q4E1B3_TRYCR	Q4e1b3 trypanosoma
759	63.5	10.8	2672	2	Q3UHH3_MOUSE	Q3uhh3 m 14 days p	832	63	10.7	3445	2	Q4DYC9_TRYCR	Q4dyc9 trypanosoma
760	63.5	10.8	2842	2	Q561H8_9FLAV	Q561h8 gb virus c.	833	63	10.7	3456	2	Q4DJN1_TRYCR	Q4djn1 trypanosoma
761	63.5	10.8	3004	2	Q24550_DROME	Q24550 drosophila	834	63	10.7	3474	2	Q4D523_TRYCR	Q4d523 trypanosoma

835	63	10.7	3483	2	Q4DTL6_TRYCR	Q4dt16 trypanosoma	908	62	10.5	272	2	Q61BN9_CAEBR	Q61bn9 caenorhabdi
836	63	10.7	5141	2	Q700K0_RAT	Q700k0 rattus norv	909	62	10.5	282	1	END4_DESVH	Q72c9 desulfovibr
837	62.5	10.6	128	2	Q6ZWD3_HUMAN	Q6zwd3 homo sapien	910	62	10.5	311	2	Q8RIG8_MOUSE	Q8r1g8 mus musculu
838	62.5	10.6	131	2	Q9YZV2_9FLAV	Q9yzv2 gb virus c.	911	62	10.5	318	2	Q6A853_PROAC	Q6a853 propionibac
839	62.5	10.6	135	2	Q9YUP8_9FLAV	Q9yup8 gb virus c.	912	62	10.5	339	2	Q9BIJ2_TOXGO	Q9bi12 toxoplasma
840	62.5	10.6	145	2	Q39219_9FLAV	Q39219 gb virus c.	913	62	10.5	347	2	Q75J66_DICTDI	Q75j66 dictyosteli
841	62.5	10.6	153	2	Q11434_ADEEN	Q11434 duck adenov	914	62	10.5	380	2	Q60214_METCA	Q60214 methylococc
842	62.5	10.6	157	2	Q5ISQ5_MAFCA	Q5isq5 macaca fasc	915	62	10.5	402	1	GUNI_HUMIN	P56680 humicola in
843	62.5	10.6	158	1	KAB3_OLDAP	P58455 oldenlandia	916	62	10.5	435	1	GUNI_HUMGT	Q12622 humicola gr
844	62.5	10.6	159	2	Q7XZ75_GRIJA	Q7xz75 griffithsia	917	62	10.5	435	2	Q616G8_CAEBR	Q616g8 caenorhabdi
845	62.5	10.6	166	2	Q4CYN2_TRYCR	Q4cyn2 trypanosoma	918	62	10.5	459	2	Q64R19_9INFA	Q64r19 influenza a
846	62.5	10.6	169	2	Q3TRB8_MOUSE	Q3trb8 m adult mal	919	62	10.5	475	1	U3IF2_MOUSE	Q31wm3 mus musculu
847	62.5	10.6	170	2	Q52VU5_CIOIN	Q52vuj5 ciona intes	920	62	10.5	476	2	Q8RIH9_MOUSE	Q8r1h9 mus musculu
848	62.5	10.6	173	2	Q3ZLCO_OREMO	Q3zlc0 oreochromis	921	62	10.5	491	2	P90850_CAEBL	P90850 caenorhabdi
849	62.5	10.6	208	2	Q4DLA7_TRYCR	Q4dlaw7 trypanosoma	922	62	10.5	493	2	Q7TNG6_MOUSE	Q7tng6 mus musculu
850	62.5	10.6	220	2	Q63404_RAT	Q63404 rattus norv	923	62	10.5	504	2	Q5ZB09_ORYSA	Q5zb09 oryza sativ
851	62.5	10.6	227	2	Q7YIM8_9SMEG	Q7yim8 hyporhamphu	924	62	10.5	522	2	Q6IS34_MOUSE	Q6is34 mus musculu
852	62.5	10.6	237	2	Q311U3_MACNE	Q311u3 macaca neme	925	62	10.5	592	2	Q58E52_MOUSE	Q58e52 mus musculu
853	62.5	10.6	286	2	Q6IKY7_DROME	Q6iky7 drosophila	926	62	10.5	625	2	Q8JQF9_9VIRU	Q8jqf9 adeno-assoc
854	62.5	10.6	288	2	Q9XYV5_TOXCA	Q9xyv5 toxocara ca	927	62	10.5	657	2	Q8R0K8_MOUSE	Q8r0k8 mus musculu
855	62.5	10.6	298	2	Q4CR12_TRYCR	Q4cr12 trypanosoma	928	62	10.5	772	1	DLA_BRARE	Q6di48 brachydanio
856	62.5	10.6	308	2	Q46370_BOVIN	Q46370 bos taurus	929	62	10.5	776	2	Q86KY7_DICTDI	Q86ky7 dictyosteli
857	62.5	10.6	352	2	Q3MZ10_9DELT	Q3mz10 syntrophoba	930	62	10.5	949	1	TSP4_BRARE	Q8jgw0 brachydanio
858	62.5	10.6	360	2	Q3MCS3_ANAVT	Q3mcs3 anabaena va	931	62	10.5	949	2	Q502R1_BRARE	Q502r1 brachydanio
859	62.5	10.6	360	2	Q8YQT4_ANASP	Q8yqt4 anabaena sp	932	62	10.5	951	2	Q4D0C3_TRYCR	Q4d0c3 trypanosoma
860	62.5	10.6	378	2	Q510R0_XENTR	Q5i0r0 xenopus tro	933	62	10.5	988	2	Q22685_CAEBL	Q22685 caenorhabdi
861	62.5	10.6	398	2	Q52VK3_CIOIN	Q52vk3 ciona intes	934	62	10.5	998	1	EPHB3_HUMAN	P54753 homo sapien
862	62.5	10.6	424	2	Q4SL08_TETNG	Q4sl08 tetraodon n	935	62	10.5	1047	2	Q566K6_MOUSE	Q566k6 mus musculu
863	62.5	10.6	430	2	Q62229_CAEBR	Q62229 caenorhabdi	936	62	10.5	1065	2	Q810H2_MOUSE	Q810h2 mus musculu
864	62.5	10.6	484	2	Q311U4_MACMU	Q311u4 macaca mula	937	62	10.5	1095	2	Q416T2_GIBZE	Q416t2 gibberella
865	62.5	10.6	544	2	Q5BW73_SCHJA	Q5bw73 schistosoma	938	62	10.5	1103	2	Q55A33_DICTDI	Q55a33 dictyosteli
866	62.5	10.6	567	2	Q8WUL3_HUMAN	Q8wul3 homo sapien	939	62	10.5	1113	1	CORIN_MOUSE	Q9z319 mus musculu
867	62.5	10.6	567	2	Q3G137_9DELT	Q3g137 pelobacter	940	62	10.5	1170	1	TSP1_HUMAN	P07996 homo sapien
868	62.5	10.6	645	2	Q02261_CAEBL	Q02261 caenorhabdi	941	62	10.5	1170	1	TSP1_MOUSE	P35441 mus musculu
869	62.5	10.6	668	2	Q4SRK6_TETNG	Q4srk6 tetraodon n	942	62	10.5	1170	2	Q3TR40_MOUSE	Q3tr40 mus musculu
870	62.5	10.6	705	1	FELNI_MOUSE	Q08879 mus musculu	943	62	10.5	1170	2	Q71SA3_RAT	Q71sa3 rattus norv
871	62.5	10.6	705	2	Q3TWK8_MOUSE	Q3twk8 mus musculu	944	62	10.5	1171	2	Q80YQ1_MOUSE	Q80yq1 mus musculu
872	62.5	10.6	812	2	Q77779_BOVIN	Q77779 bos taurus	945	62	10.5	1171	2	Q8CGB2_MOUSE	Q8cgb2 mus musculu
873	62.5	10.6	844	2	Q6Y857_MORAM	Q6y857 morone amer	946	62	10.5	1205	2	Q8KOP6_MOUSE	Q8kop6 mus musculu
874	62.5	10.6	880	1	CADHF_XENLA	P33148 xenopus lae	947	62	10.5	1225	2	Q59599_HUMAN	Q59599 homo sapien
875	62.5	10.6	907	2	Q9XTS9_CAEBL	Q9xts9 caenorhabdi	948	62	10.5	1343	2	Q4RGJ3_TETNG	Q4rgj3 tetraodon n
876	62.5	10.6	919	2	Q28659_RABIT	Q28659 oryctolagus	949	62	10.5	1361	2	Q6PD18_MOUSE	Q6pd18 mus musculu
877	62.5	10.6	925	2	Q9UB95_CAEBL	Q9ub95 caenorhabdi	950	62	10.5	1403	2	Q70E20_MOUSE	Q70e20 mus musculu
878	62.5	10.6	976	2	Q90ZNR_BRARE	Q90znr brachydanio	951	62	10.5	1443	2	Q4CNL9_TRYCR	Q4cnl9 trypanosoma
879	62.5	10.6	1031	2	Q42124_CHICK	Q42124 gallus gall	952	62	10.5	1521	2	Q4CTB2_TRYCR	Q4ctb2 trypanosoma
880	62.5	10.6	1159	2	Q41020_GIBZE	Q4i020 gibberella	953	62	10.5	1523	1	SLIT3_RAT	Q88280 rattus norv
881	62.5	10.6	1245	2	Q9Y7V5_TRICHER	Q9y7v5 trichoderma	954	62	10.5	1562	2	Q4CNY4_TRYCR	Q4cny4 trypanosoma
882	62.5	10.6	1280	2	Q60YB8_CAEBR	Q60yeb8 caenorhabdi	955	62	10.5	1599	2	Q09983_CAEBL	Q09983 caenorhabdi
883	62.5	10.6	2223	2	Q61T23_CAEBR	Q61t23 caenorhabdi	956	62	10.5	1679	2	Q51DQ1_ENTHI	Q51dq1 entamoeba h
884	62.5	10.6	2448	2	Q8WQ05_HUMAN	Q8wq05 homo sapien	957	62	10.5	1813	1	LTBP2_MOUSE	Q08999 mus musculu
885	62.5	10.6	2525	2	Q4QHT5_LEIMA	Q4qht5 leishmania	958	62	10.5	1964	2	Q4COL1_TRYCR	Q4cql1 trypanosoma
886	62.5	10.6	2549	2	Q2L697_CIOIN	Q2l697 ciona intes	959	62	10.5	2043	2	Q4Q510_LEIMA	Q4q510 leishmania
887	62.5	10.6	2571	1	STABI_MOUSE	Q8r4y4 mus musculu	960	62	10.5	2282	1	ZAN_RABIT	P57999 oryctolagus
888	62.5	10.6	2843	2	Q96899_9FLAV	Q96899 gb virus c.	961	62	10.5	2414	2	Q6DFL6_XENLA	Q6df16 xenopus lae
889	62.5	10.6	3623	1	CUBN_MOUSE	Q9j1b4 mus musculu	962	62	10.5	2427	2	Q8MQ36_CAEBL	Q8mq36 caenorhabdi
890	62.5	10.6	4135	2	Q18977_BOVIN	Q18977 bos taurus	963	62	10.5	2511	2	Q4T9V2_TETNG	Q4t9v2 tetraodon n
891	62	10.5	92	1	LCM_LOGMI	P80060 locusta mig	964	62	10.5	2651	2	Q4CTC1_TRYCR	Q4ctc1 trypanosoma
892	62	10.5	100	1	VP52_BPAPS	Q9tlp6 bacterioph	965	62	10.5	2705	2	Q4D538_TRYCR	Q4d538 trypanosoma
893	62	10.5	100	2	Q3LZQ0_SCAUD	Q3lqz0 acyrthosiph	966	62	10.5	2760	2	Q4T8G9_TETNG	Q4t8g9 tetraodon n
894	62	10.5	101	2	Q9XGJ3_GERHY	Q9xgj3 gerbera hyb	967	62	10.5	2838	2	Q4DUG4_TRYCR	Q4dug4 trypanosoma
895	62	10.5	102	2	Q24040_9ROSI	Q24040 lavatera th	968	62	10.5	2976	2	Q4CZM4_TRYCR	Q4czm4 trypanosoma
896	62	10.5	112	2	Q9ZP51_URTDI	Q9zps1 urtica dioi	969	62	10.5	3313	1	CELK3_RAT	Q88278 rattus norv
897	62	10.5	145	1	TXVE_BOTIN	Q90x24 bothrops in	970	62	10.5	3335	2	Q4D255_TRYCR	Q4d255 trypanosoma
898	62	10.5	155	2	Q3ZS88_RHOPA	Q3zsz8 rhodopsudo	971	62	10.5	3461	2	Q4D8R5_TRYCR	Q4d8r5 trypanosoma
899	62	10.5	178	2	Q8PPR1_XANAC	Q8ppr1 xanthomonas	972	62	10.5	3482	2	Q4DSH9_TRYCR	Q4dsh9 trypanosoma
900	62	10.5	198	2	Q4WAE1_ASFPF	Q4wae1 aspergillus	973	62	10.5	3483	2	Q4DWZ0_TRYCR	Q4dhw0 trypanosoma
901	62	10.5	211	2	Q6H804_CANFA	Q6h8q4 canis famil	974	62	10.5	3484	2	Q4DHR5_TRYCR	Q4dhr5 trypanosoma
902	62	10.5	211	2	Q9RK27_STRCO	Q9rk27 streptomyce	975	62	10.5	3493	2	Q4RJ20_TETNG	Q4rj20 tetraodon n
903	62	10.5	222	2	Q3U697_MOUSE	Q3u697 m bone marr	976	62	10.5	4998	2	Q8CG65_MOUSE	Q8cg65 mus musculu
904	62	10.5	240	2	Q340C6_RHOPA	Q340c6 rhodopsudo	977	61.5	10.4	83	2	Q9XXT6_CAEBL	Q9xxt6 caenorhabdi
905	62	10.5	243	2	Q4TDM7_TETNG	Q4tdm7 tetraodon n	978	61.5	10.4	93	2	Q7MS54_WOLUS	Q7ms54 wolinnella s
906	62	10.5	256	2	Q5ENU2_HETTR	Q5enu2 heterocapsa	979	61.5	10.4	131	2	Q9YZW5_9FLAV	Q9yzw5 gb virus c.
907	62	10.5	269	2	Q6AL36_DESPS	Q6al36 desulfotale	980	61.5	10.4	131	2	Q9YZX0_9FLAV	Q9yzx0 gb virus c.

981	61.5	10.4	135	2	Q77VZ0_9FLAV	Q77vz0 gb virus c.	1054	61	10.4	93	2	Q94HA1_ORYSA	Q94ha1 oryza sativ
982	61.5	10.4	135	2	Q77VZ1_9FLAV	Q77vz1 gb virus c.	1055	61	10.4	95	2	Q92GV4_ECO57	Q92gv4 escherichia
983	61.5	10.4	135	2	Q77VZ2_9FLAV	Q77vz2 gb virus c.	1056	61	10.4	111	1	COL_MTCOCO	P42889 myocastor c
984	61.5	10.4	135	2	Q77VZ3_9FLAV	Q77vz3 gb virus c.	1057	61	10.4	115	1	MERT_SHEPU	Q54462 shewanella
985	61.5	10.4	135	2	Q9W8H8_9FLAV	Q9wh8 gb virus c.	1058	61	10.4	116	2	Q5T6Z9_HUMAN	Q5t6z9 homo sapien
986	61.5	10.4	135	2	Q9YUN7_9FLAV	Q9yun7 gb virus c.	1059	61	10.4	168	2	Q6SGZ0_9BACT	Q6sgz0 uncultured
987	61.5	10.4	143	2	Q72441_9FLAV	Q72441 gb virus c.	1060	61	10.4	177	2	Q5TPK8_ANOGA	Q5tpk8 anopheles g
988	61.5	10.4	162	2	Q9BLH6_APLKU	Q9blh6 aplysia kur	1061	61	10.4	190	2	Q93518_AGKHB	Q93518 agkistrodon
989	61.5	10.4	166	1	ZCH13_HUMAN	Q8w36 homo sapien	1062	61	10.4	205	2	Q5T700_HUMAN	Q5t700 homo sapien
990	61.5	10.4	176	2	Q87WA2_PSSSM	Q87wa2 pseudomonas	1063	61	10.4	212	2	Q90Y44_AGKHP	Q90y44 agkistrodon
991	61.5	10.4	177	2	Q7RYN5_NEUCR	Q7ryn5 neurospora	1064	61	10.4	214	2	Q4RGG7_TETNG	Q4rgg7 tetraodon n
992	61.5	10.4	190	2	Q3ZDR4_PIG	Q3zdr4 sus scrofa	1065	61	10.4	227	2	Q3X072_9ACTN	Q3x072 cryptospori
993	61.5	10.4	202	2	Q55254_9FLAV	Q55254 gb virus c.	1066	61	10.4	249	2	Q5CK70_CRYHO	Q5ck70 cryptospori
994	61.5	10.4	220	2	Q92VZ0_RHIME	Q92vz0 rhizobium m	1067	61	10.4	254	2	Q2U3M4_ASPOR	Q2u3m4 aspergillus
995	61.5	10.4	228	2	Q91NG9_9PARA	Q91ng9 tioman viru	1068	61	10.4	260	2	Q3PBZ0_CABEL	Q3pbz0 paracoccus
996	61.5	10.4	277	1	TNR4_HUMAN	Q91ng9 tioman viru	1069	61	10.4	269	2	Q902B8_CABEL	Q902b8 caenorhabdi
997	61.5	10.4	277	2	Q2M312_HUMAN	Q2m312 homo sapien	1070	61	10.4	307	2	Q4C965_CROWT	Q4c965 crocospaer
998	61.5	10.4	282	1	CD330_HUMAN	Q9npf0 homo sapien	1071	61	10.4	309	2	Q69525_MYCLE	Q69525 mycobacteri
999	61.5	10.4	289	2	Q8BX61_MOUSE	Q8bx64 mus musculu	1072	61	10.4	320	2	Q8QYV4_WSV	Q8qyv4 white spot
1000	61.5	10.4	316	2	C57092_SPOKV	Q57092 ectromelia	1073	61	10.4	339	2	Q4CKA1_TRYCR	Q4cka1 trypanosoma
1001	61.5	10.4	322	1	CHIC_LYCES	Q05538 lycopersico	1074	61	10.4	352	2	Q34F99_RHOPA	Q34f99 rhodopseudo
1002	61.5	10.4	347	2	Q86T16_HUMAN	Q86t16 homo sapien	1075	61	10.4	369	2	Q7QDZ6_ANOGA	Q7qdz6 anopheles g
1003	61.5	10.4	356	2	Q60C70_METCA	Q60c70 methylococc	1076	61	10.4	402	2	Q5LGG5_BACFN	Q5lgg5 bacteroides
1004	61.5	10.4	368	2	Q82VZ2_NITEU	Q82vz2 nitrosomona	1077	61	10.4	402	2	Q64WM1_BACFR	Q64wm1 bacteroides
1005	61.5	10.4	373	2	Q18197_CAERL	Q18197 caenorhabdi	1078	61	10.4	406	2	Q3FDG7_9BURK	Q3fdg7 burkholderi
1006	61.5	10.4	373	2	Q5SN55_ERARE	Q5sn55 brachydanio	1079	61	10.4	413	2	Q23015_CABEL	Q23015 caenorhabdi
1007	61.5	10.4	415	2	Q60N48_CAEBR	Q60n48 caenorhabdi	1080	61	10.4	432	2	Q9BKP1_CABEL	Q9bkp1 caenorhabdi
1008	61.5	10.4	422	2	Q9K3H4_STRCO	Q9k3h4 streptomyce	1081	61	10.4	441	2	Q3PB67_PARDE	Q3pb67 paracoccus
1009	61.5	10.4	435	2	Q505M6_XENLA	Q505m6 xenopus lae	1082	61	10.4	447	2	Q4J3W1_AZQVI	Q4j3w1 azotobacter
1010	61.5	10.4	448	2	Q641C0_XENLA	Q641c0 xenopus lae	1083	61	10.4	451	2	Q98173_MCV1	Q98173 molluscum c
1011	61.5	10.4	452	2	Q51S12_MACFA	Q51s12 macaca fasc	1084	61	10.4	485	2	Q4H3Q6_CIOIN	Q4h3q6 ciona intes
1012	61.5	10.4	459	2	Q2TAW1_XENLA	Q2taw1 xenopus lae	1085	61	10.4	506	2	Q8C7W2_MOUSE	Q8c7w2 mus musculu
1013	61.5	10.4	504	2	Q7QWR4_GIALA	Q7qwr4 giardia lam	1086	61	10.4	525	2	P92162_BOMMO	P92162 bombyx mori
1014	61.5	10.4	587	2	Q5C3P1_SCHJA	Q5c3p1 schistosoma	1087	61	10.4	538	2	Q8CC86_MOUSE	Q8cc86 rattus norv
1015	61.5	10.4	705	1	CTL2_CAVPO	Q810f1 cavia porce	1088	61	10.4	563	2	Q7TP82_RAT	Q7tp82 rattus norv
1016	61.5	10.4	719	2	Q5XG79_HUMAN	Q5xg79 homo sapien	1089	61	10.4	571	2	Q8C1E3_MOUSE	Q8c1e3 mus musculu
1017	61.5	10.4	735	2	Q498M5_RAT	Q498m5 rattus norv	1090	61	10.4	586	2	Q8KDS0_CHLTE	Q8kds0 chlorobium
1018	61.5	10.4	774	2	Q3SEM2_PARTE	Q3sem2 paramecium	1091	61	10.4	601	2	Q7M4J3_DICDI	Q7m4j3 dictyosteli
1019	61.5	10.4	774	2	Q3SEM3_PARTE	Q3sem3 paramecium	1092	61	10.4	610	2	Q4BOK0_2BURK	Q4bok0 polaronomas
1020	61.5	10.4	774	2	Q7PDS2_PLAYO	Q7pds2 plasmodium	1093	61	10.4	657	2	Q4T6N0_TETNG	Q4t6n0 tetraodon n
1021	61.5	10.4	816	2	Q5R449_PONPY	Q5r449 pongo pygma	1094	61	10.4	703	2	Q8C122_MOUSE	Q8c122 mus musculu
1022	61.5	10.4	818	2	Q6KF79_XENLA	Q6kf79 xenopus lae	1095	61	10.4	715	2	Q9H0L5_HUMAN	Q9h0l5 homo sapien
1023	61.5	10.4	833	2	Q5R6S4_PONPY	Q5r6s4 pongo pygma	1096	61	10.4	735	2	Q8BZT2_MOUSE	Q8bzt2 mus musculu
1024	61.5	10.4	909	2	Q61GM2_CAEBR	Q61gm2 caenorhabdi	1097	61	10.4	745	2	Q8VCB2_MOUSE	Q8vcb2 mus musculu
1025	61.5	10.4	932	2	Q5Y4N8_RAT	Q5y4n8 rattus norv	1098	61	10.4	747	2	Q6P143_HUMAN	Q6p143 homo sapien
1026	61.5	10.4	941	2	Q54YP0_DICDI	Q54yp0 dictyosteli	1099	61	10.4	754	2	Q71S15_HUMAN	Q71s15 homo sapien
1027	61.5	10.4	1247	1	JAG2_MOUSE	Q9qve5 mus musculu	1100	61	10.4	754	2	Q707U4_HUMAN	Q707u4 homo sapien
1028	61.5	10.4	1316	2	Q96JUT_HUMAN	Q96ju7 homo sapien	1101	61	10.4	787	1	SMO_HUMAN	Q99835 homo sapien
1029	61.5	10.4	1373	2	Q75372_HUMAN	Q75372 homo sapien	1102	61	10.4	796	2	Q6QMHS_HUMAN	Q6qmhs homo sapien
1030	61.5	10.4	1394	2	Q8MST1_DROME	Q8mt1 drosophila	1103	61	10.4	856	2	Q91LE1_WSV	Q91le1 white spot
1031	61.5	10.4	1511	2	Q9VB21_DROME	Q9vb21 drosophila	1104	61	10.4	875	2	Q4CMA5_TRYCR	Q4cma5 trypanosoma
1032	61.5	10.4	1592	1	SORL_CHICK	Q98930 g sortilin-	1105	61	10.4	881	2	Q9W0A0_DROME	Q9w0a0 drosophila
1033	61.5	10.4	1666	1	LTBP4_MOUSE	Q8k4g1 mus musculu	1106	61	10.4	903	2	Q4RS15_TRITR	Q4rs15 trichuris t
1034	61.5	10.4	1702	2	Q6ZQA1_MOUSE	Q6zqa1 mus musculu	1107	61	10.4	915	2	Q4RS15_TETNG	Q4rs15 tetraodon n
1035	61.5	10.4	1721	2	Q614N6_CAEBR	Q614n6 caenorhabdi	1108	61	10.4	937	2	Q9BLJ1_CIOIN	Q9blj1 ciona intes
1036	61.5	10.4	1913	2	Q5SV42_HUMAN	Q5sv42 homo sapien	1109	61	10.4	968	2	Q4SNB3_TETNG	Q4snb3 tetraodon n
1037	61.5	10.4	2030	2	Q9VXV3_DROME	Q9vxv3 drosophila	1110	61	10.4	1038	2	Q5A282_CANAL	Q5a282 candida alb
1038	61.5	10.4	2045	1	AGRN_HUMAN	Q00468 homo sapien	1111	61	10.4	1062	2	Q60789_MOUSE	Q60789 mus musculu
1039	61.5	10.4	2045	2	Q60PE1_HUMAN	Q60pe1 homo sapien	1112	61	10.4	1111	2	Q80YN4_RAT	Q80yn4 rattus norv
1040	61.5	10.4	2224	2	Q44131_CAEBL	Q44131 caenorhabdi	1113	61	10.4	1123	2	Q5RD15_PONPY	Q5rd15 pongo pygma
1041	61.5	10.4	2470	1	NOTC2_MOUSE	Q35516 mus musculu	1114	61	10.4	1128	2	Q4S6G8_TETNG	Q4s6g8 tetraodon n
1042	61.5	10.4	2471	1	NOTC2_RAT	Q9q30 rattus norv	1115	61	10.4	1170	1	TSF1_BOVIN	Q28178 bos taurus
1043	61.5	10.4	2570	1	STAB1_HUMAN	Q9ny15 homo sapien	1116	61	10.4	1202	1	JAG1_RAT	P97607 brachydanio
1044	61.5	10.4	2843	2	Q89251_9FLAV	Q89251 gb virus c.	1117	61	10.4	1213	1	JAG1B_BRARE	Q90y54 trypanosoma
1045	61.5	10.4	2873	2	Q69431_9FLAV	Q69431 gb virus c.	1118	61	10.4	1270	2	Q9GPN0_CAEBR	Q9gpn0 caenorhabdi
1046	61.5	10.4	2966	2	Q4RMT7_TETNG	Q4rmt7 tetraodon n	1119	61	10.4	1382	2	Q4CPF1_TRYCR	Q4cpf1 trypanosoma
1047	61.5	10.4	3126	2	Q3VSL4_MOUSE	Q3vsl4 mus musculu	1120	61	10.4	1385	2	Q61300_CAEBR	Q613q0 caenorhabdi
1048	61.5	10.4	3333	1	LAMA3_MOUSE	Q61789 mus musculu	1121	61	10.4	1396	2	Q4RPY1_TETNG	Q4rpy1 tetraodon n
1049	61.5	10.4	3457	2	Q4E0C7_TRYCR	Q4e0c7 trypanosoma	1122	61	10.4	1418	2	Q93457_SCOMX	Q93457 scophthalmu
1050	61.5	10.4	3548	2	Q5VTE4_HUMAN	Q5vte4 homo sapien	1123	61	10.4	1476	2	Q90285_CARAU	Q90285 carassius a
1051	61.5	10.4	3574	2	Q4LDE5_HUMAN	Q4lde5 homo sapien	1124	61	10.4	1477	2	Q4H3A4_CIOIN	Q4h3a4 ciona intes
1052	61.5	10.4	4006	2	Q35452_MOUSE	Q35452 mus musculu	1125	61	10.4	1506	2	Q54U77_DICDI	Q54u77 dictyosteli
1053	61.5	10.4	4114	2	Q54796_MOUSE	Q54796 mus musculu	1126	61	10.4	1525	2	Q4D8M2_TRYCR	Q4d8m2 trypanosoma

1127	61	10.4	1747	2	Q4CQV8_TRYCR	Q4cq8 trypanosoma	1200	60.5	10.3	551	2	Q09967_CABEL	Q09967 caenorhabdi
1128	61	10.4	1827	2	Q4CQ44_TRYCR	Q4cq44 trypanosoma	1201	60.5	10.3	556	2	Q5VXW6_HUMAN	Q5vwx6 homo sapien
1129	61	10.4	1834	2	Q4CQ57_TRYCR	Q4cq57 trypanosoma	1202	60.5	10.3	562	2	Q10703_9FLAV	Q10703 gb virus c.
1130	61	10.4	1955	1	AGRN_CHICK	P31696 gallus gall	1203	60.5	10.3	569	2	Q7PMF9_ANOGA	Q7pmf9 anopheles g
1131	61	10.4	2262	2	Q4CXH5_TRYCR	Q4cxh5 trypanosoma	1204	60.5	10.3	591	2	Q6LBN5_HUMAN	Q6lbn5 homo sapien
1132	61	10.4	2345	2	Q4CX92_TRYCR	Q4cx92 trypanosoma	1205	60.5	10.3	637	2	Q7PFQ7_ANOGA	Q7pfq7 anopheles g
1133	61	10.4	2450	2	Q9P273_HUMAN	Q9p273 homo sapien	1206	60.5	10.3	664	1	DLIC_BRARE	Q9iat6 brachydanio
1134	61	10.4	2476	1	ZAN_PIG	Q28993 sus scrofa	1207	60.5	10.3	680	2	Q9QW15_9MURI	Q9qw15 mus sp. bet
1135	61	10.4	2520	2	Q5SVCT_MOUSE	Q5svct7 mus musculus	1208	60.5	10.3	700	2	Q9SW66_HUMAN	Q9sw66 homo sapien
1136	61	10.4	2806	2	Q4DH79_TRYCR	Q4dh79 trypanosoma	1209	60.5	10.3	723	1	DL11_HUMAN	Q00548 homo sapien
1137	61	10.4	3450	2	Q4D801_TRYCR	Q4d801 trypanosoma	1210	60.5	10.3	737	2	Q81YT0_HUMAN	Q81yt0 homo sapien
1138	61	10.4	3452	2	Q4D134_TRYCR	Q4d134 trypanosoma	1211	60.5	10.3	737	2	Q8NFT8_HUMAN	Q8nft8 homo sapien
1139	61	10.4	3467	2	Q4D6V4_TRYCR	Q4d6v4 trypanosoma	1212	60.5	10.3	738	2	Q90Z45_CHICK	Q90z45 gallus gall
1140	61	10.4	3473	2	Q4DAR6_TRYCR	Q4dar6 trypanosoma	1213	60.5	10.3	754	2	Q5TNY8_ANOGA	Q5tny8 anopheles g
1141	61	10.4	3476	2	Q4DS00_TRYCR	Q4ds00 trypanosoma	1214	60.5	10.3	787	1	ITB3_MOUSE	Q54890 mus musculus
1142	61	10.4	3480	2	Q4DH83_TRYCR	Q4dh83 trypanosoma	1215	60.5	10.3	787	2	Q3TZC6_MOUSE	Q3tzc6 mus musculus
1143	61	10.4	3483	2	Q4DRJ9_TRYCR	Q4drj9 trypanosoma	1216	60.5	10.3	787	2	Q4R728_MACFA	Q4r728 macaca fasc
1144	61	10.4	3487	2	Q4DLB3_TRYCR	Q4dlb3 trypanosoma	1217	60.5	10.3	833	2	Q5AB17_CANAL	Q5ab17 candida alb
1145	60.5	10.3	64	1	KX12_CONIM	P69496 conus imper	1218	60.5	10.3	834	2	Q5AAS8_CANAL	Q5aas8 candida alb
1146	60.5	10.3	64	2	Q59AAB_CONIM	Q59aas conus imper	1219	60.5	10.3	836	2	O19057_PORPY	O19057 pongo pygma
1147	60.5	10.3	81	2	Q5RLQ5_PIG	Q5rlq5 sus scrofa	1220	60.5	10.3	864	2	Q6KF80_XENLA	Q6kfst0 xenopus lae
1148	60.5	10.3	88	2	Q6UXU7_HUMAN	Q6uxu7 homo sapien	1221	60.5	10.3	871	2	Q4SCX8_TESTNG	Q4scx8 tetraodon n
1149	60.5	10.3	92	2	Q8GXV9_ARATH	Q8gxv9 arabidopsis	1222	60.5	10.3	883	2	Q9VEN1_DROME	Q9vbn1 drosophila
1150	60.5	10.3	96	2	Q9CJ11_LACLA	Q9cj11 lactococcus	1223	60.5	10.3	917	2	Q9VE20_DROME	Q9ve20 drosophila
1151	60.5	10.3	99	1	GASA3_ARATH	P46687 arabidopsis	1224	60.5	10.3	926	2	Q7LBX6_HUMAN	Q7lbn6 homo sapien
1152	60.5	10.3	99	2	Q9D638_MOUSE	Q9d638 mus musculus	1225	60.5	10.3	931	1	NRP2_HUMAN	Q60462 homo sapien
1153	60.5	10.3	117	2	Q53TQ4_HUMAN	Q53tq4 homo sapien	1226	60.5	10.3	931	2	Q7LBX7_HUMAN	Q7lbn7 homo sapien
1154	60.5	10.3	126	2	Q6F4P7_TRISC	Q6f4f7 triakis scy	1227	60.5	10.3	931	2	Q723T9_HUMAN	Q723t9 homo sapien
1155	60.5	10.3	129	2	Q9YCE5_AERPE	Q9yce5 aeropyrum p	1228	60.5	10.3	978	1	MCR_MOUSE	Q8vii8 mus musculus
1156	60.5	10.3	129	2	Q8HYT2_ORYSA	Q8hyt2 oryza sativ	1229	60.5	10.3	1074	2	Q9BX11_HUMAN	Q9bx11 homo sapien
1157	60.5	10.3	131	2	Q9YZW4_9FLAV	Q9yzw4 gb virus c.	1230	60.5	10.3	1031	2	Q9VBNO_DROME	Q9vbn0 drosophila
1158	60.5	10.3	131	2	Q9YZW6_9FLAV	Q9yzw6 gb virus c.	1231	60.5	10.3	1037	2	Q6NP66_DROME	Q6np66 drosophila
1159	60.5	10.3	131	2	Q9YZV1_9FLAV	Q9yzv1 gb virus c.	1232	60.5	10.3	1071	2	Q4RT16_TESTNG	Q4rt16 tetraodon n
1160	60.5	10.3	131	2	Q9YZV5_9FLAV	Q9yzv5 gb virus c.	1233	60.5	10.3	1104	1	NFX1_HUMAN	Q12986 homo sapien
1161	60.5	10.3	135	2	Q9YUN0_9FLAV	Q9yun0 gb virus c.	1234	60.5	10.3	1116	2	Q5SA31_DICDI	Q5sa31 dictyosteli
1162	60.5	10.3	161	2	Q35KP7_9BRAD	Q35kp7 bradyrhizob	1235	60.5	10.3	1117	2	Q86KY4_DICDI	Q86ky4 dictyosteli
1163	60.5	10.3	168	1	WFDC2_RAT	Q3chn3 rattus norv	1236	60.5	10.3	1120	2	Q96EL5_HUMAN	Q96el5 mus sapien
1164	60.5	10.3	173	2	Q3NQL2_SHEPR	Q3ngl2 shewanella	1237	60.5	10.3	1389	1	LTB1S_MOUSE	Q8cg18 mus musculus
1165	60.5	10.3	181	2	Q3F736_9BURK	Q3f736 burkholderi	1238	60.5	10.3	1394	2	Q505C9_MOUSE	Q505c9 mus musculus
1166	60.5	10.3	191	2	Q872V4_NEUCR	Q872v4 neurospora	1239	60.5	10.3	1461	2	Q9JLP3_MOUSE	Q9jlp3 mus musculus
1167	60.5	10.3	214	2	Q7NEW7_GLOVI	Q7new7 gloeobacter	1240	60.5	10.3	1577	2	Q9VS89_DROME	Q9v89 drosophila
1168	60.5	10.3	234	2	Q5C0J3_SCHUJA	Q5c0j3 schistosoma	1241	60.5	10.3	1622	2	Q3ZTN4_SALSC	Q3ztn4 salmifiri sci
1169	60.5	10.3	288	2	Q4TTR9_CABEL	Q4tt94 caenorhabdi	1242	60.5	10.3	1674	2	Q80Z18_MOUSE	Q80z18 mus musculus
1170	60.5	10.3	289	1	PIP26_ARATH	Q2zv07 arabidopsis	1243	60.5	10.3	1713	1	LTB1L_MOUSE	Q8cg19 mus musculus
1171	60.5	10.3	290	2	Q9DAU5_MOUSE	Q9daus mus musculus	1244	60.5	10.3	1914	2	Q4WHJ5_ASFPU	Q4whj5 aspergillus
1172	60.5	10.3	291	2	Q9UDM2_HUMAN	Q9udm2 homo sapien	1245	60.5	10.3	2038	2	Q7QFS2_ANOGA	Q7qfs2 anopheles g
1173	60.5	10.3	296	2	Q5M8H8_XENTR	Q5m8h8 xenopus tro	1246	60.5	10.3	2516	2	Q7TQ52_MOUSE	Q7tq52 mus musculus
1174	60.5	10.3	307	2	Q7R3F7_GIALA	Q7r3f7 giardia lam	1247	60.5	10.3	2526	2	Q7TQ51_MOUSE	Q7tq51 mus musculus
1175	60.5	10.3	313	2	Q8K3U2_MOUSE	Q8k3u2 mus musculus	1248	60.5	10.3	2531	1	NOTC1_MOUSE	Q01705 mus musculus
1176	60.5	10.3	316	1	IBP2_PIG	P24853 sus scrofa	1249	60.5	10.3	2531	2	Q7TQ50_MOUSE	Q7tq50 mus musculus
1177	60.5	10.3	324	1	CHI2_TORAC	P24091 nicotiana t	1250	60.5	10.3	2531	2	Q8K428_MOUSE	Q8k428 mus musculus
1178	60.5	10.3	324	2	Q9FEW1_NICSY	Q9few1 nicotiana s	1251	60.5	10.3	2703	1	NOTCH_DROME	Q7m207 drosophila
1179	60.5	10.3	327	2	Q37PR9_SPHAR	Q37pr9 novosphingo	1252	60.5	10.3	2783	2	Q7M559_BRARE	Q7m559 brachydanio
1180	60.5	10.3	335	2	Q4UB25_THEAN	Q4ub25 theileria a	1253	60.5	10.3	2842	2	O09804_9FLAV	Q09804 gb virus c.
1181	60.5	10.3	349	1	CTGF_HUMAN	P29279 homo sapien	1254	60.5	10.3	2842	2	O36178_9FLAV	O36178 gb virus c.
1182	60.5	10.3	349	2	Q5M8T4_HUMAN	Q5m8t4 homo sapien	1255	60.5	10.3	2850	2	Q80T03_MOUSE	Q80t03 mus musculus
1183	60.5	10.3	349	2	Q6FHL8_HUMAN	Q6fhl8 homo sapien	1256	60.5	10.3	2873	2	Q90481_9FLAV	Q90481 gb virus c.
1184	60.5	10.3	370	2	Q66A46_YERPS	Q66a46 yersinia ps	1257	60.5	10.3	2873	2	Q93070_9FLAV	Q93070 gb virus c.
1185	60.5	10.3	370	2	Q8ZE17_YERPE	Q8ze17 yersinia pe	1258	60.5	10.3	2873	2	P89967_9FLAV	P89967 gb virus c.
1186	60.5	10.3	384	1	Q8D0L6_YERPE	Q8d0l6 yersinia pe	1259	60.5	10.3	2910	2	Q9WGR8_9FLAV	Q9wgr8 gb virus c.
1187	60.5	10.3	385	1	DLK_MOUSE	Q9163 mus musculus	1260	60.5	10.3	2933	2	O09803_9FLAV	O09803 gb virus c.
1188	60.5	10.3	385	2	Q52LJ3_MOUSE	Q52lj3 m dlk (delt	1261	60.5	10.3	3486	2	Q4E492_TRYCR	Q4e492 trypanosoma
1189	60.5	10.3	386	2	Q53LE2_ORYSA	Q53le2 oryza sativ	1262	60.5	10.3	3486	2	Q4DGM4_TRYCR	Q4dgm4 trypanosoma
1190	60.5	10.3	394	2	Q6Z434_ORYSA	Q6z434 oryza sativ	1263	60.5	10.3	4071	1	Q6KXZ1_CHICK	Q6kxz1 gallus gall
1191	60.5	10.3	401	2	Q81LK6_MOUSE	Q81lk6 mus musculus	1264	60.5	10.3	4544	2	LRPL_HUMAN	Q07954 homo sapien
1192	60.5	10.3	407	2	Q961I3_DROME	Q961i3 drosophila	1265	60.5	10.3	4544	2	Q2PP12_HUMAN	Q2pp12 homo sapien
1193	60.5	10.3	452	2	Q499Z4_HUMAN	Q499z4 homo sapien	1266	60.5	10.3	5193	2	Q2QI47_MOUSE	Q2qi47 mus musculus
1194	60.5	10.3	452	2	Q9H6G5_HUMAN	Q9h6g5 homo sapien	1267	60.5	10.3	5703	1	MUC5B_HUMAN	Q9hc84 homo sapien
1195	60.5	10.3	454	2	Q8TB42_HUMAN	Q8tb42 homo sapien	1268	60	10.2	84	2	Q8MNZ8_SCHMA	Q8mnz8 schistosoma
1196	60.5	10.3	499	2	Q88714_MOUSE	Q88714 mus musculus	1269	60	10.2	93	2	Q6J0U3_BRABE	Q6j0u3 brachioesto
1197	60.5	10.3	510	2	Q3QRX7_9RHOB	Q3qrx7 silicibacte	1270	60	10.2	97	2	Q3E715_ARATH	Q3e715 arabidopsis
1198	60.5	10.3	515	1	NAGPA_HUMAN	Q9uk23 homo sapien	1271	60	10.2	102	1	108_LYCES	Q34495 lycopersico
1199	60.5	10.3	533	2	Q66HB8_RAT	Q66hb8 rattus norv	1272	60	10.2	102	2	Q8TER8_HUMAN	Q8tbr8 homo sapien

1273	60	10.2	116	2	07YX03 CAEBL	07YX03 caenorhabdi	1346	60	10.2	981	2	04CYD8 TRYCR	04CYD8 trypanosoma
1274	60	10.2	118	2	Q212F4 RHOPA	Q212f4 rhodopseudo	1347	60	10.2	996	1	LRP8 MOUSE	Q924x6 mus musculu
1275	60	10.2	121	2	Q6ZNM7 HUMAN	Q6znm7 homo sapien	1348	60	10.2	1021	2	Q6NUU4 BRARE	Q6nuu4 brachydanio
1276	60	10.2	125	2	Q4WZP5 ASPFU	Q4wzp5 aspergillus	1349	60	10.2	1035	2	Q9NEG1 DROME	Q9neg1 drosophila
1277	60	10.2	126	2	Q8T5W4 CAERE	Q8t5w4 caenorhabdi	1350	60	10.2	1061	2	Q5B110 DROME	Q5b110 drosophila
1278	60	10.2	127	2	Q8T5X2 CAERE	Q8t5x2 caenorhabdi	1351	60	10.2	1071	2	Q4DL68 TRYCR	Q4dl68 trypanosoma
1279	60	10.2	128	2	Q8T5W8 CAERE	Q8t5w8 caenorhabdi	1352	60	10.2	1083	2	Q4CM15 TRYCR	Q4cm15 trypanosoma
1280	60	10.2	129	2	Q8T5W7 CAERE	Q8t5w7 caenorhabdi	1353	60	10.2	1097	2	Q4CP75 TRYCR	Q4cp75 trypanosoma
1281	60	10.2	161	2	Q34G76 RHOPA	Q34g76 rhodopseudo	1354	60	10.2	1110	1	POL2 ARMYN	Q91hk4 arabis mosa
1282	60	10.2	184	1	ESM1 HUMAN	Q9nm30 homo sapien	1355	60	10.2	1123	2	Q75QY0 HUMAN	Q75qy0 homo sapien
1283	60	10.2	185	2	Q6XIW9 DROYA	Q6xiw9 drosophila	1356	60	10.2	1142	2	Q26615 STRPU	Q26615 stronglyloe
1284	60	10.2	211	2	Q6TPK5 CHICK	Q6tpk5 gallus gall	1357	60	10.2	1249	1	APAP RAT	Q9epv5 rattus norv
1285	60	10.2	233	1	JYT5 YEAST	Q39541 saccharomyc	1358	60	10.2	1302	1	LTPB3 HUMAN	Q9na15 homo sapien
1286	60	10.2	231	2	Q95Y21 CAEBL	Q95y21 caenorhabdi	1359	60	10.2	1508	2	Q4CNT3 TRYCR	Q4cnt3 trypanosoma
1287	60	10.2	283	2	Q18283 CAEBL	Q18283 caenorhabdi	1360	60	10.2	1512	2	Q8K3K1 RAT	Q8k3k1 rattus norv
1288	60	10.2	311	2	Q57VE2 9TRYP	Q57ve2 trypanosoma	1361	60	10.2	1523	1	SLIT3 HUMAN	Q75094 homo sapien
1289	60	10.2	320	2	Q8N780 HUMAN	Q8n780 homo sapien	1362	60	10.2	1547	1	RDRP BMV	P20951 papaya mosa
1290	60	10.2	342	2	Q18744 BOVIN	Q18744 bos taurus	1363	60	10.2	1569	2	Q4CRC1 TRYCR	Q4crc1 trypanosoma
1291	60	10.2	351	1	NOV CHICK	P28686 gallus gall	1364	60	10.2	1587	2	Q61K66 CAEBR	Q61k66 caenorhabdi
1292	60	10.2	366	2	Q46SU2 RALEBJ	Q46su2 ralestonia e	1365	60	10.2	1593	2	Q8JHV8 BRARE	Q8jlv8 brachydanio
1293	60	10.2	375	2	Q4RMC1 TETNG	Q4rmc1 tetraodon n	1366	60	10.2	1607	1	MIPR LTMST	Q25410 l putative
1294	60	10.2	383	2	Q6XVY4 CRYNV	Q6xvy4 cryptococcu	1367	60	10.2	1673	2	Q4CPB7 TRYCR	Q4cpb7 trypanosoma
1295	60	10.2	383	2	Q3KA04 PSEPF	Q3ka04 pseudomonas	1368	60	10.2	1676	2	Q4RSP7 TETNG	P30432 drosophila
1296	60	10.2	401	1	KR104 HUMAN	P60372 homo sapien	1369	60	10.2	1679	1	FUR2 DROME	Q4cgs1 trypanosoma
1297	60	10.2	416	2	Q4KEP7 PSEPF	Q4kep7 pseudomonas	1370	60	10.2	1828	2	Q4CQ51 TRYCR	Q4cgs1 trypanosoma
1298	60	10.2	419	2	Q92043 CROAT	Q92043 crocalus at	1371	60	10.2	1874	2	Q4CTN2 TRYCR	Q4ctn2 trypanosoma
1299	60	10.2	443	1	PBLNA CRIGR	O55058 cricetulus	1372	60	10.2	1876	2	Q4DQM1 TRYCR	Q4dqm1 trypanosoma
1300	60	10.2	454	2	Q8AXB6 BRARE	Q8axb6 brachydanio	1373	60	10.2	1883	2	Q4CQB2 TRYCR	Q4cqb2 trypanosoma
1301	60	10.2	463	2	Q6DHU6 IAJAP	O6duk6 influenza a	1374	60	10.2	1957	2	Q4CTM7 TRYCR	Q4ctm7 trypanosoma
1302	60	10.2	463	2	Q6PHH5 BRARE	O6phh5 brachydanio	1375	60	10.2	2016	2	Q7PF90 ANOGA	Q7pf90 anopheles g
1303	60	10.2	468	2	Q642B2 RAT	Q642b2 rattus norv	1376	60	10.2	2075	2	Q4CZP2 TRYCR	Q4czp2 trypanosoma
1304	60	10.2	507	2	Q4CKW3 TRYCR	Q4ckw3 trypanosoma	1377	60	10.2	2189	2	Q9EI05 EIMTE	Q9ei05 eineria ten
1305	60	10.2	566	2	Q617P3 CAEBR	Q617p3 caenorhabdi	1378	60	10.2	2472	2	Q4CZ74 TRYCR	Q4cz74 trypanosoma
1306	60	10.2	569	2	Q6J2K6 ORYSA	O6j2k6 oryza sativ	1379	60	10.2	2500	2	Q4RFP1 TETNG	Q4rfp1 tetraodon n
1307	60	10.2	573	2	Q5W9G8 HUMAN	Q5w9g8 homo sapien	1380	60	10.2	2685	2	Q4DH14 TRYCR	Q4dh14 trypanosoma
1308	60	10.2	600	1	EGFL5 MOUSE	Q8bb27 mus musculu	1381	60	10.2	3062	2	Q2TJF6 BRARE	Q2tjfe brachydanio
1309	60	10.2	610	2	Q9Y120 AGKHP	Q9y120 agkistrodon	1382	60	10.2	3075	2	Q45H72 BRARE	Q45h72 brachydanio
1310	60	10.2	622	2	Q5Y9B3 9VIRU	Q5y9b3 adeno-assoc	1383	60	10.2	3312	1	CELK3 HUMAN	Q9nyq7 homo sapien
1311	60	10.2	622	2	Q5Y9B5 9VIRU	Q5y9b5 adeno-assoc	1384	60	10.2	3374	2	Q4CX83 TRYCR	Q4cx83 trypanosoma
1312	60	10.2	623	2	Q56136 9VIRU	Q56136 adeno-assoc	1385	60	10.2	3431	2	Q4D1D7 TRYCR	Q4d1d7 trypanosoma
1313	60	10.2	623	2	Q9WB7 9VIRU	Q9wbp7 adeno-assoc	1386	60	10.2	3432	2	Q4D3V1 TRYCR	Q4d3v1 trypanosoma
1314	60	10.2	644	2	Q4REW4 TETNG	Q4rew4 tetraodon n	1387	60	10.2	3432	2	Q4DYW0 TRYCR	Q4dyw0 trypanosoma
1315	60	10.2	654	2	Q8IPP3 DROME	Q8ipp3 drosophila	1388	60	10.2	3452	2	Q4DKD5 TRYCR	Q4dkd5 trypanosoma
1316	60	10.2	657	2	Q8EMR4 MOUSE	Q8emr4 mus musculu	1389	60	10.2	3456	2	Q4D335 TRYCR	Q4d335 trypanosoma
1317	60	10.2	699	2	Q3WIK0 9ACTO	Q3wik0 frankia sp.	1390	60	10.2	3463	2	Q4E0A4 TRYCR	Q4e0a4 trypanosoma
1318	60	10.2	708	2	Q9NFS9 DROME	Q9nfs9 drosophila	1391	60	10.2	3464	2	Q4CYB5 TRYCR	Q4cyb5 trypanosoma
1319	60	10.2	710	2	Q91BD5 ANGJA	Q91bd5 anguilla ja	1392	60	10.2	3466	2	Q4DUP4 TRYCR	Q4dup4 trypanosoma
1320	60	10.2	717	2	Q474X2 RALEBJ	Q474x2 ralestonia e	1393	60	10.2	3476	2	Q4DZ45 TRYCR	Q4dz45 trypanosoma
1321	60	10.2	719	2	Q9U019 GIALA	Q9u019 giardia lam	1394	60	10.2	3481	2	Q4E3X3 TRYCR	Q4e3x3 trypanosoma
1322	60	10.2	719	2	Q9U021 GIALA	Q9u021 giardia lam	1395	60	10.2	3484	2	Q4E4F1 TRYCR	Q4e4f1 trypanosoma
1323	60	10.2	721	2	Q95Y60 CIOGA	Q95y60 ciona savi	1396	60	10.2	4117	2	Q8IRV9 DROME	Q8irv9 drosophila
1324	60	10.2	740	2	Q6PIA2 HUMAN	Q6pia2 homo sapien	1397	60	10.2	4179	2	Q9W4Y4 DROME	Q9w4y4 drosophila
1325	60	10.2	755	1	COMP MOUSE	Q9r0g6 mus musculu	1398	60	10.2	4186	2	Q8MPN3 DROME	Q8mpn3 drosophila
1326	60	10.2	755	2	Q8V154 MOUSE	Q8v154 mus musculu	1399	60	10.2	4223	2	Q8IRV8 DROME	Q8irv8 drosophila
1327	60	10.2	794	2	Q18742 BOVIN	Q18742 bos taurus	1400	60	10.2	4228	1	PAT2 HUMAN	Q9nyq8 homo sapien
1328	60	10.2	797	2	Q89PY0 BRAJA	Q89py0 bradyrhizob	1401	60	10.2	4349	1	Q9W4Y3 DROME	Q9w4y3 drosophila
1329	60	10.2	802	1	TMP86 HUMAN	Q8iu80 homo sapien	1402	60	10.2	4629	2	Q9W4Y3 DROME	Q61ej2 caenorhabdi
1330	60	10.2	808	2	Q7T2W9 ONCNY	Q7t2w9 oncorhynch	1403	60	10.2	4856	2	Q61EJ2 CAEBR	P82734 arabidopsis
1331	60	10.2	820	2	Q18743 BOVIN	Q18743 bos taurus	1404	59.5	10.1	75	1	LCR20 ARATH	Q98429 bacillus su
1332	60	10.2	824	2	Q6IC22 HUMAN	Q6ic22 homo sapien	1405	59.5	10.1	105	2	Q5SZ17 HUMAN	Q5sz17 homo sapien
1333	60	10.2	837	1	LDLR RABIT	P20063 oryctolagus	1406	59.5	10.1	128	1	KAPB BACSU	Q98429 bacillus su
1334	60	10.2	844	2	Q4CMY8 TRYCR	Q4cmv8 trypanosoma	1407	59.5	10.1	131	2	Q9YZW9 9FLAV	Q9yzw9 gb virus c.
1335	60	10.2	862	2	Q4CRU0 TRYCR	Q4cru0 trypanosoma	1408	59.5	10.1	131	2	Q9YZY0 9FLAV	Q9yzp0 gb virus c.
1336	60	10.2	867	1	SSPO BOVIN	P98167 bos taurus	1409	59.5	10.1	132	2	Q2Q1P4 PANTR	Q2q1p4 pan troglod
1337	60	10.2	869	2	Q42126 XENLA	Q42126 xenopus lae	1410	59.5	10.1	135	2	Q9WLF2 9FLAV	Q9wlf2 gb virus c.
1338	60	10.2	892	2	Q6NS01 XENLA	O6ns01 xenopus lae	1411	59.5	10.1	140	2	Q76LM8 HUMAN	Q76lm8 homo sapien
1339	60	10.2	892	2	Q6ZAA9 ORYSA	O6zaa9 oryza sativ	1412	59.5	10.1	141	2	Q74G89 GEOSL	Q74g89 geobacter s
1340	60	10.2	893	2	Q8MJK0 CERAE	Q8mjko cercopithec	1413	59.5	10.1	143	2	Q72440 9FLAV	Q72440 gb virus c.
1341	60	10.2	905	2	Q18741 BOVIN	O18741 bos taurus	1414	59.5	10.1	145	2	Q3F5G2 9BURK	Q3f5g2 burkholderi
1342	60	10.2	909	2	Q7JP81 CAEBL	Q7jp81 caenorhabdi	1415	59.5	10.1	145	2	Q39216 9FLAV	Q39216 gb virus c.
1343	60	10.2	911	2	Q7JP80 CAEBL	Q7jp80 caenorhabdi	1416	59.5	10.1	151	2	Q2WAI5 MAGSA	Q2wai5 magnetospir
1344	60	10.2	961	2	Q4CMN6 TRYCR	Q4cmn6 trypanosoma	1417	59.5	10.1	155	2	Q8VDY7 MOUSE	Q8vdy7 mus musculu
1345	60	10.2	967	1	YMW2 CAEBL	P34504 caenorhabdi	1418	59.5	10.1	182	2	Q4AT93 9BURK	Q4at93 polaromonas

1419	59.5	10.1	182	2	Q5P9V7	ANAMM	Q5P9V7	anaplasma m
1420	59.5	10.1	186	2	Q44621	CAEEL	Q44621	caenorhabdi
1421	59.5	10.1	211	2	Q39963	9FLAV	Q39963	gb virus c.
1422	59.5	10.1	232	2	Q2JWS8	9CYAN	Q2JWS8	cyanoabacter
1423	59.5	10.1	242	2	Q61MP2	CAEBR	Q61MP2	caenorhabdi
1424	59.5	10.1	257	2	Q6NW92	BRARE	Q6NW92	brachydanio
1425	59.5	10.1	269	2	Q89XH9	BRAJA	Q89XH9	bradyrhizob
1426	59.5	10.1	281	2	Q2JMA5	9CYAN	Q2JMA5	cyanoabacter
1427	59.5	10.1	284	2	Q8T1D1	DICDI	Q8T1D1	dictyosteli
1428	59.5	10.1	294	2	Q61H14	CAEBR	Q61H14	caenorhabdi
1429	59.5	10.1	300	2	Q3V1I2	MOUSE	Q3V1I2	mus musculus
1430	59.5	10.1	307	2	Q3IYR3	RHOSA	Q3IYR3	rhodobacter
1431	59.5	10.1	316	2	Q4SDA4	TETNG	Q4SDA4	tetraodon n
1432	59.5	10.1	320	2	Q57079	COMPX	Q57079	cowpox viru
1433	59.5	10.1	338	2	Q7U6B4	SYNFX	Q7U6B4	synchococc
1434	59.5	10.1	340	2	Q54KK1	DICDI	Q54KK1	dictyosteli
1435	59.5	10.1	343	2	Q50515	XENLA	Q50515	xenopus lae
1436	59.5	10.1	348	2	Q3RXT6	RALME	Q3RXT6	ralstonia m
1437	59.5	10.1	358	2	Q2W405	MAGSA	Q2W405	magnetospir
1438	59.5	10.1	392	2	Q52V11	CIOIN	Q52V11	ciona intes
1439	59.5	10.1	411	2	Q89YQ3	BACTN	Q89YQ3	bacteroides
1440	59.5	10.1	445	2	Q61X89	CAEBR	Q61X89	caenorhabdi
1441	59.5	10.1	448	2	Q9VJH8	DROME	Q9VJH8	drosophila
1442	59.5	10.1	484	2	Q5C268	HUMAN	Q5C268	homo sapien
1443	59.5	10.1	491	2	Q8TEK2	HUMAN	Q8TEK2	homo sapien
1444	59.5	10.1	504	2	Q7QJ41	ANOQA	Q7QJ41	anopheles g
1445	59.5	10.1	513	2	Q4S0D5	TETNG	Q4S0D5	tetraodon n
1446	59.5	10.1	523	1	FZD4	XENLA	Q9PT62	xenopus lae
1447	59.5	10.1	535	2	Q4CJG4	TRYCR	Q4CJG4	trypanosoma
1448	59.5	10.1	550	2	Q4QAE0	LEIMA	Q4QAE0	leishmania
1449	59.5	10.1	562	2	Q10697	9FLAV	Q10697	gb virus c.
1450	59.5	10.1	564	2	Q9TTS4	BOVIN	Q9TTS4	bos taurus
1451	59.5	10.1	585	2	Q3G1I4	CHLVI	Q3G1I4	protheoch
1452	59.5	10.1	658	2	Q58EW5	XENLA	Q58EW5	xenopus lae
1453	59.5	10.1	688	2	Q4RLS7	TETNG	Q4RLS7	tetraodon n
1454	59.5	10.1	694	2	Q5TW00	ANOQA	Q5TW00	anopheles g
1455	59.5	10.1	722	2	Q4SPX8	TETNG	Q4SPX8	tetraodon n
1456	59.5	10.1	747	2	Q5DTZ4	MOUSE	Q5DTZ4	mus musculus
1457	59.5	10.1	765	2	Q4SWJ3	TETNG	Q4SWJ3	tetraodon n
1458	59.5	10.1	814	2	Q7RLV1	GIALA	Q7RLV1	giardia lam
1459	59.5	10.1	836	2	Q49H10	CANFA	Q49H10	canis famil
1460	59.5	10.1	856	2	Q4H557	9DEIO	Q4H557	fad-depen
1461	59.5	10.1	861	2	Q83472	SBMV	Q83472	southern be
1462	59.5	10.1	868	2	Q4SP38	TETNG	Q4SP38	tetraodon n
1463	59.5	10.1	874	1	DNAB	MYCBO	P59666	mycobacteri
1464	59.5	10.1	886	1	EMR1	HUMAN	Q14246	homo sapien
1465	59.5	10.1	886	2	Q2I7G5	HUMAN	Q2I7G5	homo sapien
1466	59.5	10.1	898	2	Q4H387	CIOIN	Q4H387	ciona intes
1467	59.5	10.1	917	2	Q65XH7	ORYSA	Q65XH7	oryza sativ
1468	59.5	10.1	925	2	Q9UB94	CAEEL	Q9UB94	caenorhabdi
1469	59.5	10.1	932	2	Q17569	CAEEL	Q17569	caenorhabdi
1470	59.5	10.1	1034	2	Q6QRS2	LYTVA	Q6QRS2	lytechinus
1471	59.5	10.1	1061	2	Q4T8L6	TETNG	Q4T8L6	tetraodon n
1472	59.5	10.1	1070	2	Q4RJT4	TETNG	Q4RJT4	tetraodon n
1473	59.5	10.1	1081	2	Q8T4N8	PENSE	Q8T4N8	penseus sem
1474	59.5	10.1	1107	2	Q4COH9	TRYCR	Q4COH9	trypanosoma
1475	59.5	10.1	1117	2	Q6EOK3	DIDNA	Q6EOK3	didelphis m
1476	59.5	10.1	1144	2	Q4WGE0	ASPFU	Q4WGE0	aspergillus
1477	59.5	10.1	1191	2	Q7QH41	ANOQA	Q7QH41	anopheles g
1478	59.5	10.1	1245	1	NID1	MOUSE	P10493	mus musculus
1479	59.5	10.1	1245	1	Q3TKX9	MOUSE	Q3TKX9	m blastocys
1480	59.5	10.1	1299	2	Q8M037	CAEEL	Q8M037	caenorhabdi
1481	59.5	10.1	1363	2	Q4Q4Z5	LEIMA	Q4Q4Z5	leishmania
1482	59.5	10.1	1375	2	Q3US12	MOUSE	Q3US12	mus musculus
1483	59.5	10.1	1447	2	Q4CPD4	TRYCR	Q4CPD4	trypanosoma
1484	59.5	10.1	1502	2	Q2LYM1	DROPS	Q2LYM1	drosophila
1485	59.5	10.1	1524	2	Q3S2J2	BRARE	Q3S2J2	brachydanio
1486	59.5	10.1	1616	2	Q7KUB3	DROME	Q7KUB3	drosophila
1487	59.5	10.1	1616	2	Q9VSJ0	DROME	Q9VSJ0	drosophila
1488	59.5	10.1	1620	2	Q3ZTN2	SAGOE	Q3ZTN2	saguinus oe
1489	59.5	10.1	1621	2	Q3ZTN8	MACMU	Q3ZTN8	macaca mla
1490	59.5	10.1	1799	1	LAMB2	MOUSE	Q61292	mus musculus
1491	59.5	10.1	1799	2	Q8ROY0	MOUSE	Q8ROY0	mus musculus

ALIGNMENTS

RESULT 1

PROK1_HUMAN

ID PROK1_HUMAN STANDARD; PRT; 105 AA.

AC PS8294;

DT 26-SEP-2001, integrated into UniProtKB/Swiss-Prot.

DT 21-FEB-2006, entry version 35.

DE Prokineticin-1 precursor (Endocrine-gland-derived vascular endothelial

DE Growth factor) (EG-VEGF) (Mambakine).

GN Name=PROK1; ORFNames=UNQ600/PROI186;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

NCBI_TaxID=9606;

RX MEDLINE=21160229; PubMed=11259612;

RX MEDLINE=21160229; PubMed=11259612;

RA Li M., Bullock C.M., Knauer D.J., Ehler P.J., Zhou Q.-Y.;

RT "Identification of two prokineticin cDNAs: recombinant proteins

RL Mol. Pharmacol. 59:692-698(2001).

RX NUCLEOTIDE SEQUENCE [MRNA].

RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,

RT "Identification of an angiogenic mitogen selective for endocrine gland

RL Nature 412:877-884(2001).

RX NUCLEOTIDE SEQUENCE [MRNA].

RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,

RT "Identification of an angiogenic mitogen selective for endocrine gland

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RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,

RT "Identification of an angiogenic mitogen selective for endocrine gland

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RT "Identification of an angiogenic mitogen selective for endocrine gland

RL Nature 412:877-884(2001).

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RT "Identification of an angiogenic mitogen selective for endocrine gland

RL Nature 412:877-884(2001).

RX NUCLEOTIDE SEQUENCE [MRNA].

RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,

RT "Identification of an angiogenic mitogen selective for endocrine gland

RL Nature 412:877-884(2001).

RX NUCLEOTIDE SEQUENCE [MRNA].

RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,

RT "Identification of an angiogenic mitogen selective for endocrine gland

RL Nature 412:877-884(2001).

RX NUCLEOTIDE SEQUENCE [MRNA].

RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,

RT "Identification of an angiogenic mitogen selective for endocrine gland

RL Nature 412:877-884(2001).

RX NUCLEOTIDE SEQUENCE [MRNA].

RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,

RT "Identification of an angiogenic mitogen selective for endocrine gland

RL Nature 412:877-884(2001).

RX NUCLEOTIDE SEQUENCE [MRNA].

RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,

RT "Identification of an angiogenic mitogen selective for endocrine gland

RL Nature 412:877-884(2001).


```
DR HSP; P25687; l1MT.
DR Ensembl; ENSG00000143125; Homo sapiens.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
SQ SEQUENCE 105 AA; 11729 MW; E570FDE30EB52D2 CRC64;

Query Match          99.8%; Score 588; DB 2; Length 105;
Best Local Similarity 99.0%; Pred. No. 2.7e-54;
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGREGEC 60
    |||||
Db 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGREGEC 60
    |||||
Qy 61 HPGSHKVPFFRKQKHTCPCLPNLLCSRFDPDGRYCSMDLKNINF 105
    |||||
Db 61 HPGSHKIPFFRKQKHTCPCLPNLLCSRFDPDGRYCSMDLKNINF 105
    |||||

RESULT 4
PROK1_RAT STANDARD; PRT; 105 AA.
AC QBR41.4;
DT 19-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2002, sequence version 1.
DT 21-FEB-2006, entry version 24.
DE Prokineticin-1 precursor (Endocrine-gland-derived vascular endothelial
DE growth factor) (EG-VEGF).
GN Name=Prok1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Iehibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohkaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VEGF/prokineticins as cognate
RT ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
CC -1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC Induces proliferation, migration and fenestration (the formation
CC of membrane discontinuities) in capillary endothelial cells
CC derived from endocrine glands. Has little or no effect on a
CC variety of other endothelial and non-endothelial cell types (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC -1- SIMILARITY: Belongs to the prokinectin family.
CC
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC ENBL; AY089983; AA09104.1; -; mRNA.
DR HSP; P25687; l1MT.
DR Ensembl; ENSRNOG0000018201; Rattus norvegicus.
DR RGD; 620898; Prok1.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0045765; P:regulation of angiogenesis; NAS.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
DR KW Growth factor; Mitogen; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 105 Prokineticin-1.
FT FTID=PRO_0000025808.
FT DISULFID 26 38 By similarity.
FT DISULFID 32 50 By similarity.
FT DISULFID 37 78 By similarity.
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FT DISULFID 60 86 By similarity.
FT DISULFID 80 96 By similarity.
SQ SEQUENCE 105 AA; 11643 MW; 8DF0C42122B1CSB6 CRC64;

Query Match          92.5%; Score 545; DB 1; Length 105;
Best Local Similarity 89.5%; Pred. No. 9.6e-50;
Matches 94; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGREGEC 60
    |||||
Db 1 MRGAVQVFIMLLLATVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGREGEC 60
    |||||
Qy 61 HPGSHKVPFFRKQKHTCPCLPNLLCSRFDPDGRYCSMDLKNINF 105
    |||||
Db 61 HPGSHKIPFFRKQKHTCPCLPNLLCSRFDPDGRYCSMDLKNINF 105
    |||||

RESULT 5
QBR457_MOUSE PRELIMINARY; PRT; 81 AA.
ID QBR457_MOUSE
AC QBR457;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Prokineticin 1 (Fragment).
GN Name=Prok1; Synonyms=Pkl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
CC
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CC
CC ENBL; AF487281; AA049573.1; -; mRNA.
DR HSP; P25687; l1MT.
DR Ensembl; ENSMUSG00000046213; Mus musculus.
DR MGI; MGI:2180370; Prok1.
DR GO; GO:0005576; C:extracellular region; IDA.
DR GO; GO:0000187; P:activation of MAPK activity; IDA.
DR GO; GO:0007623; P:circadian rhythm; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0045765; P:regulation of angiogenesis; IDA.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
FT NON_TER 1 1
SQ SEQUENCE 81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;

Query Match          73.3%; Score 432; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 6.7e-38;
Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 25 ACERDVQCGAGTCCCAISLWLRGLRMTPLRGREGECCHPGSHKVPFFRKQKHTCPCLPNL 84
    |||||
Db 1 ACERDQQCGAGTCCCAISLWLRGLRMTPLRGREGECCHPGSHKIPFFRKQKHTCPSPSL 60
    |||||
Qy 85 LCSRFDPDGRYCSMDLKNINF 105
    |||||
Db 61 LCSRFDPDGRYCSMDLKNINF 81
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RESULT 6
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Q32FI2_BOVIN
ID Q32FI2_BOVIN PRELIMINARY; PRT; 81 AA.
AC Q32FI2;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Prokineticin-1 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15932929; DOI=10.1210/en.2005-0297;
RA Kislouk T., Podlovni H., Spanel-Borowski K., Ovadia O., Zhou Q.Y.,
RA Meidan R.;
RT "Prokineticins (endocrine gland-derived vascular endothelial growth
RT factor and BV8) in the bovine ovary: expression and role as mitogens
RT and survival factors for corpus luteum-derived endothelial cells.";
RL Endocrinology 146:3950-3958(2005).
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CC -----
DEMBL; AY877432; AAX81517.1; -; mRNA.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
FT NON TER 1
FT SEQUENCE 81 AA; 9086 MW; 228834A7B83BA536 CRC64;
SQ
Query Match 70.8%; Score 417; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 2.6e-36;
Matches 71; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 25 ACERDVQCGAGTCATSLMLRGLRMCTPLGREGECHPGSHKVPFRKRKHHTCPCLPNL 84
Db 1 ACERDVQCGAGTCATSLMLRGLRMCTPLGREGECHPGSHKVPFRKRKHHTCPCLPNL 60
QY 85 LCSRPDPGRYRCSMDLKNIF 105
Db 61 LCSRGLDGRYRCSMDLKNIF 81
RESULT 7
Q2XXR8 VARVA PRELIMINARY; PRT; 104 AA.
AC Q2XXR8;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 21-FEB-2006, entry version 4.
DE AVIToxin-VAR1 precursor.
OS Varanus varius (Lace monitor).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=8559;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16292255;
RA Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F.,
RA Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C.,
RA Ignjatovic V., Summerhayes R., Kochva E.;
RT "Early evolution of the venom system in lizards and snakes.";
RL Nature 439:584-588(2006).
CC -----
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CC -----
DEMBL; DQ139878; AAZ75583.1; -; mRNA.
DR SIGNAL.
FT SIGNAL.
FT CHAIN 1 19 AVIToxin-VAR2.
FT CHAIN 20 104 AVIToxin-VAR1.
SQ SEQUENCE 104 AA; 11191 MW; C25A83A6B59D3AA3 CRC64;
Query Match 61.6%; Score 363; DB 2; Length 104;
Best Local Similarity 56.3%; Pred. No. 1.7e-30;
Matches 58; Conservative 21; Mismatches 24; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGREGERC 60
Db 1 MRSLLCAPLLLLLSAGESAVITGACDKDLQCGEGMCCAVSLWIRSIRICTPLGSGGDC 60
QY 61 HPGSHKVPFRKRKHHTCPCLPNLCSRPDPGRYRCSMDLKNI 103
Db 61 HPLSHKVPFDGQRKHHTCPCLPNLVCGQTSPGKYKCLPEFKNV 103
RESULT 8
Q2XXR7 VARVA PRELIMINARY; PRT; 104 AA.
AC Q2XXR7;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 21-FEB-2006, entry version 4.
DE AVIToxin-VAR2 precursor.
OS Varanus varius (Lace monitor).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=8559;
RN [1]
RP TISSUE=Compound mandibular venom gland;
RC TISSUE=Compound mandibular venom gland;
RX PubMed=16292255;
RA Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F.,
RA Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C.,
RA Ignjatovic V., Summerhayes R., Kochva E.;
RT "Early evolution of the venom system in lizards and snakes.";
RL Nature 439:584-588(2006).
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CC -----
DEMBL; DQ139878; AAZ75584.1; -; mRNA.
DR SIGNAL.
FT SIGNAL.
FT CHAIN 1 19 AVIToxin-VAR2.
FT CHAIN 20 104 AVIToxin-VAR1.
SQ SEQUENCE 104 AA; 11191 MW; C25A83A6B59D3AA3 CRC64;
Query Match 61.6%; Score 363; DB 2; Length 104;
Best Local Similarity 56.3%; Pred. No. 1.7e-30;
Matches 58; Conservative 21; Mismatches 24; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCTCAISLWRLGLRMCTPLGREGERC 60
Db 1 MRSLLCAPLLLLLSAGESAVITGACDKDLQCGEGMCCAVSLWIRSIRICTPLGSGGDC 60
QY 61 HPGSHKVPFRKRKHHTCPCLPNLCSRPDPGRYRCSMDLKNI 103
Db 61 HPLSHKVPFDGQRKHHTCPCLPNLVCGQTSPGKYKCLPEFKNV 103
RESULT 9
Q4RVU3 TETNG PRELIMINARY; PRT; 106 AA.
ID Q4RVU3_TETNG
AC Q4RVU3;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 9 SCAP14991, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG0028169001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
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CC -----
DEMBL; DQ139877; AAZ75583.1; -; mRNA.
DR SIGNAL.
FT SIGNAL.
FT CHAIN 1 19 Potential.
FT CHAIN 20 104 AVIToxin-VAR1.
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DR PANTHER: PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
KW 3D-structure; Direct protein sequencing; Toxin.
FT CHAIN 1 81
FT
FT
FT DISULFID 7 19
FT DISULFID 13 21
FT DISULFID 18 59
FT DISULFID 41 67
FT DISULFID 61 77
FT VARIANT 72 77
FT CONFLICT 18 18
FT CONFLICT 22 22
FT CONFLICT 54 54
FT STRAND 5 6
FT STRAND 8 9
FT TURN 10 12
FT TURN 13 13
FT TURN 15 16
FT STRAND 17 21
FT STRAND 23 24
FT TURN 26 27
FT STRAND 29 33
FT STRAND 35 35
FT TURN 37 38
FT STRAND 40 41
FT TURN 43 44
FT STRAND 48 49
FT STRAND 52 52
FT STRAND 57 58
FT STRAND 62 62
FT TURN 64 65
FT STRAND 67 72
FT TURN 73 74
FT STRAND 75 79
SQ SEQUENCE 81 AA; 8604 MW; 5F6B703434338B03 CRC64;

Query Match 53.5%; Score 315; DB 1; Length 81;
Best Local Similarity 62.3%; Pred. No. 1.6e-25;
Matches 48; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 20 AVITGACERDVCGAGTCCATSLWRLGRLMCTPLGREGECHPGSHKVPFRKXHTCP 79
Db 1 AVITGACERDLQCGTGCACVSLWIKSVRVCTPVGTSGEDCHPASHKIPFGQRMHTCP 60

QY 80 CLPNLLCSRFPDGRYRC 96
Db 61 CAPNLACVQTSPPKFKC 77

RESULT 12
Q6ISR0 HUMAN
ID Q6ISR0 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q6ISR0
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 21-FEB-2006, entry version 6.
DE Prokineticin 2.
GN Name=PROK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC069395; AAH69395.1; -; mRNA.
DR EMBL; BC096695; AAH96695.1; -; mRNA.
DR EMBL; BC098110; AAH98110.1; -; mRNA.
DR Ensembl; ENSG00000163421; Homo sapiens.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
SQ SEQUENCE 108 AA; 11659 MW; D7AF89D8551A97FC CRC64;

Query Match 51.4%; Score 303; DB 2; Length 108;
Best Local Similarity 55.2%; Pred. No. 4e-24;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 10 MLLLVTSDCAVITGACERDVCGAGTCCATSLWRLGRLMCTPLGREGECHPGSHKVPF 69
Db 18 LLLTPRAGDAVITGACERDVCGAGTCCATSLWRLGRLMCTPLGREGECHPGSHKVPF 77

QY 70 FRKRKHHTCPCLPNLLCSRFPDGRYRC 96
Db 78 FGRRMHHTCPCLPGLACLRTSFNRFIC 104

RESULT 13
Q8JFQ0 BOMMX
ID Q8JFQ0 BOMMX PRELIMINARY; PRT; 96 AA.
AC Q8JFQ0
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Bv8 protein homolog 2.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin secretions;
RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
RA Lai R., Liu H., Lee W.H., Zhang Y.;

DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
FT NON TER 102 102
SQ SEQUENCE 102 AA; 11062 MW; 470A2CDF2D069043 CRC64;

Query Match 50.6%; Score 298; DB 2; Length 102;
Best Local Similarity 57.8%; Pred. No. 1.3e-23;
Matches 52; Conservative 9; Mismatches 15; Indels 14; Gaps 1;

Qy 11 LLVTVSDCAVITGACERDVQCAGTCCALSLWLRLGRLMCTPLGRGEECHP----- 62
Db 11 LLVSRGSSAVITGAKEKSCQCGGLCCAVLSIRLSRLCMPHGAEGDDCHPMSQATSYL 70
Qy 63 -----GSHKVPFPRKRKHHHTCPLPNLLC 86
Db 71 VEQPSSSSFQVFFGKRLHHTCPLPNLSC 100

RESULT 15
PROK2 RAT STANDARD; PRT; 107 AA.
ID AC QBR413;
DT 02-AUG-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2002, sequence version 1.
DT 21-FEB-2006, entry version 25.
GN Prokineticin-2 precursor (PK2).
DN Name=Prok2; Synonyms=Bv8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22050003; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohkaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VEGF/prokineticins as cognate
RT ligands for two orphan G-protein-coupled receptors";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
RN [2]
RP EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
RX MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus";
RL Nature 417:405-410(2002).
CC CC -1- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potentially contracts gastrointestinal (GI) smooth muscle (By
CC similarity).
CC CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC CC -1- TISSUE SPECIFICITY: Expressed at high levels in testis and at
CC lower levels in brain, lung, ovary, spleen, thymus and uterus.
CC CC -1- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC genes (CRY1 and CRY2) (Probable).
CC CC -1- SIMILARITY: Belongs to the prokineticin family.
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CC
CC EMBL; AY089984; AA009105.1; -; mRNA.
CC HSSP; P25687; 1IMT.
DR Ensembl; ENSRNOG0000010898; Rattus norvegicus.
DR RGD; 620280; Prok2.
DR GO; GO:0001664; F:G-protein-coupled receptor binding; IDA.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR

Pfam; PF06607;	Prokineticin; 1.
KW	Biological rhythms; Neuropeptide; signal.
FT SIGNAL	1 26 Potential.
FT CHAIN	27 107 Prokineticin-2. /FtId=PRO_0000025811.
FT DISULFID	33 45 By similarity.
FT DISULFID	39 57 By similarity.
FT FT DISULFID	44 85 By similarity.
FT DISULFID	67 93 By similarity.
FT DISULFID	87 103 By similarity.
SQ SEQUENCE	107 AA; 11594 MW; BDFP316DCB5PED0 CRC64; Query Match 50.6%; Score 298; DB 1; Length 107; Best Local Similarity 54.0%; Pred. No. 1.3e-23; Matches 47; Conservative 16; Mismatches 24; Indels 0; Gaps 0;
Qy	10 MLLAVTVSDCAVITGACERDVQCAGGTCCATSIWLRLGRMCTPLGREGEBCHPGSHKVPF 69 : : : : : : : :
Dd	17 LLLTPPADGAAVITGADKDSCQGCGGCCCAVSIIWKISIRICTPMGVQGDSCHLPTRKVPF 76 : : : :
Qy	70 FRKKHHTCCLPNLLCSRFPDGYRC 96 : : : :
Dd	77 WGRMHHTCPCLPGLACLRTSFNRFC 103 : : : :

Search completed: December 14, 2006, 14:13:22
Job time : 273.398 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model
Run on: December 14, 2006, 14:14:02 ; Search time 32.8691 Seconds
(without alignments)
229.018 Million cell updates/sec
Title: US-10-692-299-2_COPY_20_105
Perfect score: 498
Sequence: 1 AVITGACBRDVGCGAGTCCA.....CSRFPDGRYRCMDLKNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 650591 segs, 87530628 residues
Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents_AA*
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pap:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pap:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCUTUS_COMB.pap:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pap:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	105	2	US-09-712-529-5-5
2	498	100.0	105	2	US-10-212-201A-5
3	498	100.0	105	2	US-10-212-355-5
15	486	97.6	105	2	US-09-621-976-5350
16	357	71.7	80	2	US-09-513-998C-4698
17	291	58.4	108	2	US-09-712-523-2
18	291	58.4	108	2	US-10-212-201A-2
19	291	58.4	108	2	US-10-212-355-2
20	107.5	21.6	224	2	US-09-161-241-14
21	102	20.5	186	2	US-09-949-016-7146
22	102	20.5	207	2	US-09-161-241-13
23	102	20.5	259	2	US-09-161-241-12
24	102	20.5	259	2	US-09-949-016-6872
44	101	20.3	259	2	US-09-161-241-11
45	100.5	20.2	215	2	US-10-104-047-2196
46	100.5	20.2	350	2	US-09-161-241-9
64	100.5	20.2	375	2	US-09-949-016-7856
65	100.5	20.2	375	2	US-09-949-016-7857
66	100.5	20.2	375	2	US-09-949-016-7858
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146	71	14.3	593	2	US-09-456-886-17	Sequence 17, Appli
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160	69	13.9	677	2	US-09-949-016-111370	Sequence 11370, A	233	65.5	13.2	683	2	US-08-979-847B-208	Sequence 208, App
161	69	13.9	677	2	US-09-949-016-111371	Sequence 11371, A	234	65.5	13.2	683	2	US-08-979-847B-210	Sequence 210, App
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183	68	13.7	224	3	US-09-613-591F-134	Sequence 134, App	256	64.5	13.0	299	2	US-09-312-283C-192	Sequence 192, App
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198	68	13.7	455	2	US-09-095-094-4	Sequence 4, Appli	271	63.5	12.8	713	2	US-08-872-855-5	Sequence 5, Appli
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203	67	13.5	317	2	US-09-383-586-20	Sequence 20, Appl	276	63.5	12.8	729	2	US-09-897-427A-2	Sequence 2, Appli
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209	66.5	13.4	589	1	US-07-668-648-6	Sequence 2, Appli	282	63	12.7	1239	2	US-10-104-047-2669	Sequence 2669, Ap
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212	66.5	13.4	589	1	US-08-429-998-6	Sequence 6, Appli	285	62.5	12.6	277	2	US-08-469-633A-4	Sequence 4, Appli
213	66.5	13.4	589	1	US-08-431-333-2	Sequence 2, Appli	286	62.5	12.6	297	2	US-09-270-767-44071	Sequence 44071, A
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215	66.5	13.4	589	2	US-08-991-862-2	Sequence 2, Appli	288	62.5	12.6	5179	2	US-09-538-092-1258	Sequence 1258, Ap
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225	66	13.3	1172	2	US-09-949-016-6333	Sequence 6333, Ap	298	62	12.4	415	2	US-09-069-632-1	Sequence 1, Appli
226	66	13.3	3712	2	US-10-037-417-48	Sequence 48, Appl	299	62	12.4	435	1	US-08-361-920-27	Sequence 27, Appl

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301	12.4	435	1	US-08-483-432-27	Sequence 27, Appl	374	60.5	12.1	2601	2	US-09-436-063C-9	Sequence 9, Appli
302	12.4	435	2	US-09-069-632-3	Sequence 3, Appli	375	60.5	12.1	2703	1	US-08-185-432-19	Sequence 19, Appl
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304	12.4	578	2	US-09-908-322-13	Sequence 13, Appl	377	60.5	12.1	2703	2	US-09-121-457-4	Sequence 4, Appli
305	12.4	831	2	US-09-939-853A-97	Sequence 97, Appl	378	60	12.0	113	2	US-09-270-767-37873	Sequence 37873, A
306	12.4	831	2	US-09-939-853A-98	Sequence 98, Appl	379	60	12.0	113	2	US-09-270-767-53090	Sequence 53090, A
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308	12.4	998	1	US-08-702-367A-20	Sequence 20, Appl	381	60	12.0	184	1	US-08-468-847B-18	Sequence 18, Appl
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312	12.4	1068	2	US-09-113-825-2	Sequence 2, Appli	385	60	12.0	202	2	US-09-949-016-10546	Sequence 10546, A
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315	12.4	1833	2	US-08-479-722B-2	Sequence 2, Appli	388	60	12.0	546	2	US-09-949-016-10394	Sequence 10394, A
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317	12.4	1833	5	PCT-US95-02251-18	Sequence 18, Appl	390	60	12.0	623	2	US-09-807-802A-5	Sequence 5, Appli
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322	12.4	2556	2	US-09-121-457-2	Sequence 2, Appli	395	60	12.0	734	5	PCT-US95-07295-8	Sequence 8, Appli
323	12.3	156	2	US-09-270-767-33322	Sequence 33322, A	396	60	12.0	1227	2	US-09-252-991A-16636	Sequence 16636, A
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325	12.3	277	1	US-08-147-784-2	Sequence 2, Appli	398	59.5	11.9	230	2	US-09-252-991A-25728	Sequence 25728, A
326	12.3	277	1	US-08-195-967-2	Sequence 2, Appli	399	59.5	11.9	258	2	US-09-252-991A-28812	Sequence 28812, A
327	12.3	277	2	US-09-006-353A-12	Sequence 12, Appl	400	59.5	11.9	340	2	US-09-252-991A-18667	Sequence 18667, A
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329	12.3	277	2	US-09-573-986-12	Sequence 12, Appl	402	59.5	11.9	886	2	US-09-631-603-14	Sequence 14, Appl
330	12.3	277	2	US-09-880-939-2	Sequence 2, Appli	403	59.5	11.9	4544	1	US-08-469-486-52	Sequence 52, Appl
331	12.3	277	2	US-09-804-200-2	Sequence 2, Appli	404	59.5	11.9	4544	1	US-08-469-486-52	Sequence 52, Appl
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333	12.3	510	2	US-10-104-047-2580	Sequence 2580, Ap	406	59	11.8	298	2	US-09-902-540-12595	Sequence 12595, A
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341	12.2	1252	1	US-08-316-650-3	Sequence 3, Appli	414	59	11.8	1253	2	US-09-592-685-4	Sequence 4, Appli
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343	12.1	170	2	US-09-252-991A-22362	Sequence 22362, A	416	58.5	11.7	143	2	US-09-270-767-33302	Sequence 33302, A
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352	12.1	515	2	US-09-895-077-6	Sequence 6, Appli	425	58.5	11.7	207	2	US-08-577-788C-47	Sequence 47, Appl
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362	12.1	1104	1	US-08-327-832-5	Sequence 5, Appli	435	58.5	11.7	721	2	US-09-310-685-12	Sequence 12, Appl
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457	57.5	11.5	132	2	US-09-523-323-55	Sequence 55, Appli	542	57	11.4	2324	1	US-08-283-857-1	Sequence 1, Appli
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459	57.5	11.5	207	2	US-10-094-749-2017	Sequence 2017, Ap	544	57	11.4	2327	7	5455158-1	Patent No. 5455158
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461	57.5	11.5	443	2	US-09-461-325-147	Sequence 147, App	546	57	11.4	2386	1	US-09-016-366A-12	Sequence 12, Appli
462	57.5	11.5	443	2	US-10-012-542-147	Sequence 147, App	547	57	11.4	2386	2	US-09-961-403-1	Sequence 1, Appli
463	57.5	11.5	443	2	US-10-115-123-147	Sequence 147, App	548	57	11.4	2446	1	US-08-551-356-2	Sequence 2, Appli
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467	57.5	11.5	668	1	US-08-786-164-13	Sequence 13, Appli	552	56.5	11.3	99	2	US-09-950-933A-82	Sequence 82, Appli
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471	57.5	11.5	767	1	US-08-874-678-2	Sequence 2, Appli	556	56.5	11.3	264	2	US-09-973-278-151	Sequence 151, App
472	57.5	11.5	767	2	US-08-643-839-2	Sequence 2, Appli	557	56.5	11.3	265	2	US-09-247-357-153	Sequence 153, App
473	57.5	11.5	767	2	US-09-348-886-2	Sequence 2, Appli	558	56.5	11.3	309	2	US-09-270-767-46802	Sequence 46802, A
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478	57.5	11.5	810	2	US-09-055-699-34	Sequence 34, Appli	563	56.5	11.3	495	2	US-10-006-011A-4	Sequence 4, Appli
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481	57.5	11.5	810	2	US-09-661-468-34	Sequence 34, Appli	566	56.5	11.3	638	2	US-09-482-273-245	Sequence 245, App
482	57.5	11.5	810	2	US-09-976-165-34	Sequence 34, Appli	567	56.5	11.3	705	2	US-10-006-011A-3	Sequence 3, Appli
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499	57.5	11.5	2871	2	US-09-538-092-1076	Sequence 1076, Ap	584	56.5	11.3	1238	2	US-09-855-722-5	Sequence 5, Appli
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504	57	11.4	181	2	US-09-095-094-19	Sequence 19, Appli	589	56.5	11.3	1616	2	US-09-538-092-1016	Sequence 1016, Ap
505	57	11.4	253	2	US-10-094-749-1792	Sequence 1792, Ap	590	56	11.2	98	2	US-09-950-933A-50	Sequence 50, Appli
506	57	11.4	254	2	US-09-042-785A-4	Sequence 4, Appli	591	56	11.2	141	2	US-09-621-976-4236	Sequence 4236, Ap
507	57	11.4	254	2	US-09-422-680A-6	Sequence 6, Appli	592	56	11.2	141	2	US-09-252-991A-28121	Sequence 28121, A
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510	57	11.4	306	2	US-09-270-767-41758	Sequence 12, Appli	595	56	11.2	260	2	US-09-270-767-45600	Sequence 45600, A
511	57	11.4	498	1	US-08-660-963-12	Sequence 12, Appli	596	56	11.2	260	2	US-09-711-681-2	Sequence 2, Appli
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514	57	11.4	605	2	US-09-042-785A-23	Sequence 23, Appli	599	56	11.2	383	2	US-09-142-027A-12	Sequence 12, Appli
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607	56	11.2	691	2	US-09-252-991A-16809	Sequence 16809, A	680	55	11.0	359	2	US-09-699-266A-11	Sequence 11, Appli
608	56	11.2	748	1	US-08-920-234-2	Sequence 2, Appli	681	55	11.0	394	2	US-10-233-858-9	Sequence 9, Appli
609	56	11.2	748	1	US-08-937-931-4	Sequence 4, Appli	682	55	11.0	394	2	US-09-338-063A-9	Sequence 9, Appli
610	56	11.2	748	2	US-09-285-502-4	Sequence 4, Appli	683	55	11.0	399	1	US-08-414-926A-5	Sequence 5, Appli
611	56	11.2	748	2	US-09-030-335-9	Sequence 9, Appli	684	55	11.0	399	1	US-08-926-682-5	Sequence 5, Appli
612	56	11.2	748	2	US-09-709-126-4	Sequence 4, Appli	685	55	11.0	399	2	US-09-253-682-5	Sequence 5, Appli
613	56	11.2	748	2	US-09-871-385A-4	Sequence 4, Appli	686	55	11.0	399	2	US-09-527-687-5	Sequence 5, Appli
614	56	11.2	761	2	US-09-949-016-10631	Sequence 10631, A	687	55	11.0	399	2	US-09-892-100-5	Sequence 5, Appli
615	56	11.2	799	2	US-09-030-335-4	Sequence 4, Appli	688	55	11.0	428	2	US-09-252-991A-27023	Sequence 27023, A
616	56	11.2	1153	2	US-09-560-385A-16	Sequence 16, Appli	689	55	11.0	547	2	US-10-104-047-3096	Sequence 3096, Ap
617	56	11.2	1170	2	US-09-561-709B-12	Sequence 12, Appli	690	55	11.0	548	2	US-09-252-991A-28958	Sequence 28958, A
618	56	11.2	1170	2	US-09-560-385A-14	Sequence 14, Appli	691	55	11.0	567	1	US-08-841-483-2	Sequence 2, Appli
619	56	11.2	1194	2	US-09-092-508-2	Sequence 2, Appli	692	55	11.0	567	2	US-09-382-911-2	Sequence 2, Appli
620	56	11.2	1194	2	US-09-435-115-2	Sequence 2, Appli	693	55	11.0	574	2	US-09-248-796A-15283	Sequence 15283, A
621	56	11.2	1194	2	US-09-069-023-26	Sequence 26, Appli	694	55	11.0	582	2	US-08-334-179A-4	Sequence 4, Appli
622	56	11.2	1194	2	US-09-098-310-2	Sequence 2, Appli	695	55	11.0	583	2	US-09-641-612-2	Sequence 2, Appli
623	56	11.2	1194	2	US-09-538-092-825	Sequence 825, App	696	55	11.0	585	2	US-09-641-612-5	Sequence 5, Appli
624	56	11.2	1194	2	US-09-949-016-6030	Sequence 6030, Ap	697	55	11.0	597	2	US-09-939-853A-107	Sequence 107, App
625	56	11.2	1196	2	US-09-949-016-10065	Sequence 10065, A	698	55	11.0	750	2	US-09-270-767-42975	Sequence 42975, A
626	56	11.2	1196	2	US-09-949-016-10066	Sequence 10066, A	699	55	11.0	909	2	US-09-252-991A-30503	Sequence 30503, A
627	56	11.2	1205	2	US-09-092-508-16	Sequence 16, Appli	700	55	11.0	961	2	US-09-657-472-4	Sequence 4, Appli
628	56	11.2	1205	2	US-09-435-115-16	Sequence 16, Appli	701	55	11.0	961	5	PCT-US93-11725-4	Sequence 4, Appli
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630	56	11.2	1239	2	US-09-949-016-10063	Sequence 10063, A	703	55	11.0	1036	2	US-09-751-389-2	Sequence 2, Appli
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633	56	11.2	1935	2	US-09-949-016-10403	Sequence 8, Appli	706	55	11.0	1038	2	US-09-908-500A-2	Sequence 2, Appli
634	56	11.2	5405	2	US-08-718-388-9	Sequence 9, Appli	707	55	11.0	1171	2	US-09-560-385A-36	Sequence 36, Appli
635	55.5	11.1	44	1	US-08-050-319B-37	Sequence 37, Appli	708	55	11.0	1192	2	US-09-560-385A-34	Sequence 34, Appli
636	55.5	11.1	44	1	US-08-465-982-37	Sequence 37, Appli	709	55	11.0	1192	2	US-10-053-662A-32	Sequence 32, Appli
637	55.5	11.1	80	2	US-09-621-976-7198	Sequence 7198, Ap	710	55	11.0	1431	2	US-09-842-930A-2	Sequence 2, Appli
638	55.5	11.1	143	2	US-09-439-313-482	Sequence 482, App	711	55	11.0	2052	2	US-09-045-201A-2	Sequence 2, Appli
639	55.5	11.1	143	2	US-09-636-215-482	Sequence 482, App	712	55	11.0	2052	2	US-09-619-062-2	Sequence 2, Appli
640	55.5	11.1	143	2	US-09-685-166A-482	Sequence 482, App	713	55	11.0	2733	2	US-09-949-016-11433	Sequence 11433, A
641	55.5	11.1	143	2	US-09-679-426-482	Sequence 482, App	714	55	11.0	3259	2	US-09-949-016-6507	Sequence 6507, Ap
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643	55.5	11.1	143	2	US-09-651-236-482	Sequence 482, App	716	54.5	10.9	92	2	US-08-938-085A-41	Sequence 41, Appli
644	55.5	11.1	143	2	US-09-657-273-482	Sequence 482, App	717	54.5	10.9	92	2	US-10-072-844-41	Sequence 41, Appli
645	55.5	11.1	143	2	US-10-012-896-482	Sequence 482, App	718	54.5	10.9	92	2	US-10-072-838-41	Sequence 41, Appli
646	55.5	11.1	143	3	US-10-144-678A-482	Sequence 482, App	719	54.5	10.9	92	2	US-10-072-841A-41	Sequence 41, Appli
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648	55.5	11.1	154	2	US-09-540-245A-10	Sequence 10, Appli	721	54.5	10.9	103	2	US-09-489-039A-7227	Sequence 7227, Ap
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650	55.5	11.1	154	2	US-10-289-776-10	Sequence 10, Appli	723	54.5	10.9	190	2	US-09-902-540-12077	Sequence 12077, A
651	55.5	11.1	233	2	US-09-252-991A-18455	Sequence 18455, A	724	54.5	10.9	232	2	US-09-270-767-39931	Sequence 39931, A
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654	55.5	11.1	385	1	US-08-457-135-1	Sequence 1, Appli	727	54.5	10.9	259	2	US-09-573-986-2	Sequence 2, Appli
655	55.5	11.1	385	2	US-09-142-027A-10	Sequence 10, Appli	728	54.5	10.9	282	2	US-08-808-847-1	Sequence 1, Appli
656	55.5	11.1	407	2	US-09-252-991A-32423	Sequence 32423, A	729	54.5	10.9	299	2	US-09-153-927-3	Sequence 3, Appli
657	55.5	11.1	431	2	US-09-252-991A-18787	Sequence 18787, A	730	54.5	10.9	299	2	US-09-134-618-4	Sequence 4, Appli
658	55.5	11.1	716	2	US-09-252-991A-30683	Sequence 30683, A	731	54.5	10.9	299	2	US-09-949-016-6422	Sequence 6422, Ap
659	55.5	11.1	1742	3	US-09-958-359-23	Sequence 23, Appli	732	54.5	10.9	301	2	US-09-949-016-9189	Sequence 9189, Ap
660	55	11.0	82	2	US-10-178-213-464	Sequence 464, App	733	54.5	10.9	320	2	US-09-489-039A-8062	Sequence 8062, Ap
661	55	11.0	100	2	US-09-950-933A-40	Sequence 40, Appli	734	54.5	10.9	322	2	US-09-248-796A-15932	Sequence 15932, A
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663	55	11.0	150	2	US-09-334-179A-10	Sequence 10, Appli	736	54.5	10.9	357	2	US-10-037-417-46	Sequence 46, Appli
664	55	11.0	150	2	US-09-902-540-14820	Sequence 14820, A	737	54.5	10.9	435	2	US-09-252-991A-23753	Sequence 23753, A
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666	55	11.0	175	2	US-09-252-991A-30055	Sequence 30055, A	739	54.5	10.9	546	2	US-09-270-767-46725	Sequence 46725, A
667	55	11.0	195	2	US-10-031-607-11	Sequence 11, Appli	740	54.5	10.9	590	2	US-09-270-767-45038	Sequence 45038, A
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670	55	11.0	197	2	US-08-795-447A-49	Sequence 49, Appli	743	54.5	10.9	948	1	US-08-469-537A-101	Sequence 101, App
671	55	11.0	197	2	US-08-974-186-49	Sequence 49, Appli	744	54.5	10.9	948	2	US-09-751-389-5	Sequence 5, Appli
672	55	11.0	197	2	US-08-795-446B-49	Sequence 49, Appli	745	54.5	10.9	955	1	US-08-500-857A-10	Sequence 10, Appli
673	55	11.0	197	2	US-08-706-945D-135	Sequence 135, App	746	54.5	10.9	984	1	US-08-673-789-9	Sequence 9, Appli
674	55	11.0	197	2	US-08-577-788C-49	Sequence 49, Appli	747	54.5	10.9	984	1	US-08-449-645A-19	Sequence 19, Appli
675	55	11.0	197	3	US-09-613-591F-132	Sequence 132, App	748	54.5	10.9	984	1	US-08-702-367A-19	Sequence 19, Appli
676	55	11.0	203	2	US-10-031-607-10	Sequence 10, Appli	749	54.5	10.9	984	2	US-09-378-759-19	Sequence 19, Appli

767	54.5	10.9	984	5	PCT-US95-04681-19	Sequence 19, Appl	857	53.5	10.7	411	2	US-09-949-016-11215	Sequence 11215, A
768	54.5	10.9	991	2	US-09-949-016-7768	Sequence 7768, Ap	858	53.5	10.7	440	1	US-08-574-959A-2	Sequence 2, Appl
769	54.5	10.9	1010	2	US-08-882-046-7	Sequence 7, Appl	859	53.5	10.7	440	2	US-09-357-014-2	Sequence 2, Appl
770	54.5	10.9	1010	2	US-09-566-047-7	Sequence 7, Appl	860	53.5	10.7	440	2	US-09-949-016-6431	Sequence 546, Ap
771	54.5	10.9	1035	2	US-09-751-389-4	Sequence 6, Appl	861	53.5	10.7	506	2	US-09-303-518D-546	Sequence 28761, A
772	54.5	10.9	1036	2	US-09-068-740A-6	Sequence 6, Appl	879	53.5	10.7	526	2	US-09-252-991A-28761	Sequence 3, Appl
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774	54.5	10.9	1067	2	US-09-579-536C-18	Sequence 18, Appl	881	53.5	10.7	546	2	US-10-094-749-1953	Sequence 3, Appl
775	54.5	10.9	1187	2	US-09-068-740A-7	Sequence 7, Appl	882	53.5	10.7	559	1	US-08-424-788-3	Sequence 2, Appl
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777	54.5	10.9	1208	2	US-10-213-329-1	Sequence 1, Appl	884	53.5	10.7	575	1	US-08-110-683-4	Sequence 4, Appl
778	54.5	10.9	1218	1	US-08-400-159-6	Sequence 6, Appl	885	53.5	10.7	575	1	US-08-477-166-4	Sequence 4, Appl
779	54.5	10.9	1218	2	US-08-611-729A-6	Sequence 6, Appl	886	53.5	10.7	575	1	US-08-472-097-4	Sequence 4, Appl
780	54.5	10.9	1218	2	US-08-882-046-2	Sequence 2, Appl	887	53.5	10.7	575	2	US-09-439-672-4	Sequence 4, Appl
781	54.5	10.9	1218	2	US-09-214-278-7	Sequence 7, Appl	888	53.5	10.7	575	2	PCT-US93-11638-4	Sequence 4, Appl
782	54.5	10.9	1218	2	US-09-068-740A-11	Sequence 11, Appl	889	53.5	10.7	629	5	US-09-079-431B-4	Sequence 4, Appl
783	54.5	10.9	1218	2	US-09-855-722-7	Sequence 7, Appl	890	53.5	10.7	704	2	US-09-590-656-2	Sequence 2, Appl
784	54.5	10.9	1218	2	US-09-566-047-2	Sequence 2, Appl	891	53.5	10.7	704	2	US-09-733-764-2	Sequence 2, Appl
785	54.5	10.9	1218	2	US-09-917-254-85	Sequence 85, Appl	892	53.5	10.7	768	1	US-08-454-455-4	Sequence 4, Appl
786	54.5	10.9	1218	2	US-09-195-524-6	Sequence 6, Appl	893	53.5	10.7	784	2	US-09-949-016-9467	Sequence 9467, Ap
787	54.5	10.9	1218	2	US-09-573-536C-1	Sequence 1, Appl	894	53.5	10.7	977	2	US-09-590-656-1	Sequence 1, Appl
788	54.5	10.9	1218	2	US-09-949-016-5902	Sequence 5902, Ap	895	53.5	10.7	977	2	US-09-733-764-1	Sequence 1, Appl
789	54.5	10.9	1218	2	US-09-310-685-4	Sequence 4, Appl	896	53.5	10.7	996	2	US-09-949-016-8254	Sequence 8254, Ap
790	54.5	10.9	1254	2	US-09-949-016-10297	Sequence 10297, A	897	53.5	10.7	1111	1	US-08-317-450B-15	Sequence 15, Appl
791	54.5	10.9	1551	2	US-09-949-016-6785	Sequence 6785, Ap	898	53.5	10.7	1111	2	US-08-800-593-15	Sequence 15, Appl
792	54.5	10.9	1799	2	US-09-845-583A-6	Sequence 6, Appl	899	53.5	10.7	1111	2	US-09-756-071B-15	Sequence 15, Appl
793	54.5	10.9	2647	1	US-08-583-562B-8	Sequence 8, Appl	900	53.5	10.7	1124	1	US-08-323-474-2	Sequence 2, Appl
794	54.5	10.9	2647	1	US-08-779-113-8	Sequence 8, Appl	901	53.5	10.7	1124	1	US-09-949-016-5946	Sequence 5946, Ap
795	54.5	10.9	2647	2	US-09-949-016-6082	Sequence 6082, Ap	902	53.5	10.7	1124	5	PCT-US93-06093-2	Sequence 2, Appl
796	54.5	10.9	2666	2	US-09-949-016-10857	Sequence 10857, A	903	53.5	10.7	1157	2	US-09-949-016-9568	Sequence 9568, Ap
797	54	10.8	94	2	US-09-950-933A-47	Sequence 47, Appl	904	53.5	10.7	1172	2	US-09-560-385A-32	Sequence 32, Appl
798	54	10.8	107	1	US-07-963-538B-4	Sequence 4, Appl	905	53.5	10.7	1172	2	US-09-560-385A-28	Sequence 28, Appl
799	54	10.8	107	2	US-09-461-697-322	Sequence 32, App	906	53.5	10.7	1193	1	US-08-317-450B-13	Sequence 13, Appl
800	54	10.8	132	1	US-08-304-051-21	Sequence 21, Appl	907	53.5	10.7	1193	2	US-08-800-593-13	Sequence 13, Appl
801	54	10.8	132	5	PCT-US95-11445-21	Sequence 21, Appl	908	53.5	10.7	1193	2	US-09-560-385A-26	Sequence 26, Appl
802	54	10.8	167	2	US-09-898-659-28	Sequence 28, Appl	909	53.5	10.7	1193	2	US-09-560-385A-30	Sequence 30, Appl
803	54	10.8	167	2	US-08-928-808C-1	Sequence 1, Appl	910	53.5	10.7	1193	2	US-10-053-662A-31	Sequence 31, Appl
804	54	10.8	184	2	US-08-928-808C-1	Sequence 1, Appl	911	53.5	10.7	1193	2	US-09-756-071B-13	Sequence 13, Appl
805	54	10.8	198	2	US-09-543-681A-7611	Sequence 7611, Ap	912	53.5	10.7	1394	2	US-09-949-016-5971	Sequence 5971, Ap
806	54	10.8	213	2	US-09-336-536-58	Sequence 58, Appl	913	53.5	10.7	1394	7	517197-30	Patent No. 517197
807	54	10.8	287	1	US-07-915-934-2	Sequence 2, Appl	914	53.5	10.7	1940	1	US-08-644-271-30	Sequence 30, Appl
808	54	10.8	287	1	US-08-325-743-2	Sequence 2, Appl	915	53.5	10.7	1940	1	US-09-077-955-34	Sequence 34, Appl
809	54	10.8	291	2	US-09-902-540-15052	Sequence 15052, A	916	53.5	10.7	1940	2	US-10-016-283-34	Sequence 1, Appl
810	54	10.8	324	2	US-09-270-767-59483	Sequence 59483, A	917	53.5	10.7	2813	2	US-09-381-261A-1	Sequence 1, Appl
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812	54	10.8	476	2	US-09-189-035-1	Sequence 1, Appl	919	53	10.6	121	2	US-09-270-767-56706	Sequence 56706, A
813	54	10.8	476	2	US-09-382-086-1	Sequence 1, Appl	920	53	10.6	183	2	US-09-949-016-7915	Sequence 7915, Ap
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815	54	10.8	571	2	US-09-460-295B-13	Sequence 13, Appl	922	53	10.6	228	2	US-08-911-423-6	Sequence 6, Appl
816	54	10.8	721	2	US-09-815-048-2	Sequence 2, Appl	923	53	10.6	228	3	US-09-545-998B-6	Sequence 7, Appl
817	54	10.8	732	2	US-09-815-048-4	Sequence 4, Appl	924	53	10.6	232	2	US-08-911-423-7	Sequence 7, Appl
818	54	10.8	742	2	US-09-815-048-4	Sequence 4, Appl	925	53	10.6	232	3	US-09-545-998B-7	Sequence 7, Appl
819	54	10.8	1042	2	US-09-959-392-2	Sequence 2, Appl	926	53	10.6	233	2	US-09-902-540-14590	Sequence 2, Appl
820	54	10.8	2362	2	US-09-949-016-8985	Sequence 8985, Ap	927	53	10.6	234	2	US-09-512-363-2	Sequence 2, Appl
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822	53.5	10.7	120	2	US-08-795-445A-42	Sequence 42, Appl	929	53	10.6	234	2	US-09-155-593-2	Sequence 2, Appl
823	53.5	10.7	120	2	US-08-795-447A-42	Sequence 42, Appl	930	53	10.6	241	2	US-08-911-423-4	Sequence 4, Appl
824	53.5	10.7	120	2	US-08-795-446B-42	Sequence 42, Appl	931	53	10.6	241	2	US-09-512-363-28	Sequence 28, Appl
825	53.5	10.7	120	2	US-08-974-186-42	Sequence 42, Appl	932	53	10.6	241	2	US-09-915-593-28	Sequence 28, Appl
826	53.5	10.7	120	2	US-08-706-945D-120	Sequence 120, App	933	53	10.6	241	2	US-09-949-016-7232	Sequence 7232, Ap
827	53.5	10.7	120	2	US-08-577-788C-42	Sequence 42, Appl	934	53	10.6	241	3	US-09-545-998B-4	Sequence 4, Appl
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302 2 10.4 302 2 US-09-270-767-48543 Sequence 48543, A
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397 5 10.4 397 5 PCT-US91-07635-4 Sequence 4, Appli
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523 2 10.4 523 2 US-09-252-991A-21124 Sequence 21124, A
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600 2 10.4 600 2 US-09-422-680A-10 Sequence 10, Appl

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1268	52	10.4	735	2	US-09-540-245A-9	Sequence 9, Appl	1341	51.5	10.3	799	1	US-08-976-838-23	Sequence 23, Appl
1269	52	10.4	735	2	US-09-540-153-9	Sequence 9, Appl	1342	51.5	10.3	830	2	US-09-562-737-31	Sequence 31, Appl
1270	52	10.4	735	2	US-10-289-776-9	Sequence 9, Appl	1343	51.5	10.3	830	2	US-09-562-737-34	Sequence 34, Appl
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1273	52	10.4	787	2	US-09-398-239-4	Sequence 4, Appl	1346	51.5	10.3	834	2	US-09-196-466-2	Sequence 2, Appl
1274	52	10.4	787	2	US-09-560-876A-4	Sequence 4, Appl	1347	51.5	10.3	834	2	US-09-669-459A-2	Sequence 2, Appl
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ALIGNMENTS

RESULT 1

US-09-712-529-5
; Sequence 5, Application US/09712529
; Patent No. 6485338
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-5

Query Match 100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AVITGACERDVQCAGTCCATSLWLGRMCTPLGRGEECHPGSHKVPFFPKRKHHTCP	60
Db	20	AVITGACERDVQCAGTCCATSLWLGRMCTPLGRGEECHPGSHKVPFFPKRKHHTCP	79
Qy	61	CLPNLLCSRFPDGRYRCMDLNINF	86
Db	80	CLPNLLCSRFPDGRYRCMDLNINF	105

RESULT 2

US-10-212-201A-5
; Sequence 5, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-201A-5

Query Match 100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
20 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 79
QY 61 CLPNLLCSRFPDGRYCSMDLKNINF 86
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
80 CLPNLLCSRFPDGRYCSMDLKNINF 105

RESULT 3
US-10-212-355-5
; Sequence 5, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-355-5

Query Match 100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
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QY 61 CLPNLLCSRFPDGRYCSMDLKNINF 86
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
80 CLPNLLCSRFPDGRYCSMDLKNINF 105

RESULT 4
; Sequence 371, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC53.
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-24
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; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCAIISLWRLGLRMCTPLGREGECHPGSHKVPFFPKRKHHTCP 60
Db 20 AVITGACERDVCGAGTCCAIISLWRLGLRMCTPLGREGECHPGSHKVPFFPKRKHHTCP 79

QY 61 CLPNLLCSFPDGRYRCSMDLKNINF 86
Db 80 CLPNLLCSFPDGRYRCSMDLKNINF 105

RESULT 6
; Sequence 371, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730FIC27
; CURRENT APPLICATION NUMBER: US/09/997,333
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;
Query Match 100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVCGAGTCCCAISLWLRGLMCTPLGREGECCHPGSHKVPFFPKRKHHTCP 60
Db 20 AVITGACERDVCGAGTCCCAISLWLRGLMCTPLGREGECCHPGSHKVPFFPKRKHHTCP 79

Qy 61 CLPPLLCSRFPPDGRYRCSMDLNINF 86
Db 80 CLPPLLCSRFPPDGRYRCSMDLNINF 105

RESULT 7
; Sequence 371, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same


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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 5,2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQAGTCCCAISLWLRGRLMCTPLGREGECHPGSHKVPFPRKRKHTCP 60
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Db 20 AVITGACERDVQAGTCCCAISLWLRGRLMCTPLGREGECHPGSHKVPFPRKRKHTCP 79
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QY 61 CLPNLLCSRPDGRYRCSMDLKNINF 86
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Db 80 CLPNLLCSRPDGRYRCSMDLKNINF 105
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RESULT 8
; Sequence 371, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVQCGAGTCCATSLWLRLGRLMCTPLRGEGEECHPGSHKVPFFKRKHHTCP 60
Db 20 AVITGACERDVQCGAGTCCATSLWLRLGRLMCTPLRGEGEECHPGSHKVPFFKRKHHTCP 79
Qy 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
Db 80 CLPNLLCSRFPDGRYRCMDLKNINF 105

RESULT 9
;; Sequence 371, Application US/09989726
;; Patent No. 701811
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A..
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C60
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: US/09/989,726
;; PRIOR FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186


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; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 498; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVCGAGTCCAIISLWGLRMCTPLGREGGECHPGSHKVPFFPKRKHHTCP 60
DB 20 AVITGACERDVCGAGTCCAIISLWGLRMCTPLGREGGECHPGSHKVPFFPKRKHHTCP 79

QY 61 CLPNLLCSFPDGRYRCSMDLNINF 86
DB 80 CLPNLLCSFPDGRYRCSMDLNINF 105

RESULT 10
; Sequence 371, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;;
Query Match 100.0%; Score 498; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CLPNLLCSRFDPGRYRCSDMLKNINP 86
Db |||||
80 CLPNLLCSRFDPGRYRCSDMLKNINP 105
RESULT 11
; Sequence 371, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C72
; CURRENT APPLICATION NUMBER: US/09/989,728
; PRIOR FILING DATE: 2001-11-20
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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910


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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 498; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACRDVQAGTCCCAISLWLRLGRLMCTPLGREGEGCHPGSHKVPFFRRKHKHTCP 60
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QY 61 CLPNLLCSRPDPGRYRCSMDLKNINF 86
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Db 80 CLPNLLCSRPDPGRYRCSMDLKNINF 105
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RESULT 12
; Sequence 371, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C37
; CURRENT APPLICATION NUMBER: US/09/997,349
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-06-17
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978

;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 498; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCALSLMLRGLRMTPLRGEGECHPGSHKVPFFRKRRKHTCP 60
Db 20 AVITGACERDVQCGAGTCCALSLMLRGLRMTPLRGEGECHPGSHKVPFFRKRRKHTCP 79

QY 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
Db 80 CLPNLLCSRFPDGRYRCMDLKNINF 105

RESULT 13
; Sequence 371, Application US/09997653
; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607


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; PRIOR FILING DATE: 1998-07-09
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Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 AVITGACRDVCGAGTCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKXKHTCP 79

QY 61 CLPNLLCSRFDPGRYRCSMDLKNINF 86
Db 80 CLPNLLCSRFDPGRYRCSMDLKNINF 105

RESULT 14
; Sequence 371, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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?	PRIOR FILING DATE: 1998-07-07
?	PRIOR APPLICATION NUMBER: 60/092182
?	PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 498; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-51;

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Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 15
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; Sequence 5350, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5350
; LENGTH: 105
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; ORGANISM: Homo sapiens
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; NAME/KEY: SIGNAL
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; NAME/KEY: UNSURE
; LOCATION: 38
; OTHER INFORMATION: Xaa = Ala,Gly
US-09-621-976-5350

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Qy	61	CLPNLLCSRPDPGRYRCS	MDLKNINF	86
Db	80	CLPNLLCSRPDPGRYRCS	MDLKNINF	105

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Scoring table: BLOSUM62

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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 1500 summaries

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3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	DB	ID	Description
RESULT 1					
ID	AA070146	standard; protein; 86 AA.			
DE	Human G protein-coupled receptor protein-related sequence #2.				
PN	WO200116309-A1.				
PD	08-MAR-2001.				
PA	(TAKE) TAKEDA CHEM IND LTD.				
Query Match	100.0%;	Score 498;	DB 4;	Length 86;	
Best Local Similarity	100.0%;	Pred. No. 8.9e-47;			
RESULT 2					
ID	ABB76801	standard; protein; 86 AA.			
DE	Human ZAQ-1.				
PN	WO200208417-A1.				
PD	31-JAN-2002.				
PA	(TAKE) TAKEDA CHEM IND LTD.				
Query Match	100.0%;	Score 498;	DB 5;	Length 86;	
Best Local Similarity	100.0%;	Pred. No. 8.9e-47;			
RESULT 3					
ID	ABJ05338	standard; protein; 86 AA.			
DE	Human ZAQ protein ligand.				
PN	WO200236762-A1.				
PD	10-MAY-2002.				
PA	(TAKE) TAKEDA CHEM IND LTD.				
Query Match	100.0%;	Score 498;	DB 5;	Length 86;	
Best Local Similarity	100.0%;	Pred. No. 8.9e-47;			
RESULT 4					
ID	AA015529	standard; protein; 86 AA.			
DE	Human physiologically-active ZAQ ligand-related protein 4.				
PN	WO200257443-A1.				
PD	25-JUL-2002.				
PA	(TAKE) TAKEDA CHEM IND LTD.				
Query Match	100.0%;	Score 498;	DB 5;	Length 86;	
Best Local Similarity	100.0%;	Pred. No. 8.9e-47;			
RESULT 5					
ID	ABB06306	standard; protein; 86 AA.			
DE	Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:21.				
PN	WO200206483-A1.				
PD	24-JAN-2002.				
PA	(TAKE) TAKEDA CHEM IND LTD.				
Query Match	100.0%;	Score 498;	DB 5;	Length 86;	
Best Local Similarity	100.0%;	Pred. No. 8.9e-47;			
RESULT 6					
ID	AAE24383	standard; protein; 86 AA.			
DE	Human prokineticin 1 mature protein.				

PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 7
ID ADD69104 standard; protein; 86 AA.
DE Human ZAQ-related protein - SEQ ID 82.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 8
ID ADO05360 standard; protein; 86 AA.
DE Human prokineticin 1 (PK1), SEQ ID NO:9.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 9
ID ADM43256 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 10
ID ADR24003 standard; protein; 86 AA.
DE Human ZAQ-1 ligand protein #1.
PN WO2004065419-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 11
ID ADS86471 standard; protein; 86 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 3.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 12
ID ADS75494 standard; protein; 86 AA.
DE Human prokineticin 1 receptor protein.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 13
ID ADW00759 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 1 (PK1).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 14
ID ADZ58575 standard; protein; 86 AA.
DE Human ZAQ-1 amino acid sequence - SEQ ID 2.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 100.0%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 15
ID ABB45594 standard; protein; 86 AA.
DE Human Zven2 protein fragment.
PN US2005153322-A1.

PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 16
ID AAD00599 standard; protein; 86 AA.
DE Partial human prokineticin 1 (PK1) SEQ ID NO 11.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-47;
RESULT 17
ID AAE24395 standard; protein; 87 AA.
DE Human prokineticin 1 mutant protein #4.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 9e-47;
RESULT 18
ID ADS75509 standard; protein; 87 AA.
DE Prokineticin receptor antagonist Met PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 87;
Best Local Similarity 100.0%; Pred. No. 9e-47;
RESULT 19
ID AAE24392 standard; protein; 89 AA.
DE Human prokineticin 1 mutant protein #1.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.3e-47;
RESULT 20
ID ADS75506 standard; protein; 89 AA.
DE Prokineticin receptor related synthetic construct protein, SEQ ID 15.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.3e-47;
RESULT 21
ID AAY66745 standard; protein; 105 AA.
DE Membrane-bound protein PRO1186.
PN WO9663088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 22
ID AAB18453 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide.
PN WO200052022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 100.0%; Score 498; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 23
ID AAB70148 standard; protein; 105 AA.
DE Human G protein-coupled receptor protein-related sequence #4.
PN WO200116309-A1.
PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 24
ID AAB68427 standard; protein; 105 AA.
DE Amino acid sequence of a human Zven2 polypeptide.
PN WO200136465-A2.
PD 25-MAY-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 25
ID AAU12406 standard; protein; 105 AA.
DE Human PRO1186 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 26
ID AAB53096 standard; protein; 105 AA.
DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 27
ID AAB5268 standard; protein; 105 AA.
DE Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 28
ID AAB48175 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN WO200075327-A1.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 29
ID AAB48067 standard; protein; 105 AA.
DE Human extracellular signaling molecule (EXCS) (ID 2006548CD1).
PN WO200070049-A2.
PD 23-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 30
ID AAM50773 standard; protein; 105 AA.
DE Endocrine gland-derived vascular endothelial growth factor.
PN WO200200711-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 31
ID AAU83674 standard; protein; 105 AA.
DE Human PRO protein, Seq ID NO 166.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 32
ID ABB4902 standard; protein; 105 AA.
DE Human PRO1186 protein sequence SEQ ID NO:172.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 33
ID AAO15527 standard; protein; 105 AA.
DE Human physiologically-active ZAQ ligand-related protein 3.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 100.0%; Score 498; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 34
ID ABB06308 standard; protein; 105 AA.
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 35
ID AAE24382 standard; protein; 105 AA.
DE Human prokineticin 1 precursor protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 36
ID ABB95508 standard; protein; 105 AA.
DE Human angiogenesis related protein PRO1186 SEQ ID NO: 172.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE) BAKER K P.
PA (FERR) FERRARA N.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (MARS) MARSTERS S A.
PA (PANT) PAN J.
PA (PAON) PAONI N F.
PA (STEP) STEPHAN J F.
PA (WATA) WATANABE C K.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 100.0%; Score 498; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 37
ID ADY31906 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN WO200193983-A1.
PD 13-DEC-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 38
ID ABUS8083 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 39
ID ABUS9161 standard; protein; 105 AA.
DE Novel human secreted or transmembrane protein PRO1186.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 40
ID ABUS2673 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 41
ID ABO17850 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 42
ID ABUS0592 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, #151.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 43
ID ABUS0821 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US200303635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 44
ID ABO33787 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 45
ID ABUL3974 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 46
ID ABUS0800 standard; protein; 105 AA.
DE Human endocrine gland-derived vascular endothelial growth factor.
PN US2002192634-A1.
PD 19-DEC-2002.
PA (FERR) FERRARA N.
PA (WATA) WATANABE C.
PA (WOOD) WOOD W I.
PA (SHEK) SHEK T.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 47
ID ABUS1104 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 48
ID ABUS7603 standard; protein; 105 AA.
DE Human ZVEN2.
PN US6485938-B1.
PD 26-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 49
ID ABUS2559 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

[illegible]

Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 69
ID ADA61693 standard; protein; 105 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 70
ID ADB19478 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 71
ID ADB28019 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 72
ID ADA86498 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 73
ID ADB16062 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 74
ID ADA37882 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 75
ID ADA47848 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 76
ID ADA21568 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO1186.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 77
ID ADA10355 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, PRO1186.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 78
ID ADA67643 standard; protein; 105 AA.

DE Human PRO polypeptide #235.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 79
ID ADB30650 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 80
ID ADA85946 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 81
ID ADA17899 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 82
ID ADA97158 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 83
ID ADA79462 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 84
ID ADA87601 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 85
ID ADB16803 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 86
ID ADA28007 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 87
ID ADA91895 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082694-A1.
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 88
ID ADB14958 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 89
ID ADB18919 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 90
ID ADA94134 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 91
ID ADB20030 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 92
ID ADB1342 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 93
ID ABO4383 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US200304945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 94
ID ADA94587 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 95
ID ADA74596 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 96
ID ADB24829 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 97
ID ADA82353 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 98
ID ADA75316 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 99
ID ADA85394 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 100
ID ADA84842 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 101
ID ADB30098 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 102
ID ADA80626 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 103
ID ADA75868 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 104
ID ADA38812 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 105
ID ADA47093 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 106
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ID ADB25389 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 107
ID ADA93565 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 108
ID ADB26915 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 109
ID ADB31202 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 110
ID ABJ72438 standard; protein; 105 AA.
DE Human PRO1186 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 111
ID ADA92933 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 112
ID ADA61130 standard; protein; 105 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 113
ID ADB24277 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 114
ID ADA96606 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 115
ID ADA91178 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003054516-A1.

PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 116
ID ADA96054 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 117
ID ADB26363 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 118
ID ADB21848 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 119
ID ABO34333 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO 1186.
PN US2003049334-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 120
ID ADA77627 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 121
ID ADB18367 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 122
ID ADA97050 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 123
ID ADA88153 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 124
ID ADA46541 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003054516-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 125
ID ADB28571 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 126
ID ADB29123 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 127
ID ABO53220 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 128
ID ADA77075 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 129
ID ADA22494 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO1186.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 130
ID ADA88705 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 131
ID ADA97710 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 132
ID ADB27467 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 133
ID ADB22400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 134

ID ABO22590 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 135
ID ADA06660 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #115.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 136
ID ABJ72140 standard; protein; 105 AA.
DE Human membrane bound receptor/protein PRO1186 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 137
ID ADA39353 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 138
ID ADA67091 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 139
ID ADB22952 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 140
ID ADB23725 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 141
ID ADA92447 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 142
ID ADB15510 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 143
ID ADB83656 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073814-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 144
ID ADB80762 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 145
ID ADB73303 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 146
ID ADB38762 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 147
ID ADB96379 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 148
ID ADB78385 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 149
ID ADB38210 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 150
ID ADB66682 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 151
ID ADB85033 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 152
ID ADB89762 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 153
ID ADB30494 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 154
ID ADB39595 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 155
ID ADB78139 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 156
ID ADB87205 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 157
ID ADB84787 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 158
ID ADB47218 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 159
ID ADB83902 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003089397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 160
ID ADB86825 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 161
ID ADB73057 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 162

ID ADB77430 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 163

ID ADB34587 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
FN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 164

ID ADB35691 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
FN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 165

ID ADB34035 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
FN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 166

ID ADB35139 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
FN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 167

ID ADB36243 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
FN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 168

ID ADB46638 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 169

ID ADC57851 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
FN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 170

ID ADC55215 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
FN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

RESULT 171

ID ADC12082 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
FN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

PN US2003049681-A1.
PD 13-MAR-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 172
ID ADC56504 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003064375-A1.
PD 03-APR-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 173
ID ADC07559 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003068647-A1.
PD 10-APR-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 174
ID ADC11549 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003069403-A1.
PD 10-APR-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 175
ID ADC36895 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003088065-A1.
PD 08-MAY-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
FA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 176
ID ADC21985 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096969-A1.
PD 22-MAY-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
FA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 177
ID ADC05011 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092106-A1.
PD 15-MAY-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
FA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 178
ID ADC72058 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092107-A1.
PD 15-MAY-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
FA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 179
ID ADC60037 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092105-A1.
PD 15-MAY-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
FA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 180
ID ADC49916 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088064-A1.
PD 08-MAY-2003. Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
FA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

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RESULT 181
ID ADC49115 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 182
ID ADC49632 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 183
ID ADC47493 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 184
ID ADC53044 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 185
ID ADC57398 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 186
ID ADC60589 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 187
ID ADC51064 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 188
ID ADC65591 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 189
ID ADC54689 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 190
ID ADC3650 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 191
ID ADC59173 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 192
ID ADC56051 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 193
ID ADC58621 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 194
ID ADC14671 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 195
ID ADC47238 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 196
ID ADD08203 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 197
ID ADD03295 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 198
ID ADC90287 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 199
ID ADC82028 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003083461-A1.
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PD 01-MAY-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 200
ID ADC69706 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 201
ID ADC48595 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 202
ID ADD10124 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 203
ID ADD07670 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 204
ID ADC78113 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 205
ID ADD04699 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 206
ID ADC82561 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 207
ID ADD06348 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 208
ID ADC80655 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 209
ID ADD1162 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 210
ID ADD10461 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 211
ID ADC48043 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 212
ID ADD08741 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 213
ID ADC77867 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 214
ID ADC80103 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 215
ID ADD06990 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 216
ID ADD11421 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 217
ID ADD09572 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 218

ID ADC83237 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 219
ID ADD50830 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 220
ID ADD41285 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 221
ID ADD52424 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 222
ID ADD51076 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105230-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 223
ID ADD53164 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 224
ID ADD53716 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 225
ID ADD55344 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 226
ID ADD69106 standard; protein; 105 AA.
DE Human ZAQ-related protein - SEQ ID 84.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 227
ID ADD37214 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105012-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 228
ID ADD56302 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 229
ID ADD51872 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 230
ID ADD02671 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 231
ID ADD50557 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 232
ID ADD02105 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 233
ID ADD54287 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 234
ID ADD54740 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 235
ID ADD50311 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
Pred. No. 1.1e-46;
RESULT 236
ID ADD51322 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 237
ID ADD92604 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 238
ID ADD91500 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 239
ID ADE04114 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 240
ID ADE26894 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 241
ID ADE32411 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 242
ID ADE22343 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 243
ID ADD79567 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 244
ID ADE42103 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 245
ID ADE17920 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 246
ID ADD29252 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 247
ID ADE33515 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 248
ID ADE34067 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 249
ID ADE80119 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 250
ID ADD93156 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 251
ID ADE19576 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 252
ID ADE19024 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 253
ID ADE43220 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 254
ID ADD96009 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 255
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ID ADE22895 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 256
ID ADD79013 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 257
ID ADE26361 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 258
ID ADE32963 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 259
ID ADE42655 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 260
ID ADD80671 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 261
ID ADD89699 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 262
ID ADE40983 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 263
ID ADE04782 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 264
ID ADE92911 standard; protein; 105 AA.
DE Human PRO polypeptide #235.

PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 265
ID ADF67298 standard; protein; 105 AA.
DE Human PRO1186 amino acid sequence SEQ ID NO:371.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 266
ID ADF28070 standard; protein; 105 AA.
DE Human Zven 2.
PN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 267
ID ADG21620 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 268
ID ADG23261 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 269
ID ADF97596 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 270
ID ABG75089 standard; protein; 105 AA.
DE Prokineticin 1 (PROK1).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB) BAYER PHARM CORP.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 271
ID ABG75086 standard; protein; 105 AA.
DE Human prokineticin 1 (PROK1).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB) BAYER PHARM CORP.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 272
ID ADG80660 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 273
ID ADG80108 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207372-A1.

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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 274
ID ADH55400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 275
ID ADH55952 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 276
ID ADI35552 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 277
ID ADI64171 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 278
ID ADI65120 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 279
ID ADI63619 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 280
ID ADH82033 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 281
ID ADI00045 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003049692-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 282
ID ADH81481 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 283
ID ADJ71810 standard; protein; 105 AA.
DE Human prokineticin 1 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 284
ID ADM82650 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 285
ID ADN16049 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 286
ID ADN16678 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 287
ID ADN15497 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 288
ID ADN14945 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 289
ID ADC48869 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 290
ID ADC81207 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 291
ID ADE21040 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
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RESULT 292
ID ADE05884 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 293
ID ADE05638 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 294
ID ADD75113 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 295
ID ADD75859 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 296
ID ADD85091 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 297
ID ADE20794 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 298
ID ADE20794 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 299
ID ADE39091 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US200309362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 300
ID ADD88019 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092133-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 301
ID ADE20548 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 302
ID ADE05638 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 303
ID ADD73623 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 304
ID ADE75871 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 305
ID ADD78463 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 306
ID ADE41422 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 307
ID ADE23447 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 308
ID ADE21286 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 309
ID ADD77401 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 310
ID ADE20548 standard; protein; 105 AA.
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DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 311
ID ADD75613 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100654-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 312
ID ADD74129 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 313
ID ADD74375 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 314
ID ADD76105 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 315
ID ADD85597 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 316
ID ADE23999 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 317
ID ADE24642 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 318
ID ADD87467 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 319
ID ADE05146 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 320
ID ADD75359 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 321
ID ADD76903 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 322
ID ADD86671 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 323
ID ADE89333 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US200319062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 324
ID ADD78139 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 325
ID ADE18472 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 326
ID ADE88781 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 327
ID ADD77647 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 498; DB 8; Length 105;
RESULT 328
ID ADD77893 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100730-A1.
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PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 329
ID ADD85351 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 330
ID ADD73883 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 331
ID ADD74621 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 332
ID ADD77149 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 333
ID ADD85843 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 334
ID ADE05392 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 335
ID ADD74867 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 336
ID ADE94801 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 337
ID ADE91212 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 338
ID ADE35497 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 339
ID ADE95353 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 340
ID ADE93463 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 341
ID ADE35044 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 342
ID ADE92359 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 343
ID ADE90660 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 344
ID ADE91807 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 345
ID ADG11747 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 346
ID ADG05679 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;

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Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 347
ID ADG27233 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 348
ID ADG02386 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 349
ID ADG22172 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 350
ID ADG20242 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 351
ID ADF98148 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 352
ID ADG24365 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 353
ID ADF98719 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 354
ID ADG03550 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 355
ID ADF99271 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 356
ID ADG16856 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 357
ID ADG05315 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 358
ID ADG19582 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 359
ID ADG11296 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 360
ID ADG13419 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 361
ID ADG08476 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 362
ID ADG15646 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 363
ID ADG12075 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 364
ID ADF97044 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 365
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ID ADG06229 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 366
ID ADG33813 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 367
ID ADG35003 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 368
ID ADG04102 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 369
ID ADG57555 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 370
ID ADG07300 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 371
ID ADG07852 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 372
ID ADG06728 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 373
ID ADG55347 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 374
ID ADG61011 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 375
ID ADG62115 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 376
ID ADG82316 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 377
ID ADG57555 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 378
ID ADG57003 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 379
ID ADG55899 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 380
ID ADG58659 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 381
ID ADG71025 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 382
ID ADH39072 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 383
ID ADG58107 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.

PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 393
ID ADG56451 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 394
ID ADH12717 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 395
ID ADH21110 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 396
ID ADG61563 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 397
ID ADH20150 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 398
ID ADH28650 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 399
ID ADG54795 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 400
ID ADG59835 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 401
ID ADH43605 standard; protein; 105 AA.
DE Human PRO polypeptide #86.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 402
ID ADG54243 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 403
ID ADG81212 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194793-A1.
PD 16-OCT-2003.

PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 384
ID ADG53691 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 385
ID ADG71577 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 386
ID ADG81764 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 387
ID ADH19617 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 388
ID ADH30726 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 389
ID ADH12093 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 390
ID ADG52515 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 391
ID ADG54243 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 392
ID ADG81212 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194793-A1.
PD 16-OCT-2003.

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Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 402
ID ADG34162 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 403
ID ADI81259 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 404
ID ADI33632 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 405
ID ADH69726 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 406
ID ADG10002 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 407
ID ADI15473 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 408
ID ADG09350 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 409
ID ADI14805 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 410
ID ADI29887 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 411
ID ADI18400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 412
ID ADM27284 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 413
ID ADJ63681 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 414
ID ADJ77576 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 415
ID ADK82950 standard; protein; 105 AA.
DE Human PRO polypeptide #86.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 416
ID ADK66642 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US200404180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 417
ID ADJ65698 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 418
ID ADM27834 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 419
ID ADL66891 standard; protein; 105 AA.
DE Human extracellular signaling molecule (EXCS) -11 protein.
PN US2004048244-A1.
PD 11-MAR-2004.
PA (TANG/) TANG Y T.
PA (YUEH/) YUE H.
PA (LALP/) LAL P.
PA (BURF/) BURFORD N.
```

PA (BAND/) BANDMAN O.
PA (BAUG/) BAUGHN M.R.
PA (AZIM/) AZIMZAI Y.
PA (LUDA/) LU D A M.
PA (ARVI/) ARVIZU C.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 420
ID ADN08155 standard; protein; 105 AA.
DE Human endocrine gland vascular endothelial growth factor.
PN DE1029379-A1.
PD 29-JAN-2004.
PA (SCHD) SCHERING AG.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 421
ID ADM4258 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 422
ID ADN41842 standard; protein; 105 AA.
DE Amino acid sequence of a human Zven2 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYNO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 423
ID ADM28420 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 424
ID ADI95902 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 425
ID ADI96454 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 426
ID ADS8690 standard; protein; 105 AA.
DE Human Zven2 protein.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYNO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 427
ID ADS00454 standard; protein; 105 AA.
DE Human EG-VEGF, SEQ ID 8.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 428
ID ADS86475 standard; protein; 105 AA.

DE Human ZAQ ligand protein related to eating disorders & obesity Seq 7.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 429
ID ADS75493 standard; protein; 105 AA.
DE Human prokineticin 2 receptor protein.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 430
ID ADS32406 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 431
ID ADT03390 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 432
ID ADY86164 standard; protein; 105 AA.
DE Human EG-VEGF, SEQ ID NO:2.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 433
ID ADZ03441 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO1186 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 434
ID ADZ89922 standard; protein; 105 AA.
DE Human prokineticin 1 isoform.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 435
ID AEA38601 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, #183.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 436
ID AEB14187 standard; protein; 105 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 470.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.

PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 437
ID AEB45588 standard; protein; 105 AA.
DE Human Zven2 protein, SEQ ID NO: 5.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 438
ID AEC06124 standard; protein; 105 AA.
DE Human EG-VEGF protein.
PN WO2005076972-A2.
PD 25-AUG-2005.
PA (OHIS) UNIV OHIO STATE RES FOUND.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 439
ID AED08088 standard; protein; 105 AA.
DE Human Zven2 protein.
PN US2005214800-A1.
PD 29-SEP-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 440
ID AED06016 standard; protein; 105 AA.
DE Rhesus monkey prokineticin 1 (PK1) SEQ ID NO 28.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 441
ID AED86385 standard; protein; 105 AA.
DE Human PRO amino acid sequence, seq id 470.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
RESULT 442
ID ABJ05340 standard; protein; 125 AA.
DE Target fusion peptide production method-related protein #3.
PN WO200236762-A1.
PD 10-MAY-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.3e-46;
RESULT 443
ID ABJ05339 standard; protein; 130 AA.
DE Human PTH(1-34)-ZAQ ligand fusion protein.
PN WO200236762-A1.
PD 10-MAY-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 5; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.4e-46;
RESULT 444
ID AAB70145 standard; protein; 86 AA.
DE Human G protein-coupled receptor protein-related sequence #1.
PN WO200116309-A1.

PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 4; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.1e-46;
RESULT 445
ID AAO15528 standard; protein; 86 AA.
DE Human physiologically-active ZAQ ligand-related protein 3.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.1e-46;
RESULT 446
ID ABB06305 standard; protein; 86 AA.
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:20.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.1e-46;
RESULT 447
ID ADD69103 standard; protein; 86 AA.
DE Human ZAQ-related protein - SEQ ID 81.
PN WO200306860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 7; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.1e-46;
RESULT 448
ID ADR24004 standard; protein; 86 AA.
DE Human ZAQ-1 ligand protein #2.
PN WO2004065419-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 8; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.1e-46;
RESULT 449
ID ADS86469 standard; protein; 86 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity \$seq 1.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 8; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.1e-46;
RESULT 450
ID ADZ58576 standard; protein; 86 AA.
DE Human ZAQ-1 amino acid sequence - SEQ ID 3.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 99.8%; Score 497; DB 9; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.1e-46;
RESULT 451
ID AAB70147 standard; protein; 105 AA.
DE Human G protein-coupled receptor protein-related sequence #3.
PN WO200116309-A1.
PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 4; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.4e-46;
RESULT 452
ID AAM79066 standard; protein; 105 AA.
DE Human protein SEQ ID NO 1728.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 99.8%; Score 497; DB 4; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.4e-46;
RESULT 453
ID AAG79596 standard; protein; 105 AA.
DE GSSP4 sequence.
PN WO200269689-A2.
PD 12-SEP-2002.

PA (GEST) GENSET.
Query Match 99.8%; Score 497; DB 5; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.4e-46;
RESULT 454
ID AAO15526 standard; protein; 105 AA.
DE Human physiologically-active ZAQ ligand-related protein 2.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 5; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.4e-46;
RESULT 455
ID ABB06307 standard; protein; 105 AA.
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:22.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 5; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.4e-46;
RESULT 456
ID ABP75987 standard; protein; 105 AA.
DE Human GENSET protein SEQ ID 194.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 99.8%; Score 497; DB 6; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.4e-46;
RESULT 457
ID ADD69105 standard; protein; 105 AA.
DE Human ZAQ-related protein - SEQ ID 83.
PN WO200306860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 7; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.4e-46;
RESULT 458
ID ADS86473 standard; protein; 105 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 5.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 8; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.4e-46;
RESULT 459
ID AED00619 standard; protein; 105 AA.
DE Human prokineticin 1 (PK1).
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 99.8%; Score 497; DB 9; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.4e-46;
RESULT 460
ID AAB18475 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide clone.
PN WO200502022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.4%; Score 495; DB 3; Length 105;
Best Local Similarity 98.8%; Pred. No. 2.3e-46;
RESULT 461
ID AAB18473 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide clone.
PN WO200502022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.4%; Score 495; DB 3; Length 105;
Best Local Similarity 98.8%; Pred. No. 2.3e-46;
RESULT 462
ID AAB18474 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide clone.
PN WO200502022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 99.4%; Score 495; DB 3; Length 105;
Best Local Similarity 98.8%; Pred. No. 2.3e-46;
RESULT 463
ID AAE24393 standard; protein; 85 AA.
DE Human prokineticin 1 mutant protein #2.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 99.2%; Score 494; DB 5; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.4e-46;
RESULT 464
ID ADS75507 standard; protein; 85 AA.
DE Prokineticin receptor antagonist dela-PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 99.2%; Score 494; DB 8; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.4e-46;
RESULT 465
ID ADS75511 standard; protein; 86 AA.
DE Prokineticin receptor antagonist MV PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 99.2%; Score 494; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
RESULT 466
ID ADZ88921 standard; protein; 105 AA.
DE Rhesus monkey prokineticin 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 98.8%; Score 492; DB 9; Length 105;
Best Local Similarity 98.8%; Pred. No. 5e-46;
RESULT 467
ID ABP76151 standard; protein; 105 AA.
DE Human GENSET protein SEQ ID 477.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 98.6%; Score 491; DB 6; Length 105;
Best Local Similarity 97.7%; Pred. No. 6.5e-46;
RESULT 468
ID ABP75986 standard; protein; 105 AA.
DE Human GENSET protein SEQ ID 193.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 98.6%; Score 491; DB 6; Length 105;
Best Local Similarity 97.7%; Pred. No. 6.5e-46;
RESULT 469
ID AAE24394 standard; protein; 86 AA.
DE Human prokineticin 1 mutant protein #3.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 96.0%; Score 478; DB 5; Length 86;
Best Local Similarity 95.3%; Pred. No. 1.4e-44;
RESULT 470
ID ADS75508 standard; protein; 86 AA.
DE Prokineticin receptor related synthetic construct protein, SEQ ID 17.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 96.0%; Score 478; DB 8; Length 86;
Best Local Similarity 95.3%; Pred. No. 1.4e-44;
RESULT 471
ID ADZ88902 standard; protein; 82 AA.
DE Human prokineticin 1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 95.6%; Score 476; DB 9; Length 82;

Best Local Similarity 100.0%; Pred. No. 2.2e-44;
RESULT 472
ID ABB99154 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 5; Length 86;
Best Local Similarity 91.9%; Pred. No. 4.9e-44;
RESULT 473
ID ABB06959 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:49.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 5; Length 86;
Best Local Similarity 91.9%; Pred. No. 4.9e-44;
RESULT 474
ID ADD69160 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 138.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 7; Length 86;
Best Local Similarity 91.9%; Pred. No. 4.9e-44;
RESULT 475
ID ADN43261 standard; protein; 86 AA.
DE Amino acid sequence of rat prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 95.0%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 4.9e-44;
RESULT 476
ID ADS86481 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 13.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 4.9e-44;
RESULT 477
ID ADS75521 standard; protein; 86 AA.
DE Modified rat prokineticin 1 receptor, SEQ ID 30.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 95.0%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 4.9e-44;
RESULT 478
ID ABB99151 standard; protein; 105 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 5; Length 105;
Best Local Similarity 91.9%; Pred. No. 6.1e-44;
RESULT 479
ID ABB06956 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:43.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 5; Length 105;
Best Local Similarity 91.9%; Pred. No. 6.1e-44;
RESULT 480
ID ADD69154 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 132.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 7; Length 105;
Best Local Similarity 91.9%; Pred. No. 6.1e-44;

RESULT 481
ID ADS86487 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 19.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 8; Length 105;
Best Local Similarity 91.9%; Pred. No. 6.1e-44;
RESULT 482
ID ABB99156 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.4e-43;
RESULT 483
ID ABB06961 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:53.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.4e-43;
RESULT 484
ID ADD69164 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 142.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 7; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.4e-43;
RESULT 485
ID ADS86485 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 17.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 8; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.4e-43;
RESULT 486
ID ABB99153 standard; protein; 105 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 5; Length 105;
Best Local Similarity 90.7%; Pred. No. 1.7e-43;
RESULT 487
ID ABB06958 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:47.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 5; Length 105;
Best Local Similarity 90.7%; Pred. No. 1.7e-43;
RESULT 488
ID ADD69158 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 136.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 7; Length 105;
Best Local Similarity 90.7%; Pred. No. 1.7e-43;
RESULT 489
ID ADS86491 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 23.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 8; Length 105;
Best Local Similarity 90.7%; Pred. No. 1.7e-43;
RESULT 490

ID ABB99155 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.3e-43;
RESULT 491
ID ABB06960 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:51.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.3e-43;
RESULT 492
ID ADD69162 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 140.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 7; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.3e-43;
RESULT 493
ID ADS86483 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 15.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 8; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.3e-43;
RESULT 494
ID ABB99152 standard; protein; 105 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 5; Length 105;
Best Local Similarity 90.7%; Pred. No. 2.8e-43;
RESULT 495
ID ABB06957 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:45.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 5; Length 105;
Best Local Similarity 90.7%; Pred. No. 2.8e-43;
RESULT 496
ID ADD69156 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 134.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 7; Length 105;
Best Local Similarity 90.7%; Pred. No. 2.8e-43;
RESULT 497
ID ADS86489 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 21.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 8; Length 105;
Best Local Similarity 90.7%; Pred. No. 2.8e-43;
RESULT 498
ID ABB99149 standard; protein; 86 AA.
DE Mouse ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 5; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.7e-42;
RESULT 499
ID ADD69131 standard; protein; 86 AA.

DE Murine ZAQ-related protein - SEQ ID 109.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 7; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.7e-42;
RESULT 500
ID AD005361 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1); SEQ ID NO:10.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 7; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.7e-42;
RESULT 501
ID ADN43359 standard; protein; 86 AA.
DE Amino acid sequence of murine prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.7e-42;
RESULT 502
ID ADS86477 standard; protein; 86 AA.
DE Murine ZAQ ligand protein related to eating disorders & obesity Seq 9.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.7e-42;
RESULT 503
ID ADS75519 standard; protein; 86 AA.
DE Modified mouse prokineticin 1 receptor, SEQ ID 28.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.7e-42;
RESULT 504
ID ADW00760 standard; protein; 86 AA.
DE Amino acid sequence of murine prokineticin 1 (PK1).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.7e-42;
RESULT 505
ID AD288903 standard; protein; 86 AA.
DE Mouse prokineticin 1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.7e-42;
RESULT 506
ID AED00600 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1) SEQ ID NO 12.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.7e-42;
RESULT 507
ID ABB99148 standard; protein; 105 AA.
DE Mouse ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 5; Length 105;
Best Local Similarity 88.4%; Pred. No. 5.8e-42;
RESULT 508
ID ADD69129 standard; protein; 105 AA.
DE Murine ZAQ-related protein - SEQ ID 107.

PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 7; Length 105;
Best Local Similarity 88.4%; Pred. No. 5.8e-42;
RESULT 509
ID ADS00466 standard; protein; 105 AA.
DE Murine EG-VEGF, SEQ ID 10.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 91.4%; Score 455; DB 8; Length 105;
Best Local Similarity 88.4%; Pred. No. 5.8e-42;
RESULT 510
ID ADS86479 standard; protein; 105 AA.
DE Murine ZAQ ligand protein related to eating disorders & obesity Seq 11.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 8; Length 105;
Best Local Similarity 88.4%; Pred. No. 5.8e-42;
RESULT 511
ID AAE24391 standard; protein; 86 AA.
DE Human prokineticin chimera 21 protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 5; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
RESULT 512
ID ADO05372 standard; protein; 86 AA.
DE PK2/PK1 chimeric protein, SEQ ID NO:21.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 7; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
RESULT 513
ID ADNA3267 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 2 (PK2)/PK1 chimera.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
RESULT 514
ID ADS75505 standard; protein; 86 AA.
DE Modified human prokineticin chimeric receptor, PK2-PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
RESULT 515
ID ADM00765 standard; protein; 86 AA.
DE Amino acid sequence of a PK2/PK1 chimera.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
RESULT 516
ID ADZ88908 standard; protein; 86 AA.
DE Human prokineticin 2/prokineticin 1 chimera.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
RESULT 517
ID AED00605 standard; protein; 86 AA.
DE Human PK2-PK1 chimera SEQ ID NO 17.
PN WO2005091925-A2.

PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
RESULT 518
ID AAE24390 standard; protein; 81 AA.
DE Human prokineticin chimera 12 protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 5; Length 81;
Best Local Similarity 84.4%; Pred. No. 2e-33;
RESULT 519
ID ADO05371 standard; protein; 81 AA.
DE PK1/PK2 chimeric protein, SEQ ID NO:20.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 7; Length 81;
Best Local Similarity 84.4%; Pred. No. 2e-33;
RESULT 520
ID ADNA3266 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 1 (PK1)/PK2 chimera.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 8; Length 81;
Best Local Similarity 84.4%; Pred. No. 2e-33;
RESULT 521
ID ADS75504 standard; protein; 81 AA.
DE Modified human prokineticin chimeric receptor, PK1-PK2.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 8; Length 81;
Best Local Similarity 84.4%; Pred. No. 2e-33;
RESULT 522
ID ADM00764 standard; protein; 81 AA.
DE Amino acid sequence of a PK1/PK2 chimera.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 2e-33;
RESULT 523
ID ADZ88907 standard; protein; 81 AA.
DE Human prokineticin 1/prokineticin 2 chimera.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 2e-33;
RESULT 524
ID AED00604 standard; protein; 81 AA.
DE Human PK1-PK2 chimera SEQ ID NO 16.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 2e-33;
RESULT 525
ID AAV11745 standard; protein; 81 AA.
DE Human 5' EST secreted protein SEQ ID NO: 345.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 72.5%; Score 361; DB 2; Length 81;
Best Local Similarity 98.4%; Pred. No. 9.1e-32;
RESULT 526
ID AAG00617 standard; protein; 80 AA.
DE Human secreted protein, SEQ ID NO: 4698.
PN EP1033401-A2.
PD 06-SEP-2000.

PA (GEST) GENSET.
Query Match 71.7%; Score 357; DB 3; Length 80;
Best Local Similarity 98.4%; Pred. No. 2.5e-31;
RESULT 527
ID ABG94399 standard; protein; 80 AA.
DE Dendroaspis polylepis MIT1 protein.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 528
ID ABB99160 standard; protein; 80 AA.
DE Polylepis MIT1.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 529
ID ABB06310 standard; protein; 80 AA.
DE Dendroaspis polylepis MIT1 protein sequence SEQ ID NO:34.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 530
ID ADD69043 standard; protein; 80 AA.
DE Dendroaspis polylepis MIT1-related protein.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 531
ID ADJ71812 standard; protein; 80 AA.
DE Black mamba intestinal toxin protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 63.3%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 532
ID ADO05364 standard; protein; 80 AA.
DE Snake prokineticin orthologue MIT1, SEQ ID NO:13.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.3%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 533
ID ADS86504 standard; protein; 80 AA.
DE D polylepis MIT1 protein related to eating disorders & obesity Seq 36.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 8; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 534
ID ADW00763 standard; protein; 80 AA.
DE Amino acid sequence of snake MIT1.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.3%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 535
ID ADZ88906 standard; protein; 80 AA.
DE Snake prokineticin 1 homologue, MIT1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.

Query Match 63.3%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 536
ID AED0603 standard; protein; 80 AA.
DE Snake MIT1 SEQ ID NO 15.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.3%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 1e-26;
RESULT 537
ID ADY86167 standard; protein; 79 AA.
DE Black mamba venom protein A (VPRA), SEQ ID NO:5.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 62.6%; Score 311.5; DB 9; Length 79;
Best Local Similarity 63.6%; Pred. No. 2.4e-26;
RESULT 538
ID ADN43263 standard; protein; 81 AA.
DE Amino acid sequence of MIT1.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 62.3%; Score 310.5; DB 8; Length 81;
Best Local Similarity 62.8%; Pred. No. 3.2e-26;
RESULT 539
ID ADS75503 standard; protein; 81 AA.
DE Modified black mamba prokineticin receptor, MIT1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 62.3%; Score 310.5; DB 8; Length 81;
Best Local Similarity 62.8%; Pred. No. 3.2e-26;
RESULT 540
ID ABG94400 standard; protein; 80 AA.
DE C-terminal Lys truncated human GPCR ligand Bv8 protein.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 5; Length 80;
Best Local Similarity 58.4%; Pred. No. 4.3e-24;
RESULT 541
ID ADD69044 standard; protein; 80 AA.
DE Human Bv8-related protein - SEQ ID 22.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 7; Length 80;
Best Local Similarity 58.4%; Pred. No. 4.3e-24;
RESULT 542
ID ABG94398 standard; protein; 81 AA.
DE Human GPCR ligand Bv8 protein sequence #2.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 5; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 543
ID AAO15530 standard; protein; 81 AA.
DE Human physiologically-active ZAQ ligand-related protein 5.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 5; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 544
ID AAE24385 standard; protein; 81 AA.
DE Human prokineticin 2 mature protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 5; Length 81;

Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 545
ID AEB45593 standard; protein; 81 AA.
DE Human Zven1 protein fragment.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 546
ID ADO05356 standard; protein; 81 AA.
DE Human major prokineticin 2 (PK2); SEQ ID NO:5.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 7; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 547
ID ADN43258 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 2 (PK2) isoform 2.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 548
ID ADR24005 standard; protein; 81 AA.
DE Human ZAQ-1 ligand-associated protein.
PN WO2004065419-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 549
ID ADS86493 standard; protein; 81 AA.
DE Human BV8 protein related to eating disorders & obesity Seq 25.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 550
ID ADS75497 standard; protein; 81 AA.
DE Human prokineticin 1 receptor protein isoform 1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 551
ID ADW00755 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 552
ID ADZ88900 standard; protein; 81 AA.
DE Human prokineticin 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 553
ID ADZ58574 standard; protein; 81 AA.
DE Human ZAQ-2 amino acid sequence - SEQ ID 1.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 554
ID AEB45593 standard; protein; 81 AA.
DE Human Zven1 protein fragment.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 555
ID AED00597 standard; protein; 81 AA.
DE Human prokineticin receptor 2 (PKR2) SEQ ID NO 9.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.4e-24;
RESULT 556
ID ADY86166 standard; protein; 100 AA.
DE Human BV8 homolog protein, SEQ ID NO:4.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 9; Length 100;
Best Local Similarity 58.4%; Pred. No. 5.4e-24;
RESULT 557
ID AAB68426 standard; protein; 108 AA.
DE Amino acid sequence of a human Zven1 polypeptide.
PN WO200136465-A2.
PD 25-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 4; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 558
ID ABG34397 standard; protein; 108 AA.
DE Human GPCR ligand BV8 protein sequence #1.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 5; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 559
ID AAO15531 standard; protein; 108 AA.
DE Human physiologically-active ZAQ ligand-related protein 6.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 5; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 560
ID AAE24384 standard; protein; 108 AA.
DE Human prokineticin 2 precursor protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 5; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 561
ID ABU07602 standard; protein; 108 AA.
DE Human ZVEN1.
PN US6485938-B1.
PD 26-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 6; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 562
ID AAE36789 standard; protein; 108 AA.
DE Human BV8 homologue splice variant protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 6; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 563
ID AAE36789 standard; protein; 108 AA.
DE Human BV8 homologue splice variant protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 6; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 563

ID ADD69039 standard; protein; 108 AA.
DE Human Bv8-related protein - SEQ ID 17.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 7; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 564
ID ADF28067 standard; protein; 108 AA.
DE Human Zven 1.
PN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 7; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 565
ID ABG75087 standard; protein; 108 AA.
DE Human prokineticin 2 (PROK2).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB) BAYER PHARM CORP.
Query Match 58.4%; Score 291; DB 7; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 566
ID ADJ71811 standard; protein; 108 AA.
DE Human prokineticin 2 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 58.4%; Score 291; DB 7; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 567
ID ADN41839 standard; protein; 108 AA.
DE Amino acid sequence of a human Zven1 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 568
ID ADO24421 standard; protein; 108 AA.
DE Human PRO28691 protein SEQ ID NO:60.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 569
ID ADS86957 standard; protein; 108 AA.
DE Human Zven1 protein.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 570
ID ADS00460 standard; protein; 108 AA.
DE Human Bv8 homologue variant #2, SEQ ID 4.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 571
ID ADS86495 standard; protein; 108 AA.
DE Human Bv8 protein related to eating disorders & obesity Seq 27.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 572
ID ADS75496 standard; protein; 108 AA.

DE Human prokineticin 1 receptor protein isoform 2.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 573
ID AEA23706 standard; protein; 108 AA.
DE Human PRO polypeptide SEQ ID NO 248.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 9; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 574
ID AEA45585 standard; protein; 108 AA.
DE Human Zven1 protein, SEQ ID NO: 2.
PN US2005153222-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 9; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 575
ID AED08085 standard; protein; 108 AA.
DE Human Zven1 protein.
PN US2005214800-A1.
PD 29-SEP-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 9; Length 108;
Best Local Similarity 58.4%; Pred. No. 5.9e-24;
RESULT 576
ID ADN41861 standard; protein; 116 AA.
DE Amino acid sequence of a human Zven1 with Glu-Glu tag and Gly linker.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 8; Length 116;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 577
ID ADS86981 standard; protein; 116 AA.
DE Human Zven1 protein expressed in baculovirus cell expression system.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 8; Length 116;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 578
ID AD288901 standard; protein; 80 AA.
DE Mouse prokineticin 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 9; Length 80;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 579
ID AED00598 standard; protein; 80 AA.
DE Mouse/rat prokineticin receptor 2 (PKR2) SEQ ID NO 10.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 9; Length 80;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 580
ID ABG94402 standard; protein; 81 AA.
DE Rat GPCR ligand Bv8 protein sequence #2.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 581
ID ABB06963 standard; protein; 81 AA.
DE Rat G protein-coupled receptor protein sequence SEQ ID NO:71.

PN WO200216607-A1.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 582
ID ADD69061 standard; protein; 81 AA.
DE Rat Bv8-related protein - SEQ ID 39.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 7; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 583
ID ADO05358 standard; protein; 81 AA.
DE Mouse major prokineticin 2 (PK2), SEQ ID NO:7.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 7; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 584
ID ADN43260 standard; protein; 81 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 585
ID ADN43262 standard; protein; 81 AA.
DE Amino acid sequence of rat prokineticin 2 (PK2).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 586
ID ADS96497 standard; protein; 81 AA.
DE Rat/ murine Bv8 protein related to eating disorders & obesity Seq 29.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 587
ID ADS75520 standard; protein; 81 AA.
DE Modified mouse prokineticin 2 receptor, SEQ ID 29.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 588
ID ADS75522 standard; protein; 81 AA.
DE Modified rat prokineticin 2 receptor, SEQ ID 31.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 589
ID ADM00757 standard; protein; 81 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 9; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.5e-23;
RESULT 590
ID ABG94408 standard; protein; 107 AA.
DE Mouse GPCR ligand Bv8 protein.
PN WO200262944-A2.

PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.1e-23;
RESULT 591
ID ABG94401 standard; protein; 107 AA.
DE Rat GPCR ligand Bv8 protein sequence #1.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.1e-23;
RESULT 592
ID ABB06962 standard; protein; 107 AA.
DE Rat G protein-coupled receptor protein sequence SEQ ID NO:69.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.1e-23;
RESULT 593
ID AAE36790 standard; protein; 107 AA.
DE Mouse Bv8 homologue protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 57.4%; Score 286; DB 6; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.1e-23;
RESULT 594
ID ADD69059 standard; protein; 107 AA.
DE Rat Bv8-related protein - SEQ ID 37.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 7; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.1e-23;
RESULT 595
ID ADD69077 standard; protein; 107 AA.
DE Murine Bv8-related protein - SEQ ID 55.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 7; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.1e-23;
RESULT 596
ID ADS00462 standard; protein; 107 AA.
DE Murine Bv8 homologue, SEQ ID 6.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 57.4%; Score 286; DB 8; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.1e-23;
RESULT 597
ID ADS86500 standard; protein; 107 AA.
DE Rat Bv8 protein related to eating disorders & obesity Seq 32.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 8; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.1e-23;
RESULT 598
ID ADS86502 standard; protein; 107 AA.
DE Murine Bv8 peptide DNA related to eating disorders & obesity Seq 34.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 8; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.1e-23;
RESULT 599
ID AD288897 standard; protein; 108 AA.
DE Rhesus monkey prokineticin receptor 2.
PN WO2005042717-A2.
PD 12-MAY-2005.

PA (REGC) UNIV CALIFORNIA.
Query Match 54.3%; Score 270.5; DB 8; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.3e-21;
RESULT 609
ID ADS00458 standard; protein; 129 AA.
DE Human Bv8 homologue variant #1, SEQ ID 2.
FN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 54.3%; Score 270.5; DB 8; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.3e-21;
RESULT 610
ID ADO05362 standard; protein; 77 AA.
DE Xenopus laevis prokineticin orthologue Bv8, SEQ ID NO:11.
FN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.7%; Score 267.5; DB 7; Length 77;
Best Local Similarity 57.7%; Pred. No. 1.6e-21;
RESULT 611
ID ADN43264 standard; protein; 77 AA.
DE Amino acid sequence of Bv8.
FN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.7%; Score 267.5; DB 8; Length 77;
Best Local Similarity 57.7%; Pred. No. 1.6e-21;
RESULT 612
ID ADW00761 standard; protein; 77 AA.
DE Amino acid sequence of frog Bv8.
FN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.7%; Score 267.5; DB 9; Length 77;
Best Local Similarity 57.7%; Pred. No. 1.6e-21;
RESULT 613
ID AD288905 standard; protein; 77 AA.
DE Frog prokineticin 1 homologue, Bv8.
FN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.7%; Score 267.5; DB 9; Length 77;
Best Local Similarity 57.7%; Pred. No. 1.6e-21;
RESULT 614
ID AED00602 standard; protein; 77 AA.
DE Frog Bv8 SEQ ID NO 14.
FN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.7%; Score 267.5; DB 9; Length 77;
Best Local Similarity 57.7%; Pred. No. 1.6e-21;
RESULT 615
ID ADJ71813 standard; protein; 96 AA.
DE Toad Bv8 protein.
FN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 53.7%; Score 267.5; DB 7; Length 96;
Best Local Similarity 57.7%; Pred. No. 2e-21;
RESULT 616
ID ADS75502 standard; protein; 96 AA.
DE Modified frog prokineticin receptor, Bv8.
FN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.7%; Score 267.5; DB 8; Length 96;
Best Local Similarity 57.7%; Pred. No. 2e-21;
RESULT 617
ID ADO05359 standard; protein; 102 AA.
DE Mouse minor prokineticin 2 (PK2), SEQ ID NO:8.
FN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.3%; Score 265.5; DB 7; Length 102;

PA (REGC) UNIV CALIFORNIA.
Query Match 57.0%; Score 284; DB 9; Length 108;
Best Local Similarity 57.1%; Pred. No. 3.4e-23;
RESULT 600
ID ABD00594 standard; protein; 108 AA.
DE Rhesus monkey prokineticin receptor 2 (PKR2) SEQ ID NO 6.
FN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.0%; Score 284; DB 9; Length 108;
Best Local Similarity 57.1%; Pred. No. 3.4e-23;
RESULT 601
ID ADN43265 standard; protein; 77 AA.
DE Amino acid sequence of a Bv8 homologue.
FN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 55.9%; Score 278.5; DB 8; Length 77;
Best Local Similarity 61.5%; Pred. No. 9.7e-23;
RESULT 602
ID ADS75523 standard; protein; 77 AA.
DE Modified toad prokineticin receptor.
FN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 55.9%; Score 278.5; DB 8; Length 77;
Best Local Similarity 61.5%; Pred. No. 9.7e-23;
RESULT 603
ID ADN43257 standard; protein; 102 AA.
DE Amino acid sequence of human prokineticin 2 (PK2) isoform 1.
FN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 54.3%; Score 270.5; DB 8; Length 102;
Best Local Similarity 45.9%; Pred. No. 9.8e-22;
RESULT 604
ID ADJ71808 standard; protein; 124 AA.
DE Human Bv8 protein.
FN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 54.3%; Score 270.5; DB 7; Length 124;
Best Local Similarity 45.9%; Pred. No. 1.2e-21;
RESULT 605
ID AAE36788 standard; protein; 129 AA.
DE Human Bv8 homologue protein.
FN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 54.3%; Score 270.5; DB 6; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.3e-21;
RESULT 606
ID ADJ71815 standard; protein; 129 AA.
DE Human prokineticin 2 precursor protein.
FN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 54.3%; Score 270.5; DB 7; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.3e-21;
RESULT 607
ID ADN41864 standard; protein; 129 AA.
DE Amino acid sequence of a longer human Zven1 polypeptide.
FN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 54.3%; Score 270.5; DB 8; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.3e-21;
RESULT 608
ID ADS86984 standard; protein; 129 AA.
DE Human Zven1 protein longer form.
FN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.

Best Local Similarity 44.9%; Pred. No. 3.5e-21;
RESULT 618
ID ADW00758 standard; protein; 102 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.3%; Score 265.5; DB 9; Length 102;
Best Local Similarity 44.9%; Pred. No. 3.5e-21;
RESULT 619
ID ADJ71809 standard; protein; 128 AA.
DE Mouse Bv8 variant 1 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 45.2%; Score 235; DB 7; Length 126;
Best Local Similarity 43.9%; Pred. No. 1.2e-16;
RESULT 620
ID ADF17105 standard; peptide; 77 AA.
DE Bombina maxima neurotrophic peptide.
PN CN1390849-A.
PD 15-JAN-2003.
PA (KUNM-) KUNMING ZOOLOGY INST CHINESE ACAD SCI.
Query Match 51.1%; Score 254.5; DB 7; Length 77;
Best Local Similarity 56.4%; Pred. No. 4.2e-20;
RESULT 621
ID ADO05357 standard; protein; 100 AA.
DE Human tissue specific (testis) prokineticin 2 (PK2), SEQ ID NO:6.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.5%; Score 251.5; DB 7; Length 100;
Best Local Similarity 44.9%; Pred. No. 1.2e-19;
RESULT 622
ID ADW00756 standard; protein; 100 AA.
DE Amino acid sequence of human prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.5%; Score 251.5; DB 9; Length 100;
Best Local Similarity 44.9%; Pred. No. 1.2e-19;
RESULT 623
ID ADO05363 standard; protein; 75 AA.
DE Toad prokineticin orthologue Bv8, SEQ ID NO:12.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.3%; Score 250.5; DB 7; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.1e-19;
RESULT 624
ID ADM00762 standard; protein; 75 AA.
DE Amino acid sequence of toad Bv8.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.3%; Score 250.5; DB 9; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.1e-19;
RESULT 625
ID ADZ88904 standard; protein; 75 AA.
DE Toad prokineticin 1 homologue, Bv8.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.3%; Score 250.5; DB 9; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.1e-19;
RESULT 626
ID AED00601 standard; protein; 75 AA.
DE Toad Bv8 SEQ ID NO 13.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.3%; Score 250.5; DB 9; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.1e-19;
RESULT 627
ID ADI60152 standard; protein; 126 AA.
DE Secreted polypeptide #36.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 45.2%; Score 235; DB 7; Length 126;
Best Local Similarity 43.9%; Pred. No. 1.2e-16;
RESULT 628
ID ADJ71800 standard; protein; 126 AA.
DE Human prokineticin-like protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 45.2%; Score 235; DB 7; Length 126;
Best Local Similarity 43.9%; Pred. No. 1.2e-16;
RESULT 629
ID AED53711 standard; peptide; 56 AA.
DE Amino acid sequence of human PK2beta peptide.
PN WO2005097826-A2.
PD 20-OCT-2005.
PA (JANC) JANSSEN PHARM NV.
Query Match 37.3%; Score 186; DB 9; Length 56;
Best Local Similarity 52.7%; Pred. No. 9.8e-13;
RESULT 630
ID AED53712 standard; peptide; 56 AA.
DE Amino acid sequence of human PK2beta peptide #2.
PN WO2005097826-A2.
PD 20-OCT-2005.
PA (JANC) JANSSEN PHARM NV.
Query Match 36.9%; Score 184; DB 9; Length 56;
Best Local Similarity 57.4%; Pred. No. 1.6e-12;
RESULT 631
ID AAO27072 standard; peptide; 30 AA.
DE Monkey AXOR8 receptor N-terminal peptide, SEQ ID NO 20.
PN GB2378183-A.
PD 05-FEB-2003.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 31.3%; Score 156; DB 6; Length 30;
Best Local Similarity 90.0%; Pred. No. 1e-09;
RESULT 632
ID AEA18405 standard; peptide; 24 AA.
DE R. saharica insulin releasing peptide #1.
PN WO2005047316-A2.
PD 26-MAY-2005.
PA (UYUL-) UNIV ULSTER.
Query Match 24.1%; Score 120; DB 9; Length 24;
Best Local Similarity 91.3%; Pred. No. 7.1e-06;
RESULT 633
ID AAY44934 standard; protein; 271 AA.
DE Human dickkopf-1 homolog 3 protein.
PN WO200006714-A1.
PD 10-FEB-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 22.5%; Score 112; DB 3; Length 271;
Best Local Similarity 32.9%; Pred. No. 0.00067;
RESULT 634
ID ADF28074 standard; peptide; 23 AA.
DE Human Zven polypeptide motif #2.
PN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 21.9%; Score 109; DB 7; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.00011;
RESULT 635
ID ADN1845 standard; peptide; 23 AA.
DE Motif found in Zven1 and Zven1 polypeptides.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 21.9%; Score 109; DB 8; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.00011;

RESULT 636					
ID	ADS86964 standard; peptide; 23 AA.				
DE	Human Zven1 protein motif #2.				
PN	WO2004031367-A2.				
PD	15-APR-2004.				
PA	(ZYMO) ZYMOGENETICS INC.				
Query Match					
Best Local Similarity	21.9%; Score 109; DB 8; Length 23;				
RESULT 637					
ID	ARB45592 standard; peptide; 23 AA.				
DE	Human Zven1 and Zven2 motif peptide, SEQ ID NO: 9.				
PN	US2005153322-A1.				
PD	14-JUL-2005.				
PA	(ZYMO) ZYMOGENETICS INC.				
Query Match					
Best Local Similarity	21.9%; Score 109; DB 9; Length 23;				
RESULT 638					
ID	AED08092 standard; peptide; 23 AA.				
DE	Human Zven1/Zven2 motif peptide - SEQ ID 9.				
PN	US2005214800-A1.				
PD	29-SEP-2005.				
PA	(ZYMO) ZYMOGENETICS INC.				
Query Match					
Best Local Similarity	21.9%; Score 109; DB 9; Length 23;				
RESULT 639					
ID	AEA16257 standard; protein; 221 AA.				
DE	Mouee Dickkopf-4 (Dkk-4) protein.				
PN	WO2005049797-A2.				
PD	02-JUN-2005.				
PA	(MERI) MERCK & CO INC.				
Query Match					
Best Local Similarity	21.8%; Score 108.5; DB 9; Length 221;				
RESULT 640					
ID	ASC06122 standard; peptide; 18 AA.				
DE	Human EG-vgrg peptide (amino acids 50-67).				
PN	WO2005076972-A2.				
PD	25-AUG-2005.				
PA	(OHIS) UNIV OHIO STATE RES FOUND.				
Query Match					
Best Local Similarity	21.7%; Score 108; DB 9; Length 18;				
RESULT 641					
ID	ADI60388 standard; protein; 40 AA.				
DE	Secreted polypeptide encoded by gene splice variant #24.				
PN	WO2003025142-A2.				
PD	27-MAR-2003.				
PA	(HYSE-) HYSEQ INC.				
Query Match					
Best Local Similarity	21.7%; Score 108; DB 7; Length 40;				
RESULT 642					
ID	ADJ71801 standard; protein; 40 AA.				
DE	Human prokineticin-like protein.				
PN	WO2003040326-A2.				
PD	15-MAY-2003.				
PA	(HYSE-) HYSEQ INC.				
Query Match					
Best Local Similarity	21.7%; Score 108; DB 7; Length 40;				
RESULT 643					
ID	AEB28655 standard; protein; 161 AA.				
DE	Human NOV9c protein - SEQ ID 32.				
PN	WO2003040330-A2.				
PD	15-MAY-2003.				
PA	(CURA-) CURAGEN CORP.				
Query Match					
Best Local Similarity	21.6%; Score 107.5; DB 7; Length 161;				
RESULT 644					
ID	ADM93400 standard; protein; 161 AA.				
DE	Human NOVX polypeptide #16.				
PN	US2004067882-A1.				
PD	08-APR-2004.				
PA	(ALSO/) ALSOBROOK J P.				
PA	(ALVA/) ALVAREZ E.				
PA	(ANDE/) ANDERSON D W.				
PA	(BARO/) BARON M.				
PA	(BOLD/) BOLDOG F L.				
PA	(BURG/) BURGESS C E.				
PA	(CASM/) CASMAN S J.				
PA	(CHAP/) CHAPOVAL A.				
PA	(DHAN/) DHANABAL M.				
PA	(EDIN/) EDINGER S R.				

PA (EISE/) EISEN A.
 PA (ELLE/) ELLERMAN K.
 PA (ETTE/) ETTERBERG S.
 PA (GANG/) GANGOLLI E A.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GROS/) GROSSE W M.
 PA (GUOX/) GUO X.
 PA (HACK/) HACKETT C.
 PA (JIWU/) JI W.
 PA (KEKU/) KEKUDA R.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LEPL/) LEPLEY D M.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MAZU/) MAZUR A.
 PA (MCQU/) MCQUEENEY K.
 PA (MEZE/) MEZES P S.
 PA (MILL/) MILLER C E.
 PA (MILL/) MILLET I.
 PA (MISH/) MISHRA V.
 PA (PADI/) PADIGARU M.
 PA (PATT/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D K.
 PA (ROTH/) ROTHENBERG M E.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (SMIT/) SMITHSON G.
 PA (SPAD/) SPADERNA S K.
 PA (STAR/) STARLING G.
 PA (SPYT/) SPYTEK K A.
 PA (STON/) STONE D J.
 PA (TCHER/) TCHERNEV V T.
 PA (TOMW/) TWOMLOW N.
 PA (VERN/) VERNET C A M.
 PA (ZERH/) ZERHUSEN B D.
 PA (VOSS/) VOSS E Z.
 PA (ZHON/) ZHONG M.
 Query Match 21.6%; Score 107.5; DB 8; Length 173;
 Best Local Similarity 35.5%; Pred. No. 0.0013;
 RESULT 647
 ID ADE28657 standard; protein; 180 AA.
 DE Human NOV9d protein - SEQ ID 34.
 PN WO2003040330-A2.
 PD 15-MAY-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 21.6%; Score 107.5; DB 7; Length 180;
 Best Local Similarity 35.5%; Pred. No. 0.0014;
 RESULT 648
 ID ADM93402 standard; protein; 180 AA.
 DE Human NOVX polypeptide #17.
 PN US2004067882-A1.
 PD 08-APR-2004.
 PA (ALSO/) ALSOBROOK J P.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (BARO/) BARON M.
 PA (BOLD/) BOLDOG F L.
 PA (BURG/) BURGESS C E.
 PA (CASW/) CASMAN S J.
 PA (CHAF/) CHAPOVAL A.
 PA (DHAN/) DHANABAL M.
 PA (EDIN/) EDINGER S R.
 PA (EISE/) EISEN A.
 PA (ELLE/) ELLERMAN K.
 PA (ETTE/) ETTERBERG S.
 PA (GANG/) GANGOLLI E A.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 (GROS/) GROSSE W M.
 (GUOX/) GUO X.
 (HACK/) HACKETT C.
 (JIWU/) JI W.
 (KEKU/) KEKUDA R.
 (KHRA/) KHRAMTSOV N V.
 (LEPL/) LEPLEY D M.
 (LILL/) LI L.
 (MACD/) MACDOUGALL J R.
 (MALY/) MALYANKAR U M.
 (MAZU/) MAZUR A.
 (MCQU/) MCQUEENEY K.
 (MEZE/) MEZES P S.
 (MILL/) MILLER C E.
 (MILL/) MILLET I.
 (MISH/) MISHRA V.
 (PADI/) PADIGARU M.
 (PATT/) PATTURAJAN M.
 (PENA/) PENA C E A.
 (PEYM/) PEYMAN J A.
 (RAST/) RASTELLI L.
 (RIEG/) RIEGER D K.
 (ROTH/) ROTHENBERG M E.
 (SHEN/) SHENOY S G.
 (SHIM/) SHIMKETS R A.
 (SMIT/) SMITHSON G.
 (SPAD/) SPADERNA S K.
 (STAR/) STARLING G.
 (SPYT/) SPYTEK K A.
 (STON/) STONE D J.
 (TCHER/) TCHERNEV V T.
 (TOMW/) TWOMLOW N.
 (VERN/) VERNET C A M.
 (ZERH/) ZERHUSEN B D.
 (VOSS/) VOSS E Z.
 (ZHON/) ZHONG M.
 Query Match 21.6%; Score 107.5; DB 8; Length 180;
 Best Local Similarity 35.5%; Pred. No. 0.0014;
 RESULT 649
 ID AAW73017 standard; protein; 224 AA.
 DE Human cysteine-rich secreted protein CRSP-2.
 PN WO9846755-A1.
 PD 22-OCT-1998.
 PA (MILL-) MILLENNIUM BIOTHEAPEUTICS INC.
 Query Match 21.6%; Score 107.5; DB 2; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0017;
 RESULT 650
 ID AAY92075 standard; protein; 224 AA.
 DE Human DKR-4.
 PN WO200018914-A2.
 PD 06-APR-2000.
 PA (AMGE-) AMGEN INC.
 Query Match 21.6%; Score 107.5; DB 3; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0017;
 RESULT 651
 ID AAB08875 standard; protein; 224 AA.
 DE Amino acid sequence of a human Dickkopf (Dkk)-4 protein.
 PN WO200052047-A2.
 PD 08-SEP-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 21.6%; Score 107.5; DB 3; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0017;
 RESULT 652
 ID ABUS5916 standard; protein; 224 AA.
 DE Human protein DKK4.
 PN WO200277204-A2.
 PD 03-OCT-2002.
 PA (AXOR-) AXORDIA LTD.
 Query Match 21.6%; Score 107.5; DB 6; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0017;
 RESULT 653
 ID AAE34070 standard; protein; 224 AA.
 DE DKK 4 protein.

PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 21.6%; Score 107.5; DB 6; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0017;
RESULT 654
ID ADE28651 standard; protein; 224 AA.
DE Human NOV9a protein - SEQ ID 28.
PN WO2003040330-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 21.6%; Score 107.5; DB 7; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0017;
RESULT 655
ID ADJ68529 standard; protein; 224 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID335.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 21.6%; Score 107.5; DB 7; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0017;
RESULT 656
ID ADN19310 standard; protein; 224 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO.628.
PN WO2003042861-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 21.6%; Score 107.5; DB 7; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0017;
RESULT 657
ID ADM93396 standard; protein; 224 AA.
DE Human NOVX polypeptide #14.
PN US2004067882-A1.
PD 08-APR-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (BARO/) BARON M.
PA (BOLD/) BOLDG F L.
PA (BURG/) BURGESS C E.
PA (CASW/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (DHAN/) DHANABAL M.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETTENBERG S.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JIHW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCQU/) MCQUEENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C B.
PA (MILL/) MILLET I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHE/) TCHERNEV V T.
PA (TWOM/) TWOMLOW N.
PA (VERN/) VERNET C A M.
PA (ZERH/) ZERHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match 21.6%; Score 107.5; DB 8; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0017;
RESULT 658
ID AEA16256 standard; protein; 224 AA.
DE Human Dickkopf-4 (Dkk-4) protein.
PN WO2005049797-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 21.6%; Score 107.5; DB 9; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0017;
RESULT 659
ID AEA16254 standard; protein; 224 AA.
DE Cynomolgus monkey Dickkopf-4 (cdkk-4) protein.
PN WO2005049797-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 21.6%; Score 107.5; DB 9; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0017;
RESULT 660
ID AAW73019 standard; protein; 179 AA.
DE Human cysteine-rich secreted protein CRSP-4.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 20.5%; Score 102; DB 2; Length 179;
Best Local Similarity 31.5%; Pred. No. 0.0055;
RESULT 661
ID AAB08877 standard; protein; 179 AA.
DE A partial human Dickkopf (Dkk)-2 protein.
PN WO20052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 20.5%; Score 102; DB 3; Length 179;
Best Local Similarity 31.5%; Pred. No. 0.0055;
RESULT 662
ID ADO35297 standard; protein; 179 AA.
DE Human Dkk2 carboxy terminal cysteine rich region.
PN US2004014209-A1.
PD 22-JAN-2004.
PA (LASS/) LASSAR A B.
PA (MERC/) MERCOLA M.
PA (GUPT/) GUPTA R.
PA (MARV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZAH/) TZAHOR E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match 20.5%; Score 102; DB 8; Length 179;
Best Local Similarity 31.5%; Pred. No. 0.0055;
RESULT 663
ID AAY92074 standard; protein; 207 AA.
DE Human DKK-2 splice variant, DKK-2a.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 20.5%; Score 102; DB 3; Length 207;
Best Local Similarity 31.5%; Pred. No. 0.0064;
RESULT 664
ID AAY92073 standard; protein; 259 AA.

DE Human DKR-2.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 20.5%; Score 102; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 665
ID AAY99360 standard; protein; 259 AA.
DE Human PRO1316 (UNQ682) amino acid sequence SEQ ID NO:70.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 666
ID AAB66109 standard; protein; 259 AA.
DE Protein of the invention #21.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 4; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 667
ID AAU29148 standard; protein; 259 AA.
DE Human PRO polypeptide sequence #125.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 4; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 668
ID ABUS8524 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003027272-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 669
ID ABUS88072 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032127-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 670
ID ABUS4387 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032112-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 671
ID ABR66261 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027278-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 672
ID ABR65651 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036159-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 673
ID ABUS9591 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040070-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 674
ID ABUS9862 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.

ID ABUS2830 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032113-A1.
PD 13-FEB-2003.
PA (AMGE-) AMGEN INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 675
ID ABUS9951 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036147-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 676
ID ABR68200 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027264-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 677
ID ABUS96253 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036144-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 678
ID ABUS2684 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036149-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 679
ID ABO08761 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044923-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 680
ID ABO02813 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040062-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 681
ID ABR74967 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040056-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 682
ID ABR94729 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044926-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 683
ID ABUS5702 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 684
ID ABUS9862 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.

PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 685
ID ABU98077 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 686
ID ABU91783 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 687
ID ABU89476 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 688
ID ABU86317 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 689
ID ABU67530 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 690
ID ABU80558 standard; protein; 259 AA.
DE Human PRO protein #125.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 691
ID ABR99476 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 692
ID ABR98866 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 693
ID ABO16389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 694
ID ABR92289 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.

PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 695
ID ABO18930 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 696
ID ABR78351 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 697
ID ABU85087 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 698
ID ABO00226 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 699
ID ABO11558 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 700
ID ABO22023 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 701
ID ABU55914 standard; protein; 259 AA.
DE Human protein DKK2.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 702
ID ABU88777 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 703
ID ABU83472 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 704
ID ABO06273 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003022294-A1.

PD 30-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 705
ID ABR59309 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 706
ID ABO09371 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 707
ID ABO19235 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 708
ID ABO11253 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 709
ID ABR66871 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 710
ID ABO16084 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 711
ID ABO13790 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 712
ID ABO07541 standard; protein; 259 AA.
DE Human secreted/transmembrane protein, SEQ ID 250.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 713
ID ABO07541 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 714
ID ABO03728 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 715
ID ABR67176 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 716
ID ABO15779 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 717
ID ABR34068 standard; protein; 259 AA.
DE DKK 2 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 718
ID ABU56060 standard; protein; 259 AA.
DE Human secreted/transmembrane protein, PRO1316.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 719
ID ABU65388 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 720
ID ABU95333 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 721
ID ABU71236 standard; protein; 259 AA.
DE Human PRO1316 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 722
ID ABO07846 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 723
ID ABR70087 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 724
ID ABR69420 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;

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RESULT 725					
ID	ABO01561 standard; protein; 259 AA.				
DE	Human PRO polypeptide #125.				
PN	US2003008353-A1.				
PD	09-JAN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 726					
ID	ABU81363 standard; protein; 259 AA.				
DE	Human PRO polypeptide #125.				
PN	US2003017542-A1.				
PD	23-JAN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 727					
ID	ABR60160 standard; protein; 259 AA.				
DE	Human secreted polypeptide PRO1316, SEQ ID NO:250.				
PN	US2003032137-A1.				
PD	13-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 728					
ID	ABR67895 standard; protein; 259 AA.				
DE	Human secreted polypeptide PRO1316, SEQ ID NO:250.				
PN	US2003027269-A1.				
PD	06-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 729					
ID	ABR65283 standard; protein; 259 AA.				
DE	Human secreted polypeptide PRO1316, SEQ ID NO:250.				
PN	US2003027268-A1.				
PD	06-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 730					
ID	ABR68505 standard; protein; 259 AA.				
DE	Human secreted polypeptide PRO1316, SEQ ID NO:250.				
PN	US2003027274-A1.				
PD	06-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 731					
ID	ABR71917 standard; protein; 259 AA.				
DE	Human secreted polypeptide PRO1316, SEQ ID NO:250.				
PN	US2003032135-A1.				
PD	13-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 732					
ID	ABU85397 standard; protein; 259 AA.				
DE	Human PRO polypeptide #125.				
PN	US2003022295-A1.				
PD	30-JAN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 733					
ID	ABU89087 standard; protein; 259 AA.				
DE	Human secreted/transmembrane protein (PRO) #125.				
PN	US2003022297-A1.				
PD	30-JAN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 734					
ID	ABU83167 standard; protein; 259 AA.				
DE	Human secreted/transmembrane protein (PRO) #125.				
PN	US2003032105-A1.				
PD	13-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 735					
ID	ABU95023 standard; protein; 259 AA.				
DE	Novel human secreted and transmembrane protein PRO1316.				
PN	US2003032123-A1.				
PD	13-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				
RESULT 736					
ID	ABU90571 standard; protein; 259 AA.				
DE	Novel human secreted and transmembrane protein PRO1316.				
PN	US2003032108-A1.				
PD	13-FEB-2003.				
PA	(GETH) GENENTECH INC.				
Query Match	20.5%; Score 102; DB 6; Length 259;				
Best Local Similarity	31.5%; Pred. No. 0.008;				

DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 746
ID ABU94411 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 757
ID ABU79293 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 758
ID ABU86622 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 759
ID ABU86927 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 760
ID ABU94716 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 761
ID AB004643 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 762
ID ABR70392 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 763
ID ABU98557 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032301-A1.
PD 30-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 764
ID ABR65956 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 765
ID ABR64673 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 766
ID ABR90984 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040058-A1.

DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 746
ID ABU94411 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 757
ID ABU79293 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 758
ID ABU86622 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 759
ID ABU86927 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 760
ID ABU94716 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 761
ID AB004643 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 762
ID ABR70392 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 763
ID ABU98557 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032301-A1.
PD 30-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 764
ID ABR65956 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 765
ID ABR64673 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 766
ID ABR90984 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040058-A1.

Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 766
ID ABU79598 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 767
ID ABU92989 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 768
ID ABU95948 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 769
ID ABU91168 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 770
ID ABU90261 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 771
ID ABO09676 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 772
ID ABO10948 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 773
ID ABR71002 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 774
ID ABU87610 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US200302293-A1.
PD 30-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 775
ID ABU91478 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 776
ID ABU84692 standard; protein; 259 AA.

DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 777
ID ABR69782 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 778
ID ABU80159 standard; protein; 259 AA.
DE Human PRO protein #125.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 779
ID ABU93428 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 780
ID ABO09981 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 781
ID ABO09066 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 782
ID ABU10634 standard; protein; 259 AA.
DE Human secreted/transmembrane protein #125.
PN US2002127584-A1.
PD 12-SEP-2002.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 783
ID ABU95643 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 784
ID ABU96852 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 785
ID ABR70697 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040076-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 786
ID ABO05048 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.

PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 787
ID ABO08456 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 788
ID ABO05663 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 789
ID ABR74052 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 790
ID ABR95644 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 791
ID ABR80941 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 792
ID ABR81246 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 793
ID ABM00942 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 794
ID ABR88544 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 795
ID ABM77365 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 796
ID ABR90374 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 797
ID ABO31594 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 798
ID ABM08011 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 799
ID ABO40491 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 800
ID ABO35916 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 801
ID ABO44055 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 802
ID ADA78002 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 803
ID ABM24850 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 804
ID ABO03118 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 805
ID ABR90374 standard; protein; 259 AA.

DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 806
ID ABM17288 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 807
ID ABR95034 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 808
ID ABR95339 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 809
ID ABO21577 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 810
ID ABR97841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 811
ID ABR87629 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 812
ID ABM77670 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 813
ID ABM27900 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 814
ID ABM06181 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 815
ID ABM03687 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 816
ID ABM35138 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 817
ID ABM26375 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 818
ID ABO48157 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 819
ID ABR92899 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 820
ID ABO24660 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 821
ID ABM1671 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 822
ID ABM02772 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 823
ID ABM16068 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;

Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 824
ID ABO27629 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 825
ID ABM29120 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 826
ID ABM07096 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 827
ID ABM21190 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 828
ID ABM09536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 829
ID ABO41406 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 830
ID ABO36221 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 831
ID ABO43750 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 832
ID ABM76450 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 833

ID ABM76146 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 834
ID ABM25765 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 835
ID ABM26070 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 836
ID ABO03423 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 837
ID ABO02508 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 838
ID ABR30679 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 839
ID ABR73747 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 840
ID ABO16999 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 841
ID ABR94424 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US200304917-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 842
ID ABR75931 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US200304929-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 843

ID ABR71307 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059860-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 844
ID ABR93204 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 845
ID ABR93509 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 846
ID ABR87934 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 847
ID ABO33602 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 848
ID ABO27934 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 849
ID ABO30069 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 850
ID ABO33278 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 851
ID ABO404966 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 852
ID ABR97231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054481-A1.

DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 853
ID ABO36526 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 854
ID ABO35611 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 855
ID ABO39576 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 856
ID ABO10451 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 857
ID ABO11976 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 858
ID ABO52122 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 859
ID ABO52427 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 860
ID ABO23745 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 861
ID ABR97231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054481-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 862
ID ABR87019 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 863
ID ABM11061 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 864
ID ABM28205 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 865
ID ABO32204 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 866
ID ABM15331 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 867
ID ABM06486 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 868
ID ABM04297 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 869
ID ABM22410 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 870
ID ABM07706 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068751-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 871
ID ABO40796 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 872
ID ABM35443 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 873
ID ABM33206 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 874
ID ABO52732 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 875
ID ABO50292 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 876
ID ABU99286 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 877
ID ABO04338 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 878
ID ABO05968 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 879
ID ABM18508 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 880
ID ABR97536 standard; protein; 259 AA.

DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 891
ID ABR80636 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 892
ID ABM01247 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 883
ID ABR88849 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 884
ID ABM13501 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 885
ID ABM20885 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 886
ID ABO42016 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 887
ID ABO42626 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 888
ID ABM10146 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 889
ID ABO38661 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068773-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 890
ID ABM32901 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 891
ID ABM22715 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 892
ID ABM74926 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 893
ID ADA79794 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 894
ID ABR96316 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 895
ID ABM02467 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 896
ID ABR86409 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 897
ID ABR86714 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 898
ID ABM16678 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 899

ID ABM29730 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 900
ID ABO29154 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 901
ID ABM23325 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 902
ID ABM23325 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 903
ID ABM22105 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 904
ID ABO37746 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 905
ID ABM28510 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 906
ID ABM28815 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 907
ID ABM66459 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 908
ID ABM75841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104547-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 909
ID ABM34121 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 910
ID ABM34426 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 911
ID ABO20357 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 912
ID ABO21272 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 913
ID ABO22187 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 914
ID ABR96621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 915
ID ABR85799 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 916
ID ABR99781 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 917
ID ABM00332 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;

RESULT 918
ID ABM0637 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 919
ID ABO29764 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 920
ID ABM23630 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 921
ID ABM29425 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 922
ID ABO38356 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 923
ID ABO45656 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 924
ID ABM20580 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 925
ID ADA81521 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 926
ID ABO16694 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 927
ID ABO18320 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 928
ID ABO22747 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 929
ID ABO23052 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 930
ID ABR92594 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 931
ID ABR81551 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 932
ID ABM77975 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 933
ID ABR89764 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 934
ID ABM26680 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 935
ID ABM13806 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 936
ID ABO28544 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;

RESULT 937
ID ABO30374 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 938
ID ABO7401 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 939
ID ABO3992 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 940
ID ABO37136 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 941
ID ABO41711 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 942
ID ABO35306 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 943
ID ABO25155 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 944
ID ABO47547 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 945
ID ABO47852 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 946
ID ABO48462 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 947
ID ABO51512 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 948
ID ABO51817 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 949
ID ABO50597 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 950
ID ABR79721 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 951
ID ABM16983 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 952
ID ABO18015 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 953
ID ABO20967 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 954
ID ABR96926 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 955
ID ABM12281 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 956
ID ABM16373 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 957
ID ABM24240 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 958
ID ABM14721 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 959
ID ABM04602 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 960
ID ABM06791 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 961
ID ABM09231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 962
ID AB039271 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 963
ID ABM75536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 964
ID ABM25460 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 965
ID ABM19970 standard; protein; 259 AA.

DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 966
ID ABO46876 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 967
ID ABO47181 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 968
ID ADA83319 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 969
ID ABR71612 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 970
ID ABR72222 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 971
ID ABR98561 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 972
ID ABO06931 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 973
ID ABR84884 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 974
ID ABR73442 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;

RESULT 975
ID ABR76536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 976
ID ABR73137 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 977
ID ABM18203 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 978
ID ABO20662 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 979
ID ABO25405 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 980
ID ABO25710 standard; protein; 259 AA.
DE Human secreted polypeptide #125.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 981
ID ABR94119 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 982
ID ABR80026 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 983
ID ABM11366 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 984
ID ABO22973 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 985
ID ABO30679 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 986
ID ABO30984 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 987
ID ABM27290 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 988
ID ABM30035 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 989
ID ABM05571 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 990
ID ABM15636 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 991
ID ABM08621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 992
ID ABO42321 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 993
ID ABO38051 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

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Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 994
ID ABO45961 standard; protein; 259 AA.
DE Human secreted polypeptide #125.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 995
ID ABM66764 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 996
ID AD820362 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 997
ID ABM19665 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 998
ID ABO49377 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 999
ID ABO49682 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1000
ID ADA78614 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1001
ID ABR88239 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1002
ID ABM26985 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1003
ID ABM03382 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1004
ID ABO39881 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1005
ID ABO49987 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1006
ID ABO50902 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1007
ID ABO05358 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1008
ID ABR74662 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1009
ID ABO44455 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1010
ID ABR77141 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1011
ID ABM17898 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1012
ID ABR95949 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040073-A1.
PD 27-FEB-2003.
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Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1013
ID ABO21882 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1014
ID ABO20052 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1015
ID ABO24355 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1016
ID ABR86104 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1017
ID ABM10756 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1018
ID ABM76755 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1019
ID ABR89459 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1020
ID ABM12586 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1021
ID ABM05876 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1022
ID ABR74357 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1023
ID ABO35001 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1024
ID ABM03077 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1025
ID ABM19360 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1026
ID ABO46571 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1027
ID ABO49072 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1028
ID ABR69115 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1029
ID ABR89154 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1030
ID ABR72527 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1031
ID ABR74357 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036161-A1.
PD 20-FEB-2003.
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PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1032
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1033
ID ABO18625 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1034
ID ABO18625 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1035
ID ABO18625 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1036
ID ABO18625 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1037
ID ABO12891 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1038
ID ABO12891 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1039
ID ABO12891 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1040
ID ABO12891 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1041
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1042
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1043
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1044
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1045
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1046
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1047
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US200306158-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1048
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US200306151-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1049
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1050
ID ABO11289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054456-A1.
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PD 20-MAR-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1051
ID ABO24050 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1052
ID ABR93814 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1053
ID ABR93814 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1054
ID ABR78280 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1055
ID ABO33479 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1056
ID ABR90069 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1057
ID ABM27595 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1058
ID ABM13196 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1059
ID ABO31899 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1060
ID ABM14111 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1061
ID ABM08316 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1062
ID ABO40186 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1063
ID ABM74621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1064
ID ABM33816 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1065
ID ABM20275 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1066
ID ABO48767 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1067
ID ABR72832 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1068
ID ABO15474 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1069
ID ABR85189 standard; protein; 259 AA.

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DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1070
ID ABO15169 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US20030404919-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1071
ID ABO17304 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1072
ID ABM17593 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US20030404928-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1073
ID ABR85494 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US20030409746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1074
ID ABM77060 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US20030504464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1075
ID ABO28239 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1076
ID ABM23020 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1077
ID ABM30340 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1078
ID ABM21800 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1079
ID ABM21495 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1080
ID ABM15026 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1081
ID ABO41101 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1082
ID ABO36831 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1083
ID ABO37441 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1084
ID ABM75231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1085
ID ABM33511 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1086
ID ABO46266 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1087
ID ADA82685 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
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RESULT 1088
ID ABM31865 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1089
ID ABM31255 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1090
ID ADB85993 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1091
ID ABM32170 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1092
ID ABM32475 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1093
ID ABM31560 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1094
ID ABM30950 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1095
ID ADC17939 standard; protein; 259 AA.
DE Human PRO polypeptide #21.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1096
ID ADD05723 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003083736-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1097
ID ADD70585 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US200309625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1098
ID ADD39662 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1099
ID ADD70108 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1100
ID ADD38229 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1101
ID ADD39185 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1102
ID ADD38708 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1103
ID ADD40139 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1104
ID ADE50360 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1105
ID ADE19972 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1106
ID ADE49883 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.

PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1107
ID ADE21441 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1108
ID ADF29866 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1109
ID ADF55759 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1110
ID ADG02718 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1111
ID ADG01425 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1112
ID ADF95600 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1113
ID ADG12415 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1114
ID ADH09075 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1115
ID ADH99263 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003065142-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1116
ID ADL32856 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1117
ID ADM30390 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1118
ID ADN39361 standard; protein; 259 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:B45.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1119
ID ADE74387 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1120
ID ADE74599 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1121
ID ADE96443 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1122
ID ADF25754 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1123
ID ADF24653 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1124
ID ADF29389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;

RESULT 1125
ID ADE96920 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1126
ID ADF96212 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1127
ID ADG04483 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1128
ID ADG00643 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1129
ID ADG82899 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1130
ID ADH02958 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1131
ID ADH03912 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1132
ID ADH03435 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1133
ID ADH26180 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1134
ID ADH33149 standard; protein; 259 AA.
DE Human Dkk family protein Dkk2.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1135
ID ADH04389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1136
ID ADH61390 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1137
ID ADJ54888 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1138
ID ADJ64659 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1139
ID ADM31555 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1140
ID ADM36602 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1141
ID ADM40407 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1142
ID ADL94589 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1143
ID ADO35295 standard; protein; 259 AA.
DE Human Dkk family protein Dkk2.

PN US2004014209-A1.
PD 22-JAN-2004.
PA (LASS/) LASSAR A B.
PA (MERC/) MERCOLA M.
PA (GUPT/) GUPTA R.
PA (MARV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZA/) TZAHOOR E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1144
ID AED38015 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1145
ID AED44976 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316, SEQ:70.
PN US2005181478-A1.
PD 18-AUG-2005.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
Query Match 20.5%; Score 102; DB 9; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1146
ID AED50245 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2005163766-A1.
PD 28-JUL-2005.
Query Match 20.5%; Score 102; DB 9; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.008;
RESULT 1147
ID AAB08880 standard; protein; 263 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-2 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 20.5%; Score 102; DB 3; Length 263;
Best Local Similarity 31.5%; Pred. No. 0.0082;
RESULT 1148
ID AAY92072 standard; protein; 259 AA.
DE Murine DKR-2.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 20.3%; Score 101; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.01;
RESULT 1149
ID AEA38732 standard; protein; 272 AA.
DE Mouse dickkopf-1 (Dkk-1) protein, SEQ ID NO: 22.
PN WO20005049640-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 20.3%; Score 101; DB 9; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.011;
RESULT 1150
ID AEF80274 standard; protein; 272 AA.
DE Mouse dickkopf-1 (Dkk-1) protein sequence.
PN WO2006015373-A2.
PD 09-FEB-2006.
PA (AMGE-) AMGEN INC.
Query Match 20.3%; Score 101; DB 10; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.011;
RESULT 1151
ID ADY86168 standard; protein; 83 AA.
DE Human dickkopf-3 protein, SEQ ID NO:6.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 9; Length 83;
Best Local Similarity 37.7%; Pred. No. 0.0036;
RESULT 1152
ID ADB64042 standard; protein; 215 AA.
DE Human protein encoded by clone BRAMY20227860.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 20.2%; Score 100.5; DB 7; Length 215;
Best Local Similarity 37.7%; Pred. No. 0.0097;
RESULT 1153
ID AAW73016 standard; protein; 350 AA.
DE Human cysteine-rich secreted protein CRSP-1.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 20.2%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1154
ID AAW62595 standard; protein; 350 AA.
DE Homo sapiens cerebellum and embryo specific protein.
PN WO9827932-A2.
PD 02-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.2%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1155
ID AAY13384 standard; protein; 350 AA.
DE Amino acid sequence of protein PRO295.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1156
ID AAY92070 standard; protein; 350 AA.
DE Human DKR-3.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 20.2%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1157
ID AAB08874 standard; protein; 350 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-3 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 20.2%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1158
ID ADC78556 standard; protein; 350 AA.
DE Human PRO295 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1159
ID AAB80252 standard; protein; 350 AA.
DE Human PRO295 protein.
PN WO200104311-A1.
PD 18-JAN-2001.

PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1160
ID AAG80271 standard; protein; 350 AA.
DE Human DKK-3 protein.
PN WO200163295-A2.
PD 30-AUG-2001.
PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
Query Match 20.2%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1161
ID AAB87529 standard; protein; 350 AA.
DE Human PRO295.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1162
ID AAG62468 standard; protein; 350 AA.
DE Human reduced expression in immortalised cells protein.
PN WO200138528-A1.
PD 31-MAY-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 20.2%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1163
ID ABB90735 standard; protein; 350 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 202.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 20.2%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1164
ID ABG95854 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1165
ID ABB84841 standard; protein; 350 AA.
DE Human PRO295 protein sequence SEQ ID NO:50.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1166
ID ABB95447 standard; protein; 350 AA.
DE Human angiogenesis related protein PRO295 SEQ ID NO: 50.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1167
ID ABU71630 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1168
ID ABU71485 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002192859-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1169
ID ABU54442 standard; protein; 350 AA.
DE Human tumour endothelial marker TEM 4.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1170
ID ABU71931 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1171
ID ABO01814 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1172
ID ABU90879 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1173
ID ABO33938 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1174
ID ABU71955 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1175
ID ABU55915 standard; protein; 350 AA.
DE Human protein DKK3.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;

RESULT 1176
ID ABU54387 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1177
ID ABO47402 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO295.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1178
ID ABU71509 standard; protein; 350 AA.
DE Human secreted polypeptide PRO295.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1179
ID AAE34069 standard; protein; 350 AA.
DE DKK 3 protein.
PN WO20029092-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1180
ID ABU72290 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1181
ID ABUS0963 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1182
ID ABO27284 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO295.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1183
ID ABU64539 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #43.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1184
ID ABU67385 standard; protein; 350 AA.
DE Human secreted protein PRO295.
PN US2003020354-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1185
ID ABU92479 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1186
ID ABO14905 standard; protein; 350 AA.
DE Human secreted / transmembrane polypeptide PRO295.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1187
ID ABU81149 standard; protein; 350 AA.
DE Human secreted polypeptide PRO295.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1188
ID ABO53264 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1189
ID ABU98266 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1190
ID ABUS9271 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1191
ID ABU82478 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1192
ID ABU69662 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1193
ID ABU96442 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1194
ID ABU72112 standard; protein; 350 AA.

DE Human PRO polypeptide #4.
PN US2003023042-A1.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1195
ID ABO14844 standard; protein; 350 AA.
DE Human secreted / transmembrane polypeptide PRO295.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1196
ID ADB29441 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1197
ID ADB17065 standard; protein; 350 AA.
DE Human transmembrane PRO polypeptide (seqID 8).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1198
ID ABO44242 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1199
ID ADA18297 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1200
ID ABO32796 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1201
ID ADA19870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1202
ID ADB17253 standard; protein; 350 AA.
DE Human transmembrane PRO polypeptide (seqID 8).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1203
ID ABO34856 standard; protein; 350 AA.
DE Human PRO polypeptide #41.

PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1204
ID ADA16272 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1205
ID ADA20042 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1206
ID ABO34170 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1207
ID ADA42417 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1208
ID ABO17534 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1209
ID ADA00339 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1210
ID ADA16696 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US20030319969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1211
ID ADA13125 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1212
ID ADA41993 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082540-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1213
ID ADA17340 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1214
ID ADA42843 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1215
ID ABO17595 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1216
ID ADB85581 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1217
ID ADB77762 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1218
ID ADB74898 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1219
ID ADB68260 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1220
ID ADB68067 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1221
ID ADB90884 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1222
ID ADC28544 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1223
ID ADC39744 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1224
ID ADC40258 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1225
ID ADC19082 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1226
ID ADC34382 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1227
ID ADC29437 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1228
ID ADC28968 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1229
ID ADC40853 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1230
ID ADC19510 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1231
ID ADC06964 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1232
ID ADC17143 standard; protein; 350 AA.
DE Mammalian PRO polypeptide (SeqID 8).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1233
ID ADC33958 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1234
ID ADC13028 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1235
ID ADC14841 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1236
ID ADC52336 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1237
ID ADC12480 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1238
ID ADD10339 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1239
ID ADD05035 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1240
ID ADD11299 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1241
ID ADD04041 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1242
ID ADD03617 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1243
ID ADD37092 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1244
ID ADD36012 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1245
ID ADE34869 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1246
ID ADG01013 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1247
ID ADG08566 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1248
ID ADF95187 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
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RESULT 1249
ID ADH24040 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1250
ID ADH34066 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1251
ID ADH29899 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1252
ID ADH23870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1253
ID ADG85274 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1254
ID ADH24550 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1255
ID ADH37406 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1256
ID ADH01995 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1257
ID ADH37576 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1258
ID ADH59352 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1259
ID ADH24210 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1260
ID ADH38504 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1261
ID ADG83625 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1262
ID ADH29433 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1263
ID ADH27549 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1264
ID ADH37746 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1265
ID ADH37923 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1266
ID ADH57343 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1267
ID ADH59352 standard; protein; 350 AA.
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DE Human secreted/transmembrane protein, #45.
PN US2003039972-A1.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1268
ID ADH53485 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1269
ID ADH53655 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1270
ID ADH51991 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1271
ID ADH49846 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1272
ID ADI25356 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1273
ID ADH90149 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1274
ID ADI25526 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181659-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1275
ID ADH97700 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1276
ID ADI38131 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054352-A1.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1277
ID ADI03548 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1278
ID ADI11905 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1279
ID ADH89979 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1280
ID ADH98380 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1281
ID ADI11055 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1282
ID ADI11565 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1283
ID ADH98210 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1284
ID ADH98550 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1285
ID ADH98040 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181673-A1.

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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1286
ID ADI05028 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1287
ID ADI03378 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1288
ID ADI04773 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1289
ID ADH78227 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1290
ID ADI19571 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1291
ID ADH90319 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1292
ID ADI03038 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1293
ID ADH77887 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1294
ID ADH97870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1295
ID ADI01255 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1296
ID ADI01950 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1297
ID ADI03208 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1298
ID ADI11395 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1299
ID ADI02297 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1300
ID ADI11735 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1301
ID ADI05372 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1302
ID ADH79444 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1303
ID ADI19401 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1304
ID ADI05202 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1305
ID ADH9614 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1306
ID ADI01440 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1307
ID ADI01610 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1308
ID ADI01780 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1309
ID ADH9784 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1310
ID ADI04602 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1311
ID ADI02738 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1312
ID ADH78057 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;

Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1313
ID ADI25696 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1314
ID ADI25866 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1315
ID ADK65378 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1316
ID ADH98720 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1317
ID ADH79961 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1318
ID ADJ26399 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1319
ID ADL93692 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1320
ID ADP65205 standard; protein; 350 AA.
DE Human dickkopf homologue 3, RIG-like 7-1, RIG-like 5-6.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHILU-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1321
ID ADC52146 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;

RESULT 1322
ID ADE79314 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003135025-A1.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 17-JUL-2003.
RESULT 1323
ID ADE79738 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 10-JUL-2003.
RESULT 1324
ID ADE73414 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 10-JUL-2003.
RESULT 1325
ID ADE41300 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 29-MAY-2003.
RESULT 1326
ID ADE73949 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 07-AUG-2003.
RESULT 1327
ID ADE99503 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 13-NOV-2003.
RESULT 1328
ID ADE98622 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 13-NOV-2003.
RESULT 1329
ID ADE99049 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 13-NOV-2003.
RESULT 1330
ID ADG40519 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN) DESNOYERS L.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 04-DEC-2003.
RESULT 1331
ID ADF73913 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 25-SEP-2003.
RESULT 1332
ID ADF73489 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US200316051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 04-SEP-2003.
RESULT 1333
ID ADH06578 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 25-SEP-2003.
RESULT 1334
ID ADH06408 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 25-SEP-2003.
RESULT 1335
ID ADG6829 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 25-SEP-2003.
RESULT 1336
ID ADH27719 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 25-SEP-2003.
RESULT 1337
ID ADH25060 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 25-SEP-2003.
RESULT 1338
ID ADH33692 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
PD 25-SEP-2003.
RESULT 1339
ID ADG92332 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003027145-A1.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1340
ID ADH02335 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1341
ID ADH07942 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1342
ID ADG9339 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1343
ID ADH39160 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1344
ID ADG92759 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1345
ID ADG83900 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1346
ID ADG85444 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1347
ID ADH06238 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1348
ID ADH30068 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180856-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1349
ID ADH24380 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1350
ID ADG69509 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1351
ID ADH07772 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180951-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1352
ID ADG85784 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1353
ID ADH39330 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1354
ID ADH33522 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1355
ID ADH33862 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1356
ID ADH01072 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1357
ID ADG69679 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1358
ID ADH02165 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1359
ID ADG69169 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1360
ID ADG85954 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1361
ID ADH24890 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1362
ID ADH39507 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1363
ID ADH02505 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1364
ID ADG68999 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1365
ID ADH07602 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1366
ID ADG86124 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1367
ID ADH24720 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1368
ID ADH25768 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1369
ID ADH38334 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1370
ID ADH20548 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1371
ID ADH57173 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1372
ID ADH43483 standard; protein; 350 AA.
DE Human PRO polypeptide #25.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1373
ID ADH07403 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A. J.
PA (GODO/) GODOWSKI P. J.
PA (GURN/) GURNEY A. L.
PA (MATH/) MATHER J. P.
PA (WILL/) WILLIAMS P. M.
PA (WOOD/) WOOD W. I.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1374
ID ADH52161 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1375
ID ADH59948 standard; protein; 350 AA.
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DE Human secreted/transmembrane protein, #45.
PN US2003215904-A1.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
ID' ADH90659 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1385
ID ADI37697 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1386
ID ADH97497 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1387
ID ADI65865 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1388
ID ADH60608 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1389
ID ADJ99665 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1390
ID ADL08858 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1391
ID ADJ98534 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
DE Human secreted/transmembrane protein, #45.
PN US2003215904-A1.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
ID' ADH9527 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1377
ID ADH06976 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1378
ID ADH90489 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1379
ID ADI11225 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1380
ID ADI18718 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1381
ID ADH98890 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1382
ID ADI65438 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1383
ID ADI02120 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190699-A1.
PD 09-OCT-2003.

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RESULT 1392
ID ADJ98704 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1393
ID ADH78863 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1394
ID ADJ99097 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1395
ID ADJ99267 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1396
ID ADJ98885 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1397
ID ADH79033 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1398
ID ADK00893 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1399
ID ADK1414 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1400
ID ADM25199 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1401
ID ADM29949 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1402
ID ADR82828 standard; protein; 350 AA.
DE Human PRO polypeptide #25.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1403
ID ADM80863 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1404
ID AD006271 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1405
ID ADR11123 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1406
ID ADR18032 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1407
ID ADS74671 standard; protein; 350 AA.
DE Human secreted/transmembrane protein #45.
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PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1413
ID AEF12534 standard; protein; 350 AA.
DE Human PRO295 protein SEQ ID NO:8.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1414
ID AEF74223 standard; protein; 350 AA.
DE Human PRO295 protein SEQ ID NO:8.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1415
ID AEF68232 standard; protein; 350 AA.
DE Human Dickkopf homolog 3 (DKK-3) protein.
PN WO2006010534-A1.
PD 02-FEB-2006.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1416
ID AAW73021 standard; protein; 349 AA.
DE Mouse cysteine-rich secreted protein-1.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 19.8%; Score 98.5; DB 2; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.027;
RESULT 1417
ID AAY92069 standard; protein; 349 AA.
DE Murine DKK-3.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 19.8%; Score 98.5; DB 3; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.027;
RESULT 1418
ID AAB08979 standard; protein; 349 AA.
DE A murine Dickkopf (Dkk)-3 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.8%; Score 98.5; DB 3; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.027;
RESULT 1419
ID AEF68233 standard; protein; 349 AA.
DE Murine Dickkopf homolog 3 (DKK-3) protein.
PN WO2006010534-A1.
PD 02-FEB-2006.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 19.8%; Score 98.5; DB 10; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.027;
RESULT 1420
ID ADE82539 standard; protein; 84 AA.
DE Antibody that binds to DKK #6.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.

PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1408
ID ADT03708 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1409
ID ADY77703 standard; protein; 350 AA.
DE Neoplastic disease detection protein PRO295.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 9; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1410
ID ABA37946 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 9; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1411
ID AED23980 standard; protein; 350 AA.
DE Human secreted protein PRO 295, SEQ ID 236.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 9; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.016;
RESULT 1412
ID AEE69149 standard; protein; 350 AA.
DE Integrin homologous PRO295 protein, SEQ ID 236.
PN US6974689-B1.
PD 13-DEC-2005.

PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 84;
Best Local Similarity 32.3%; Pred. No. 0.0088;
RESULT 1421
ID ADB82541 standard; protein; 107 AA.
DE Antibody that binds to DKK #8.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 107;
Best Local Similarity 32.3%; Pred. No. 0.011;
RESULT 1422
ID ADU66981 standard; protein; 108 AA.
DE Human DDX-1 LRP-6 binding domain.
PN US2004235166-A1.
PD 25-NOV-2004.
PA (PROC/) PROCKOP D.
PA (SEKI/) SEKIYA I.
PA (GREG/) GREGORY C.
PA (SPEE/) SPEES J.
PA (SMIT/) SMITH J.
PA (POCH/) POCHAMPALLY R.
Query Match 19.5%; Score 97; DB 8; Length 108;
Best Local Similarity 32.3%; Pred. No. 0.011;
RESULT 1423
ID AD251669 standard; protein; 108 AA.
DE Dickkopf-1 LDL receptor-related protein 6 binding site.
PN US2005084494-A1.
PD 21-APR-2005.
PA (PROC/) PROCKOP D.
PA (GREG/) GREGORY C.
PA (GUNN/) GUNN W.
Query Match 19.5%; Score 97; DB 9; Length 108;
Best Local Similarity 32.3%; Pred. No. 0.011;
RESULT 1424
ID ADE82538 standard; protein; 128 AA.
DE Antibody that binds to DKK #5.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 128;
Best Local Similarity 32.3%; Pred. No. 0.014;
RESULT 1425
ID ADE82540 standard; protein; 149 AA.
DE Antibody that binds to DKK #7.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 149;
Best Local Similarity 32.3%; Pred. No. 0.016;
RESULT 1426
ID ADB99065 standard; protein; 151 AA.
DE LRPS constrained peptide OST264.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 151;
Best Local Similarity 32.3%; Pred. No. 0.016;
RESULT 1427
ID ADE82633 standard; protein; 151 AA.
DE LRPS peptide aptamer #10.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 151;
Best Local Similarity 32.3%; Pred. No. 0.016;
RESULT 1428
ID ADE82537 standard; protein; 170 AA.

DE Antibody that binds to DKK #4.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 170;
Best Local Similarity 32.3%; Pred. No. 0.018;
RESULT 1429
ID ADB99066 standard; protein; 172 AA.
DE LRPS constrained peptide OST265.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 172;
Best Local Similarity 32.3%; Pred. No. 0.019;
RESULT 1430
ID ADE82634 standard; protein; 172 AA.
DE LRPS peptide aptamer #11.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 172;
Best Local Similarity 32.3%; Pred. No. 0.019;
RESULT 1431
ID AD035296 standard; protein; 180 AA.
DE Human Dkk1 carboxy terminal cysteine rich region.
PN US2004014209-A1.
PD 22-JAN-2004.
PA (LASS/) LASSAR A B.
PA (MERC/) MERCOLA M.
PA (GUPT/) GUPTA R.
PA (MARV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZAH/) TZAHOR E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match 19.5%; Score 97; DB 8; Length 180;
Best Local Similarity 32.3%; Pred. No. 0.019;
RESULT 1432
ID ADE82535 standard; protein; 212 AA.
DE Antibody that binds to DKK #2.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 212;
Best Local Similarity 32.3%; Pred. No. 0.023;
RESULT 1433
ID ADE82534 standard; protein; 233 AA.
DE Antibody that binds to DKK #1.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 233;
Best Local Similarity 32.3%; Pred. No. 0.025;
RESULT 1434
ID AEA38731 standard; protein; 265 AA.
DE Human dickkopf-1 (Dkk-1) protein, SEQ ID NO: 21 #1.
PN WO2005049640-A2.
PD 02-JUN-2005.
PA (MERI/) MERCK & CO INC.
Query Match 19.5%; Score 97; DB 9; Length 265;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1435
ID AA73018 standard; protein; 266 AA.
DE Human cyteine-rich secreted protein CRSP-3.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 19.5%; Score 97; DB 2; Length 266;

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Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1436
ID AAY1757 standard; protein; 266 AA.
DE Human PRO1008 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 2; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1437
ID AAY92071 standard; protein; 266 AA.
DE Human DKR-1.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 19.5%; Score 97; DB 3; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1438
ID AAB4433 standard; protein; 266 AA.
DE Human PRO1008 (UNQ492) protein sequence SEQ ID NO:456.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 3; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1439
ID AAB08876 standard; protein; 266 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-1 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.5%; Score 97; DB 3; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1440
ID AAU12385 standard; protein; 266 AA.
DE Human PRO1008 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 4; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1441
ID AAM78517 standard; protein; 266 AA.
DE Human protein SEQ ID NO 1179.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 19.5%; Score 97; DB 4; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1442
ID ABO17829 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1443
ID ABO25259 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1444
ID ABU81083 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1445
ID ABO25054 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #214.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1446
ID ABU66783 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1447
ID ABUS5913 standard; protein; 266 AA.
DE Human protein DKK1.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1448
ID ABU84945 standard; protein; 266 AA.
DE Human secreted and transmembrane PRO polypeptide #21.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1449
ID AAE34067 standard; protein; 266 AA.
DE DKK1 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1450
ID ABUS9864 standard; protein; 266 AA.
DE Novel secreted and transmembrane protein PRO1008.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1451
ID ABU61143 standard; protein; 266 AA.
DE Human PRO1008 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1452
ID ABUS7630 standard; protein; 266 AA.
DE Differentially expressed breast cancer associated protein #17.
PN US2002156263-A1.
PD 24-OCT-2002.
PA (CHEN/) CHEN H.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1453
ID ABO25054 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #214.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1454
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ID ABR01793 standard; protein; 266 AA.
DE Human cancer-related protein, 151PIC7A.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSVS INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1455
ID ABU80412 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO1008.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1456
ID ABU67059 standard; protein; 266 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 428.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1457
ID ADA45947 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1458
ID ADA76378 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1459
ID ADA19028 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1460
ID ADA61651 standard; protein; 266 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1461
ID ADB19436 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1462
ID ADB27977 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1463
ID ADA66456 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1464
ID ADB16020 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1465
ID ADA47806 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1466
ID ADA67601 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1467
ID ADB30608 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1468
ID ADA85904 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1469
ID ADA97116 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1470
ID ADA79420 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1471
ID ADA87559 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1472
ID ADB16761 standard; protein; 266 AA.
DE Human PRO polypeptide #214.

PN US2003087349-A1.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1473
ID ADA91853 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1474
ID ADB14916 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1475
ID ADA94995 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1476
ID ADB18877 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1477
ID ADA94092 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1478
ID ADB19988 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1479
ID ADB13300 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1480
ID ABO43362 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1481
ID ABO19714 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003050240-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1482
ID ADA12656 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO1008.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1483
ID ADA74554 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1484
ID ADB24787 standard; protein; 266 AA.
DE Human PRO polypeptide SEQ ID NO 428.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1485
ID ADA82311 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1486
ID ADA75274 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1487
ID ADA85352 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1488
ID ADA84800 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1489
ID ADB30056 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1490
ID ADA80584 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082761-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1491
ID ADA75826 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1492
ID ADA47051 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1493
ID ADB25347 standard; protein; 266 AA.
DE Human PRO polypeptide SEQ ID NO 428.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1494
ID ADA93523 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1495
ID ADB26873 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1496
ID ADB31160 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1497
ID ADA61088 standard; protein; 266 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1498
ID ADB24235 standard; protein; 266 AA.
DE Human PRO polypeptide SEQ ID NO 428.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1499
ID ADA96564 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.029;
RESULT 1500
ID ADA81136 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
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GenCore version 5.1.9
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 OM protein - protein search, using sw model
 Run on: December 14, 2006, 14:30:22 ; Search time 113.466 Seconds
 (without alignments)
 351.087 Million cell updates/sec

Title: US-10-692-299-2_COPY_20_105
 Perfect score: 498
 Sequence: 1 AVITGACERDVCGAGTCCA.....CSRFPDGRYRCMDLKNINF 86

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues
 Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Listing first 1500 summaries

Database : Published Applications AA Main:
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 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	498	100.0	86	4	US-10-016-481-3
2	498	100.0	86	4	US-10-323-157-3
3	498	100.0	86	4	US-10-417-426-9
4	498	100.0	86	4	US-10-333-192-21
5	498	100.0	86	5	US-10-680-554-5
6	498	100.0	86	5	US-10-713-567-3
7	498	100.0	86	5	US-10-912-907-3
8	498	100.0	86	5	US-10-912-907-3
9	498	100.0	86	5	US-10-415-724-3
10	498	100.0	86	5	US-10-871-152-22
11	498	100.0	86	5	US-10-503-554A-82
12	498	100.0	86	5	US-10-343-095A-117
13	498	100.0	86	6	US-11-073-420-11
14	498	100.0	87	4	US-10-016-481-18
15	498	100.0	87	4	US-10-323-157-18
16	498	100.0	87	5	US-10-713-567-18
17	498	100.0	87	5	US-10-811-328-18
18	498	100.0	87	5	US-10-912-907-18
19	498	100.0	87	5	US-10-415-724-18
20	498	100.0	89	4	US-10-016-481-15
21	498	100.0	89	4	US-10-323-157-15
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24	498	100.0	89	5	US-10-912-907-15
25	498	100.0	89	5	US-10-415-724-15
39	498	100.0	105	3	US-09-886-242A-2
41	498	100.0	105	3	US-09-965-528-11

54	498	100.0	105	3	US-09-997-428-371	Sequence 371, App
58	498	100.0	105	3	US-09-796-753-64	Sequence 64, Appl
100	498	100.0	105	3	US-09-969-984-11	Sequence 11, Appl
101	498	100.0	105	4	US-10-016-481-2	Sequence 2, Appl
102	498	100.0	105	4	US-10-027-603-2	Sequence 2, Appl
135	498	100.0	105	4	US-10-132-812-16	Sequence 16, Appl
284	498	100.0	105	4	US-10-223-085-172	Sequence 172, App
290	498	100.0	105	4	US-10-219-065-166	Sequence 166, App
318	498	100.0	105	4	US-10-223-084-172	Sequence 172, App
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325	498	100.0	105	4	US-10-212-355-5	Sequence 5, Appl
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327	498	100.0	105	4	US-10-323-157-2	Sequence 2, Appl
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672	498	100.0	105	5	US-10-912-907-2	Sequence 2, Appl
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676	498	100.0	105	5	US-10-977-113-31	Sequence 31, Appl
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681	498	100.0	105	5	US-10-982-168-5	Sequence 5, Appl
683	498	100.0	105	5	US-10-973-115B-470	Sequence 470, App
689	498	100.0	105	5	US-10-504-588-4	Sequence 4, Appl
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693	498	100.0	105	6	US-11-290-153-470	Sequence 470, App
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697	497	99.8	105	4	US-10-333-192-22	Sequence 22, Appl
698	497	99.8	105	5	US-10-467-554-3	Sequence 3, Appl
699	497	99.8	105	5	US-10-503-554A-83	Sequence 83, Appl
700	497	99.8	105	5	US-10-475-075-194	Sequence 194, App
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703	494	99.2	85	5	US-10-713-567-16	Sequence 16, Appl
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707	494	99.2	86	5	US-10-713-567-20	Sequence 20, Appl
708	494	99.2	86	5	US-10-811-328-20	Sequence 20, Appl
709	492	98.8	105	5	US-10-977-113-30	Sequence 30, Appl
710	492	98.8	105	6	US-11-073-420-28	Sequence 28, Appl
711	491	98.6	105	5	US-10-475-075-193	Sequence 193, App
712	491	98.6	105	5	US-10-475-075-477	Sequence 477, App
713	489	98.2	105	6	US-11-073-420-31	Sequence 31, Appl
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715	478	96.0	86	4	US-10-713-567-17	Sequence 17, Appl
716	478	96.0	86	5	US-10-811-328-17	Sequence 17, Appl
717	478	96.0	86	5	US-10-912-907-17	Sequence 17, Appl
718	478	96.0	86	5	US-10-415-724-17	Sequence 17, Appl
719	478	96.0	86	5	US-10-016-481-15	Sequence 15, Appl
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721	473	95.0	86	4	US-10-470-951-37	Sequence 37, Appl
722	473	95.0	86	4	US-10-362-504-49	Sequence 49, Appl
723	473	95.0	86	5	US-10-680-554-10	Sequence 10, Appl
724	473	95.0	86	5	US-10-713-567-30	Sequence 30, Appl
725	473	95.0	86	5	US-10-811-328-30	Sequence 30, Appl
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727	473	95.0	105	4	US-10-470-951-31	Sequence 31, Appl	800	291	58.4	81	5	US-10-680-554-7	Sequence 7, Appl
728	473	95.0	105	4	US-10-362-504-43	Sequence 43, Appl	801	291	58.4	81	5	US-10-713-567-6	Sequence 6, Appl
729	473	95.0	105	5	US-10-503-554A-132	Sequence 132, App	802	291	58.4	81	5	US-10-811-328-6	Sequence 6, Appl
730	469	94.2	86	4	US-10-470-951-41	Sequence 41, Appl	803	291	58.4	81	5	US-10-912-907-6	Sequence 6, Appl
731	469	94.2	86	4	US-10-362-504-53	Sequence 53, Appl	804	291	58.4	81	5	US-10-415-724-6	Sequence 9, Appl
732	469	94.2	86	5	US-10-503-554A-142	Sequence 142, App	805	291	58.4	81	5	US-10-977-113-9	Sequence 9, Appl
733	469	94.2	105	4	US-10-470-951-35	Sequence 35, Appl	806	291	58.4	81	5	US-10-871-152-18	Sequence 18, Appl
734	469	94.2	105	4	US-10-362-504-47	Sequence 47, Appl	807	291	58.4	81	5	US-10-503-554A-19	Sequence 19, Appl
735	469	94.2	105	5	US-10-503-554A-136	Sequence 136, App	808	291	58.4	81	6	US-11-073-420-9	Sequence 9, Appl
736	467	93.8	86	4	US-10-470-951-39	Sequence 39, Appl	809	291	58.4	100	3	US-09-886-242A-4	Sequence 4, Appl
737	467	93.8	86	4	US-10-362-504-51	Sequence 51, Appl	810	291	58.4	100	4	US-10-027-603-4	Sequence 4, Appl
738	467	93.8	86	5	US-10-503-554A-140	Sequence 140, App	811	291	58.4	100	5	US-10-692-399-4	Sequence 4, Appl
739	467	93.8	105	4	US-10-470-951-33	Sequence 33, Appl	812	291	58.4	108	4	US-10-016-481-5	Sequence 5, Appl
740	467	93.8	105	4	US-10-362-504-45	Sequence 45, Appl	813	291	58.4	108	4	US-10-231-411-4	Sequence 4, Appl
741	467	93.8	105	5	US-10-503-554A-134	Sequence 134, App	814	291	58.4	108	4	US-10-212-355-2	Sequence 2, Appl
742	455	91.4	86	4	US-10-417-426-10	Sequence 10, Appl	815	291	58.4	108	4	US-10-323-157-5	Sequence 5, Appl
743	455	91.4	86	4	US-10-470-951-8	Sequence 8, Appl	816	291	58.4	108	4	US-10-212-201-2	Sequence 2, Appl
744	455	91.4	86	5	US-10-680-554-8	Sequence 8, Appl	817	291	58.4	108	4	US-10-467-019-17	Sequence 17, Appl
745	455	91.4	86	5	US-10-713-567-28	Sequence 28, Appl	818	291	58.4	108	4	US-10-680-755A-2	Sequence 2, Appl
746	455	91.4	86	5	US-10-811-328-28	Sequence 28, Appl	819	291	58.4	108	4	US-10-680-500A-2	Sequence 2, Appl
747	455	91.4	86	5	US-10-977-113-12	Sequence 12, Appl	820	291	58.4	108	5	US-10-713-567-5	Sequence 5, Appl
748	455	91.4	86	5	US-10-871-152-23	Sequence 23, Appl	821	291	58.4	108	5	US-10-811-328-5	Sequence 5, Appl
749	455	91.4	86	5	US-10-503-554A-109	Sequence 109, App	822	291	58.4	108	5	US-10-912-907-5	Sequence 5, Appl
750	455	91.4	86	6	US-11-073-420-12	Sequence 12, Appl	823	291	58.4	108	5	US-10-415-724-5	Sequence 5, Appl
751	455	91.4	105	4	US-10-470-951-6	Sequence 6, Appl	824	291	58.4	108	5	US-10-990-246-2	Sequence 2, Appl
752	455	91.4	105	5	US-10-503-554A-107	Sequence 107, App	825	291	58.4	108	5	US-10-503-554A-17	Sequence 17, Appl
753	413	82.9	86	4	US-10-016-481-14	Sequence 14, Appl	826	291	58.4	108	5	US-10-982-168-2	Sequence 2, Appl
754	413	82.9	86	4	US-10-323-157-14	Sequence 14, Appl	827	291	58.4	108	5	US-10-504-588-6	Sequence 6, Appl
755	413	82.9	86	5	US-10-417-426-21	Sequence 21, Appl	828	291	58.4	116	4	US-10-680-755A-26	Sequence 26, Appl
756	413	82.9	86	5	US-10-680-554-16	Sequence 16, Appl	829	291	58.4	116	4	US-10-680-800A-26	Sequence 26, Appl
757	413	82.9	86	5	US-10-713-567-14	Sequence 14, Appl	830	286	57.4	80	5	US-10-977-113-10	Sequence 10, Appl
758	413	82.9	86	5	US-10-811-328-14	Sequence 14, Appl	831	286	57.4	80	6	US-11-073-420-10	Sequence 10, Appl
759	413	82.9	86	5	US-10-912-907-14	Sequence 14, Appl	832	286	57.4	81	4	US-10-417-426-7	Sequence 7, Appl
760	413	82.9	86	5	US-10-415-724-14	Sequence 14, Appl	833	286	57.4	81	4	US-10-467-019-39	Sequence 39, Appl
761	413	82.9	86	5	US-10-977-113-17	Sequence 17, Appl	834	286	57.4	81	4	US-10-362-504-71	Sequence 71, Appl
762	413	82.9	86	5	US-10-871-152-28	Sequence 28, Appl	835	286	57.4	81	5	US-10-680-554-9	Sequence 9, Appl
763	413	82.9	86	6	US-11-073-420-17	Sequence 17, Appl	836	286	57.4	81	5	US-10-680-554-11	Sequence 11, Appl
764	376	75.5	81	4	US-10-016-481-13	Sequence 13, Appl	837	286	57.4	81	5	US-10-713-567-29	Sequence 29, Appl
765	376	75.5	81	4	US-10-323-157-13	Sequence 13, Appl	838	286	57.4	81	5	US-10-713-567-31	Sequence 31, Appl
766	376	75.5	81	4	US-10-417-426-20	Sequence 20, Appl	839	286	57.4	81	5	US-10-811-328-29	Sequence 29, Appl
767	376	75.5	81	5	US-10-680-554-15	Sequence 15, Appl	840	286	57.4	81	5	US-10-811-328-31	Sequence 31, Appl
768	376	75.5	81	5	US-10-713-567-13	Sequence 13, Appl	841	286	57.4	81	5	US-10-871-152-20	Sequence 20, Appl
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770	376	75.5	81	5	US-10-912-907-13	Sequence 13, Appl	843	286	57.4	107	4	US-10-132-812-10	Sequence 10, Appl
771	376	75.5	81	5	US-10-415-724-13	Sequence 13, Appl	844	286	57.4	107	4	US-10-231-411-6	Sequence 6, Appl
772	376	75.5	81	5	US-10-977-113-16	Sequence 16, Appl	845	286	57.4	107	4	US-10-467-019-37	Sequence 37, Appl
773	376	75.5	81	5	US-10-871-152-27	Sequence 27, Appl	846	286	57.4	107	4	US-10-467-019-55	Sequence 55, Appl
774	376	75.5	81	6	US-11-073-420-16	Sequence 16, Appl	847	286	57.4	107	4	US-10-362-504-69	Sequence 69, Appl
775	315	63.3	80	4	US-10-417-426-13	Sequence 13, Appl	848	286	57.4	107	5	US-10-503-554A-37	Sequence 37, Appl
776	315	63.3	80	4	US-10-467-019-21	Sequence 21, Appl	849	286	57.4	107	5	US-10-503-554A-55	Sequence 55, Appl
777	315	63.3	80	4	US-10-470-951-64	Sequence 64, Appl	850	284	57.0	81	6	US-11-073-420-37	Sequence 37, Appl
778	315	63.3	80	4	US-10-333-192-34	Sequence 34, Appl	851	284	57.0	108	5	US-10-713-567-34	Sequence 34, Appl
779	315	63.3	80	5	US-10-977-113-15	Sequence 15, Appl	852	284	57.0	108	5	US-10-977-113-6	Sequence 6, Appl
780	315	63.3	80	5	US-10-871-152-26	Sequence 26, Appl	853	284	57.0	108	6	US-11-073-420-6	Sequence 6, Appl
781	315	63.3	80	5	US-10-503-554A-21	Sequence 21, Appl	854	278.5	55.9	77	5	US-10-680-554-14	Sequence 14, Appl
782	315	63.3	79	3	US-11-073-420-15	Sequence 15, Appl	855	278.5	55.9	77	5	US-10-713-567-32	Sequence 32, Appl
783	311.5	62.6	79	3	US-09-886-242A-5	Sequence 5, Appl	856	278.5	55.9	77	5	US-10-811-328-32	Sequence 32, Appl
784	311.5	62.6	79	5	US-10-027-603-5	Sequence 5, Appl	857	270.5	54.3	102	5	US-10-680-554-6	Sequence 6, Appl
785	310.5	62.3	81	4	US-10-692-299-5	Sequence 5, Appl	858	270.5	54.3	129	4	US-10-132-812-14	Sequence 14, Appl
786	310.5	62.3	81	4	US-10-016-481-12	Sequence 12, Appl	859	270.5	54.3	129	4	US-10-231-411-2	Sequence 2, Appl
787	310.5	62.3	81	4	US-10-132-812-19	Sequence 19, Appl	860	270.5	54.3	129	4	US-10-680-755A-29	Sequence 29, Appl
788	310.5	62.3	81	4	US-10-323-157-12	Sequence 12, Appl	861	270.5	54.3	129	4	US-10-417-426-11	Sequence 11, Appl
789	310.5	62.3	81	5	US-10-680-554-12	Sequence 12, Appl	862	267.5	53.7	77	4	US-10-417-426-13	Sequence 13, Appl
790	310.5	62.3	81	5	US-10-713-567-12	Sequence 12, Appl	863	267.5	53.7	77	5	US-10-680-554-13	Sequence 13, Appl
791	310.5	62.3	81	5	US-10-811-328-12	Sequence 12, Appl	864	267.5	53.7	77	5	US-10-977-113-14	Sequence 14, Appl
792	310.5	62.3	81	5	US-10-912-907-12	Sequence 12, Appl	865	267.5	53.7	77	5	US-10-871-152-24	Sequence 24, Appl
793	310.5	62.3	81	5	US-10-415-724-12	Sequence 12, Appl	866	267.5	53.7	77	6	US-11-073-420-14	Sequence 14, Appl
794	291	58.4	80	4	US-10-467-019-22	Sequence 22, Appl	867	267.5	53.7	96	4	US-10-016-481-11	Sequence 11, Appl
795	291	58.4	80	5	US-10-503-554A-22	Sequence 22, Appl	868	267.5	53.7	96	4	US-10-132-812-12	Sequence 12, Appl
796	291	58.4	81	4	US-10-016-481-6	Sequence 6, Appl	869	267.5	53.7	96	4	US-10-323-157-11	Sequence 11, Appl
797	291	58.4	81	4	US-10-323-157-6	Sequence 6, Appl	870	267.5	53.7	96	5	US-10-713-567-11	Sequence 11, Appl
798	291	58.4	81	4	US-10-417-426-5	Sequence 5, Appl	871	267.5	53.7	96	5	US-10-811-328-11	Sequence 11, Appl
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886	107.5	21.6	173	4	US-10-287-971-30	Sequence 30, Appl
887	107.5	21.6	180	4	US-10-287-971-34	Sequence 34, Appl
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893	107.5	21.6	224	4	US-10-408-765A-335	Sequence 335, Appl
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897	107.5	21.6	344	4	US-10-201-310-3	Sequence 3, Appl
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3	498	100.0	86	US-11-304-129-21	Sequence 21, Appl
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5	498	100.0	86	US-11-384-222-7	Sequence 7, Appl
6	498	100.0	87	US-10-415-724-18	Sequence 18, Appl
7	498	100.0	89	US-10-415-724-15	Sequence 15, Appl
8	498	100.0	105	US-10-415-724-2	Sequence 2, Appl
9	498	100.0	105	US-10-549-241-8	Sequence 8, Appl
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17	497	99.8	105	US-11-371-354-76648	Sequence 76648, A
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114	67	13.5	1620	7	US-11-217-997-42	Sequence 42, Appl	187	62.5	12.6	2380	7	US-11-174-307B-1698	Sequence 1698, Ap
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137	65	13.1	1198	7	US-11-217-997-14	Sequence 14, Appl	210	62	12.4	2556	7	US-11-264-243-6	Sequence 6, Appl
138	65	13.1	1248	7	US-11-174-307B-934	Sequence 934, App	211	62	12.4	2556	7	US-11-071-796A-22	Sequence 22, Appl
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148	64.5	13.0	2214	6	US-10-570-909-25	Sequence 25, Appl	221	61.5	12.3	636	7	US-11-265-762-100	Sequence 100, App
149	64.5	13.0	2214	6	US-10-570-909-52	Sequence 52, Appl	222	61.5	12.3	636	7	US-11-265-762-124	Sequence 124, App
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153	64	12.9	310	7	US-11-090-997-1042	Sequence 1042, Ap	226	61.5	12.3	1676	7	US-11-174-307B-628	Sequence 628, App
154	64	12.9	383	7	US-11-090-997-1040	Sequence 1040, Ap	227	61.5	12.3	1681	7	US-11-174-307B-416	Sequence 416, App
155	64	12.9	1568	7	US-11-174-307B-2546	Sequence 2546, Ap	228	61.5	12.3	1859	7	US-11-174-307B-940	Sequence 940, App
156	64	12.9	1597	7	US-11-174-307B-2100	Sequence 2100, Ap	229	61.5	12.3	2514	7	US-11-174-307B-2064	Sequence 2064, App
157	64	12.9	1883	7	US-11-174-307B-708	Sequence 708, App	230	61.5	12.3	2670	7	US-11-174-307B-1786	Sequence 1786, Ap
158	64	12.9	3334	7	US-11-165-586-20	Sequence 20, Appl	231	61	12.2	569	6	US-10-449-902-46970	Sequence 46970, A
159	63.5	12.8	713	7	US-11-175-714-5	Sequence 5, Appl	232	61	12.2	1144	7	US-11-174-307B-2720	Sequence 2720, Ap
160	63.5	12.8	729	7	US-11-175-714-8	Sequence 8, Appl	233	61	12.2	1170	6	US-10-525-610-38	Sequence 38, Appl
161	63.5	12.8	841	6	US-10-725-037-5	Sequence 5, Appl	234	61	12.2	1170	6	US-10-525-573-482	Sequence 482, Appl
162	63.5	12.8	841	6	US-10-725-488-5	Sequence 5, Appl	235	61	12.2	1255	7	US-11-174-307B-1594	Sequence 1594, Ap
163	63.5	12.8	1176	7	US-11-090-997-1018	Sequence 1018, Ap	236	61	12.2	1345	7	US-11-174-307B-2248	Sequence 2248, Ap
164	63.5	12.8	1353	7	US-11-174-307B-66	Sequence 66, Appl	237	61	12.2	1620	7	US-11-174-307B-1132	Sequence 1132, Ap
165	63.5	12.8	1509	7	US-11-174-307B-1838	Sequence 1838, Ap	238	61	12.2	1673	7	US-11-174-307B-1178	Sequence 1178, Ap
166	63.5	12.8	1510	7	US-11-174-307B-838	Sequence 838, App	239	61	12.2	1736	7	US-11-174-307B-664	Sequence 664, App
167	63.5	12.8	1801	7	US-11-174-307B-2660	Sequence 2660, Ap	240	61	12.2	1865	7	US-11-174-307B-2174	Sequence 2174, Ap
168	63	12.7	250	7	US-11-320-192-11	Sequence 11, Appl	241	61	12.2	1870	7	US-11-174-307B-4998	Sequence 4998, Ap
169	63	12.7	258	6	US-10-643-589-4	Sequence 4, Appl	242	61	12.2	1914	7	US-11-174-307B-20	Sequence 20, Appl
170	63	12.7	1379	7	US-11-174-307B-646	Sequence 646, App	243	61	12.2	1962	7	US-11-174-307B-1748	Sequence 1748, Ap
171	63	12.7	1581	7	US-11-174-307B-906	Sequence 906, App	244	61	12.2	1962	7	US-11-174-307B-2754	Sequence 2754, Ap
172	63	12.7	2344	7	US-11-174-307B-1496	Sequence 1496, Ap	245	61	12.2	2016	7	US-11-174-307B-2188	Sequence 2188, Ap
173	63	12.7	2451	6	US-10-669-920-908	Sequence 908, App	246	61	12.2	2124	7	US-11-174-307B-2768	Sequence 2768, Ap
174	63	12.7	2503	6	US-10-539-228-723	Sequence 723, App	247	61	12.2	2128	7	US-11-174-307B-1384	Sequence 1384, Ap
175	63	12.7	2508	7	US-11-174-307B-1998	Sequence 1998, Ap	248	60.5	12.1	98	6	US-10-449-902-38997	Sequence 38997, A

249	60.5	12.1	484	7	US-11-231-494-56	Sequence 56, Appl	Sequence 56, Appl	323	59	11.8	159	7	US-11-377-336-45	Sequence 45, Appl
250	60.5	12.1	542	7	US-11-054-369A-7	Sequence 7, Appl1	Sequence 7, Appl1	324	59	11.8	209	7	US-11-056-355B-25121	Sequence 25121, A
251	60.5	12.1	723	7	US-11-178-723A-18	Sequence 18, Appl	Sequence 18, Appl	325	59	11.8	254	7	US-11-030-653-18	Sequence 18, Appl
252	60.5	12.1	723	7	US-11-071-796A-17	Sequence 17, Appl	Sequence 17, Appl	326	59	11.8	314	7	US-11-056-355B-88093	Sequence 88093, A
253	60.5	12.1	723	7	US-11-188-417A-18	Sequence 18, Appl	Sequence 18, Appl	327	59	11.8	315	6	US-10-374-780A-2390	Sequence 2390, Ap
254	60.5	12.1	723	7	US-11-231-494-18	Sequence 18, Appl	Sequence 18, Appl	328	59	11.8	315	7	US-11-056-355B-88092	Sequence 88092, A
255	60.5	12.1	864	7	US-11-178-724-27	Sequence 27, Appl	Sequence 27, Appl	329	59	11.8	454	6	US-10-449-902-33449	Sequence 33449, A
256	60.5	12.1	864	7	US-11-188-417A-98	Sequence 98, Appl	Sequence 98, Appl	330	59	11.8	454	6	US-10-449-902-44623	Sequence 44623, A
257	60.5	12.1	864	7	US-11-231-494-34	Sequence 34, Appl	Sequence 34, Appl	331	59	11.8	836	6	US-10-509-131-35	Sequence 35, Appl
258	60.5	12.1	1081	7	US-11-174-307B-308	Sequence 308, Appl	Sequence 308, Appl	332	59	11.8	836	7	US-11-293-697-3700	Sequence 3700, Ap
259	60.5	12.1	1309	7	US-11-174-307B-1610	Sequence 1610, Ap	Sequence 1610, Ap	333	59	11.8	1170	7	US-11-174-307B-1988	Sequence 1988, Ap
260	60.5	12.1	1309	7	US-11-174-307B-1176	Sequence 1176, Ap	Sequence 1176, Ap	334	59	11.8	1245	7	US-11-174-307B-850	Sequence 850, App
261	60.5	12.1	1309	7	US-11-174-307B-934	Sequence 934, App	Sequence 934, App	335	59	11.8	1300	7	US-11-174-307B-112	Sequence 112, App
262	60.5	12.1	1811	7	US-11-174-307B-924	Sequence 924, App	Sequence 924, App	336	59	11.8	1302	7	US-11-174-307B-2152	Sequence 2152, Ap
263	60.5	12.1	1942	7	US-11-174-307B-1096	Sequence 1096, Ap	Sequence 1096, Ap	337	59	11.8	1303	7	US-11-174-307B-430	Sequence 430, App
264	60.5	12.1	2143	7	US-11-174-307B-1284	Sequence 1284, Ap	Sequence 1284, Ap	338	59	11.8	1553	7	US-11-174-307B-380	Sequence 380, App
265	60	12.0	314	7	US-11-293-697-2665	Sequence 2665, Ap	Sequence 2665, Ap	339	59	11.8	1703	7	US-11-174-307B-558	Sequence 558, App
266	60	12.0	399	7	US-11-430-226-9	Sequence 9, Appl1	Sequence 9, Appl1	340	59	11.8	1733	7	US-11-174-307B-814	Sequence 814, App
267	60	12.0	579	7	US-11-371-354-70301	Sequence 70301, A	Sequence 70301, A	341	59	11.8	1744	7	US-11-174-307B-2750	Sequence 2750, Ap
268	60	12.0	623	7	US-11-430-226-2	Sequence 2, Appl1	Sequence 2, Appl1	342	59	11.8	1814	7	US-11-174-307B-1182	Sequence 1182, Ap
269	60	12.0	623	7	US-11-430-226-5	Sequence 5, Appl1	Sequence 5, Appl1	343	59	11.8	1948	7	US-11-174-307B-2702	Sequence 2702, Ap
270	60	12.0	716	7	US-11-371-354-65201	Sequence 65201, A	Sequence 65201, A	344	59	11.8	2047	7	US-11-174-307B-680	Sequence 680, App
271	60	12.0	734	7	US-11-238-282-19	Sequence 19, Appl	Sequence 19, Appl	345	58.5	11.7	84	7	US-11-412-325-214	Sequence 214, App
272	60	12.0	734	7	US-11-300-928-11	Sequence 11, Appl	Sequence 11, Appl	346	58.5	11.7	92	7	US-11-417-317-79	Sequence 79, Appl
273	60	12.0	1050	7	US-11-265-762-114	Sequence 114, App	Sequence 114, App	347	58.5	11.7	92	7	US-11-360-450-79	Sequence 79, Appl
274	60	12.0	1192	7	US-11-174-307B-394	Sequence 394, App	Sequence 394, App	348	58.5	11.7	92	7	US-11-417-953-79	Sequence 79, Appl
275	60	12.0	1192	7	US-11-174-307B-1832	Sequence 1832, Ap	Sequence 1832, Ap	349	58.5	11.7	92	7	US-11-417-954-79	Sequence 79, Appl
276	60	12.0	1263	7	US-11-174-307B-2848	Sequence 2848, Ap	Sequence 2848, Ap	350	58.5	11.7	92	7	US-11-418-410-79	Sequence 79, Appl
277	60	12.0	1290	6	US-11-174-307B-832	Sequence 832, App	Sequence 832, App	351	58.5	11.7	92	7	US-11-418-270-79	Sequence 79, Appl
278	60	12.0	1506	6	US-10-669-920-1142	Sequence 1142, Ap	Sequence 1142, Ap	352	58.5	11.7	139	7	US-11-293-697-3259	Sequence 3259, Ap
279	60	12.0	1506	6	US-10-669-920-1153	Sequence 1153, Ap	Sequence 1153, Ap	353	58.5	11.7	189	7	US-11-412-325-213	Sequence 213, App
280	60	12.0	1713	7	US-11-174-307B-2224	Sequence 2224, Ap	Sequence 2224, Ap	354	58.5	11.7	291	7	US-11-412-325-212	Sequence 212, App
281	60	12.0	2000	6	US-10-533-519-666	Sequence 666, App	Sequence 666, App	355	58.5	11.7	397	7	US-11-412-325-211	Sequence 211, App
282	60	12.0	2117	7	US-11-174-307B-2836	Sequence 2836, Ap	Sequence 2836, Ap	356	58.5	11.7	486	7	US-11-174-307B-82	Sequence 82, Appl
283	60	12.0	2368	7	US-11-174-307B-2844	Sequence 2844, Ap	Sequence 2844, Ap	357	58.5	11.7	584	6	US-10-540-898-468	Sequence 468, App
284	60	12.0	2391	7	US-11-174-307B-1386	Sequence 1386, Ap	Sequence 1386, Ap	358	58.5	11.7	584	6	US-10-540-898-470	Sequence 470, App
285	60	12.0	2608	6	US-10-669-920-1144	Sequence 1144, Ap	Sequence 1144, Ap	359	58.5	11.7	721	7	US-11-175-714-7	Sequence 7, Appl1
286	60	12.0	2608	6	US-10-669-920-1155	Sequence 1155, Ap	Sequence 1155, Ap	360	58.5	11.7	787	7	US-11-412-325-70	Sequence 70, Appl
287	60	12.0	2802	6	US-10-669-920-1150	Sequence 1150, Ap	Sequence 1150, Ap	361	58.5	11.7	863	7	US-11-056-355B-82720	Sequence 82720, A
288	60	12.0	2902	6	US-10-669-920-1161	Sequence 1161, Ap	Sequence 1161, Ap	362	58.5	11.7	863	7	US-11-056-355B-82719	Sequence 82719, A
289	60	12.0	2904	6	US-10-669-920-1146	Sequence 1146, Ap	Sequence 1146, Ap	363	58.5	11.7	893	7	US-11-056-355B-82718	Sequence 82718, A
290	60	12.0	2904	6	US-10-669-920-1148	Sequence 1148, Ap	Sequence 1148, Ap	364	58.5	11.7	893	7	US-11-054-369A-5	Sequence 5, Appl1
291	60	12.0	2904	6	US-10-669-920-1157	Sequence 1157, Ap	Sequence 1157, Ap	365	58.5	11.7	1067	7	US-11-178-724-22	Sequence 22, Appl
292	60	12.0	3259	7	US-11-174-307B-1020	Sequence 1020, Ap	Sequence 1020, Ap	366	58.5	11.7	1238	7	US-11-071-796A-21	Sequence 21, Appl
293	60	12.0	3259	7	US-11-174-307B-2622	Sequence 2622, Ap	Sequence 2622, Ap	367	58.5	11.7	1238	7	US-11-188-417A-22	Sequence 22, Appl
294	60	12.0	3259	7	US-11-371-354-70845	Sequence 70845, A	Sequence 70845, A	368	58.5	11.7	1238	7	US-11-231-494-22	Sequence 22, Appl
295	59.5	11.9	98	7	US-11-377-336-14	Sequence 14, Appl	Sequence 14, Appl	369	58.5	11.7	1238	7	US-11-174-307B-1640	Sequence 1640, Ap
296	59.5	11.9	173	7	US-11-303-169-26	Sequence 26, Appl	Sequence 26, Appl	370	58.5	11.7	1299	7	US-11-174-307B-1066	Sequence 1066, Ap
297	59.5	11.9	173	7	US-10-449-902-50182	Sequence 50182, A	Sequence 50182, A	371	58.5	11.7	1347	7	US-11-174-307B-4560	Sequence 4560, Ap
298	59.5	11.9	394	6	US-11-174-307B-3800	Sequence 3800, Ap	Sequence 3800, Ap	372	58.5	11.7	1368	7	US-11-174-307B-2074	Sequence 2074, Ap
299	59.5	11.9	475	7	US-11-174-307B-3272	Sequence 3272, Ap	Sequence 3272, Ap	373	58.5	11.7	1437	7	US-11-174-307B-2302	Sequence 2302, Ap
300	59.5	11.9	521	7	US-11-174-307B-3272	Sequence 3272, Ap	Sequence 3272, Ap	374	58.5	11.7	1571	7	US-11-174-307B-2074	Sequence 2074, Ap
301	59.5	11.9	729	7	US-11-174-307B-230	Sequence 230, App	Sequence 230, App	375	58.5	11.7	1595	7	US-11-174-307B-4562	Sequence 4562, Ap
302	59.5	11.9	821	7	US-11-371-354-67925	Sequence 67925, A	Sequence 67925, A	376	58.5	11.7	1660	7	US-11-174-307B-2132	Sequence 2132, Ap
303	59.5	11.9	886	6	US-10-533-519-1196	Sequence 1196, Ap	Sequence 1196, Ap	377	58.5	11.7	1661	7	US-11-174-307B-1792	Sequence 1792, Ap
304	59.5	11.9	894	7	US-11-174-307B-1892	Sequence 1892, Ap	Sequence 1892, Ap	378	58.5	11.7	1830	7	US-11-174-307B-1478	Sequence 1478, Ap
305	59.5	11.9	957	7	US-11-174-307B-1976	Sequence 1976, Ap	Sequence 1976, Ap	379	58.5	11.7	1845	7	US-11-174-307B-1980	Sequence 1980, Ap
306	59.5	11.9	972	7	US-11-174-307B-1318	Sequence 1318, Ap	Sequence 1318, Ap	380	58.5	11.7	1965	7	US-11-174-307B-1092	Sequence 1092, Ap
307	59.5	11.9	1038	7	US-11-174-307B-2356	Sequence 2356, Ap	Sequence 2356, Ap	381	58.5	11.7	1994	6	US-10-544-731-2	Sequence 2, Appl1
308	59.5	11.9	1094	7	US-11-174-307B-1356	Sequence 1356, Ap	Sequence 1356, Ap	382	58.5	11.7	2012	7	US-11-174-307B-528	Sequence 528, App
309	59.5	11.9	1132	7	US-11-174-307B-892	Sequence 892, App	Sequence 892, App	383	58.5	11.7	2061	7	US-11-174-307B-1216	Sequence 1216, Ap
310	59.5	11.9	1155	7	US-11-174-307B-1546	Sequence 1546, Ap	Sequence 1546, Ap	384	58.5	11.7	4391	7	US-11-183-325-56	Sequence 56, Appl
311	59.5	11.9	1284	7	US-11-174-307B-1880	Sequence 1880, Ap	Sequence 1880, Ap	385	58.5	11.7	197	7	US-11-293-697-3943	Sequence 3943, Ap
312	59.5	11.9	1432	7	US-11-174-307B-2846	Sequence 2846, Ap	Sequence 2846, Ap	386	58	11.6	299	6	US-10-374-780A-535	Sequence 535, App
313	59.5	11.9	1573	7	US-11-174-307B-770	Sequence 770, App	Sequence 770, App	387	58	11.6	299	6	US-10-374-780A-536	Sequence 536, App
314	59.5	11.9	1860	7	US-11-174-307B-612	Sequence 612, App	Sequence 612, App	388	58	11.6	299	6	US-10-374-780A-537	Sequence 537, App
315	59.5	11.9	1896	7	US-11-174-307B-1376	Sequence 1376, Ap	Sequence 1376, Ap	389	58	11.6	525	7	US-11-056-355B-76541	Sequence 76541, A
316	59.5	11.9	2430	7	US-11-174-307B-96	Sequence 96, Appl	Sequence 96, Appl	390	58	11.6	539	7	US-11-056-355B-76540	Sequence 76540, A
317	59.5	11.9	2499	7	US-11-174-307B-138	Sequence 138, App	Sequence 138, App	391	58	11.6	710	7	US-11-174-307B-4112	Sequence 4112, Ap
318	59.5	11.9	2627	6	US-10-669-920-475	Sequence 475, App	Sequence 475, App	392	58	11.6	1026	7	US-11-174-307B-1834	Sequence 1834, Ap
319	59.5	11.9	2627	7	US-11-174-307B-2676	Sequence 2676, Ap	Sequence 2676, Ap	393	58	11.6	1075	7	US-11-174-307B-3060	Sequence 3060, Ap
320	59.5	11.9	2841	7	US-11-174-307B-2530	Sequence 2530, Ap	Sequence 2530, Ap	394	58	11.6	1103	7	US-11-174-307B-2450	Sequence 2450, Ap
321	59.5	11.9	4465	6	US-10-669-920-477	Sequence 477, App	Sequence 477, App	395	58	11.6				
322	59.5	11.9	5738	6	US-10-505-928-150	Sequence 150, App	Sequence 150, App							

396	58	11.6	1123	7	US-11-330-403-3085	Sequence 3085, Ap	472	57	11.4	35	7	US-11-155-989-122	Sequence 122, App
397	58	11.6	1217	6	US-10-537-102-28	Sequence 28, Appl	473	57	11.4	115	7	US-11-174-307B-5376	Sequence 5376, Ap
398	58	11.6	1259	7	US-11-174-307B-5038	Sequence 5038, Ap	474	57	11.4	143	6	US-10-525-610-44	Sequence 44, Appl
399	58	11.6	1271	7	US-11-174-307B-2618	Sequence 2618, Ap	475	57	11.4	468	7	US-11-371-354-62463	Sequence 62463, A
400	58	11.6	1272	7	US-11-174-307B-422	Sequence 422, App	476	57	11.4	497	7	US-11-265-762-116	Sequence 116, App
401	58	11.6	1375	7	US-11-174-307B-622	Sequence 622, App	477	57	11.4	523	7	US-11-392-436-14	Sequence 14, Appl
402	58	11.6	1431	7	US-11-174-307B-132	Sequence 132, App	478	57	11.4	598	6	US-10-540-898-465	Sequence 465, App
403	58	11.6	1431	7	US-11-174-307B-2332	Sequence 2332, Ap	479	57	11.4	642	6	US-10-562-469-2	Sequence 2, Appl
404	58	11.6	1489	7	US-11-174-307B-2422	Sequence 2422, Ap	480	57	11.4	655	6	US-10-505-928-843	Sequence 843, App
405	58	11.6	1490	7	US-11-174-307B-2534	Sequence 2534, Ap	480	57	11.4	655	6	US-10-505-928-843	Sequence 843, App
406	58	11.6	1491	7	US-11-174-307B-382	Sequence 382, App	483	57	11.4	722	7	US-11-371-354-69529	Sequence 69529, A
407	58	11.6	1492	7	US-11-174-307B-2094	Sequence 2094, Ap	484	57	11.4	737	7	US-11-296-092-15	Sequence 15, Appl
408	58	11.6	1575	7	US-11-174-307B-2648	Sequence 2648, Ap	488	57	11.4	737	7	US-11-296-155-15	Sequence 15, Appl
409	58	11.6	1577	7	US-11-174-307B-396	Sequence 396, App	489	57	11.4	850	7	US-11-174-307B-534	Sequence 534, App
410	58	11.6	1638	7	US-11-174-307B-660	Sequence 660, App	489	57	11.4	856	7	US-11-174-307B-5482	Sequence 5482, Ap
411	58	11.6	1656	7	US-11-174-307B-3004	Sequence 3004, Ap	490	57	11.4	917	7	US-11-419-672-4	Sequence 4, Appl
412	58	11.6	1689	7	US-11-174-307B-1196	Sequence 1196, Ap	492	57	11.4	984	7	US-11-174-307B-1592	Sequence 1592, Ap
413	58	11.6	1745	7	US-11-174-307B-960	Sequence 960, App	493	57	11.4	1001	7	US-11-174-307B-1460	Sequence 1460, Ap
414	58	11.6	1773	7	US-11-174-307B-1710	Sequence 1710, Ap	494	57	11.4	1027	7	US-11-174-307B-4296	Sequence 4296, Ap
415	58	11.6	1953	7	US-11-264-243-16	Sequence 16, Appl	495	57	11.4	1131	7	US-11-174-307B-1604	Sequence 1604, Ap
416	58	11.6	2088	7	US-11-174-307B-4996	Sequence 4996, Ap	496	57	11.4	1215	7	US-11-174-307B-2800	Sequence 2800, Ap
417	58	11.6	2628	7	US-11-174-307B-2692	Sequence 2692, Ap	497	57	11.4	1242	7	US-11-174-307B-1678	Sequence 1678, Ap
420	57.5	11.5	98	7	US-11-377-336-13	Sequence 13, Appl	498	57	11.4	1247	7	US-11-174-307B-1848	Sequence 1848, Ap
421	57.5	11.5	173	6	US-11-303-169-43	Sequence 43, Appl	499	57	11.4	1310	7	US-11-174-307B-1186	Sequence 1186, Ap
422	57.5	11.5	225	6	US-10-953-349-2321	Sequence 2321, Ap	500	57	11.4	1365	7	US-11-174-307B-2290	Sequence 2290, Ap
423	57.5	11.5	230	6	US-10-953-349-2320	Sequence 2320, Ap	501	57	11.4	1396	7	US-11-174-307B-466	Sequence 466, App
424	57.5	11.5	237	6	US-10-953-349-2319	Sequence 2319, Ap	502	57	11.4	1418	7	US-11-174-307B-950	Sequence 950, App
425	57.5	11.5	327	7	US-11-401-340-6	Sequence 6, Appl	503	57	11.4	1432	7	US-11-174-307B-1100	Sequence 1100, Ap
426	57.5	11.5	328	7	US-11-056-355B-9512	Sequence 9512, Ap	504	57	11.4	1444	7	US-11-174-307B-2626	Sequence 2626, Ap
427	57.5	11.5	368	7	US-11-330-403-1357	Sequence 1357, Ap	505	57	11.4	1445	7	US-11-174-307B-1452	Sequence 1452, Ap
428	57.5	11.5	368	7	US-11-330-403-12992	Sequence 12992, A	506	57	11.4	1486	7	US-11-174-307B-2522	Sequence 2522, Ap
429	57.5	11.5	383	7	US-11-330-403-13153	Sequence 13153, A	507	57	11.4	1533	7	US-11-174-307B-78	Sequence 78, Appl
430	57.5	11.5	420	7	US-11-056-355B-9511	Sequence 9511, Ap	508	57	11.4	1555	7	US-11-174-307B-1366	Sequence 1366, Ap
431	57.5	11.5	442	7	US-11-366-486-939	Sequence 939, App	509	57	11.4	1596	7	US-11-174-307B-792	Sequence 792, App
432	57.5	11.5	493	7	US-11-056-355B-9510	Sequence 9510, Ap	510	57	11.4	1709	7	US-11-174-307B-3210	Sequence 3210, Ap
433	57.5	11.5	594	7	US-11-371-354-62585	Sequence 62585, A	511	57	11.4	1737	7	US-11-174-307B-674	Sequence 674, App
434	57.5	11.5	678	7	US-11-174-307B-3924	Sequence 3924, A	512	57	11.4	1750	7	US-11-174-307B-570	Sequence 570, App
436	57.5	11.5	745	7	US-11-293-697-3826	Sequence 3826, Ap	513	57	11.4	1751	7	US-11-174-307B-2426	Sequence 2426, Ap
437	57.5	11.5	767	7	US-11-401-340-49	Sequence 49, Appl	514	57	11.4	1764	7	US-11-174-307B-2034	Sequence 2034, Ap
438	57.5	11.5	783	6	US-10-449-902-37539	Sequence 37539, A	515	57	11.4	1867	7	US-11-174-307B-406	Sequence 406, App
439	57.5	11.5	783	6	US-10-449-902-54417	Sequence 54417, A	516	57	11.4	1867	7	US-11-174-307B-2604	Sequence 2604, Ap
440	57.5	11.5	810	6	US-10-781-841-34	Sequence 34, App	517	57	11.4	1868	7	US-11-174-307B-2266	Sequence 2266, Ap
441	57.5	11.5	1070	7	US-11-174-307B-2300	Sequence 2300, Ap	518	57	11.4	1872	7	US-11-174-307B-1664	Sequence 1664, Ap
442	57.5	11.5	1092	7	US-11-174-307B-912	Sequence 912, App	519	57	11.4	1945	7	US-11-174-307B-1972	Sequence 1972, Ap
443	57.5	11.5	1223	7	US-11-174-307B-2472	Sequence 2472, Ap	520	57	11.4	2017	7	US-11-174-307B-2682	Sequence 2682, Ap
444	57.5	11.5	1232	7	US-11-174-307B-2840	Sequence 2840, Ap	521	57	11.4	2045	7	US-11-174-307B-2726	Sequence 2726, Ap
445	57.5	11.5	1356	6	US-10-508-580-18	Sequence 18, Appl	522	57	11.4	2072	7	US-11-174-307B-1184	Sequence 1184, Ap
446	57.5	11.5	1356	7	US-11-365-989-144	Sequence 144, App	523	57	11.4	2079	7	US-11-174-307B-2126	Sequence 2126, Ap
447	57.5	11.5	1356	7	US-11-401-340-4	Sequence 4, Appl	524	57	11.4	2079	7	US-11-174-307B-2408	Sequence 2408, Ap
448	57.5	11.5	1356	7	US-11-404-555-2	Sequence 2, Appl	525	57	11.4	2265	6	US-10-562-469-11	Sequence 11, Appl
449	57.5	11.5	1396	7	US-11-174-307B-1102	Sequence 1102, Ap	526	57	11.4	2355	6	US-10-530-187-272	Sequence 272, App
450	57.5	11.5	1504	7	US-11-174-307B-932	Sequence 932, App	527	57	11.4	2355	6	US-10-700-439-135	Sequence 135, App
451	57.5	11.5	1506	7	US-11-174-307B-1992	Sequence 1992, Ap	528	57	11.4	2355	6	US-11-105-233-158	Sequence 158, App
452	57.5	11.5	1530	7	US-11-174-307B-1862	Sequence 1862, Ap	529	57	11.4	2386	6	US-10-530-187-271	Sequence 271, App
453	57.5	11.5	1709	7	US-11-174-307B-2970	Sequence 2970, Ap	530	57	11.4	2472	7	US-11-174-307B-1716	Sequence 1716, Ap
454	57.5	11.5	1754	7	US-11-174-307B-2600	Sequence 2600, Ap	531	57	11.4	2643	7	US-11-174-307B-1864	Sequence 1864, Ap
455	57.5	11.5	1758	7	US-11-174-307B-2310	Sequence 2310, Ap	532	57	11.4	3230	7	US-11-174-307B-2262	Sequence 2262, Ap
456	57.5	11.5	1765	7	US-11-174-307B-2282	Sequence 2282, Ap	533	57	11.4	3331	7	US-11-174-307B-1574	Sequence 1574, Ap
457	57.5	11.5	1783	7	US-11-174-307B-902	Sequence 902, App	534	57	11.4	3682	7	US-11-174-307B-2486	Sequence 2486, Ap
458	57.5	11.5	1821	7	US-11-174-307B-2108	Sequence 2108, Ap	535	57	11.4	4393	6	US-10-525-573-366	Sequence 366, App
459	57.5	11.5	1915	7	US-11-174-307B-1702	Sequence 1702, Ap	536	57	11.4	4393	7	US-11-450-360-1	Sequence 1, Appl
460	57.5	11.5	2000	6	US-10-533-519-1676	Sequence 1676, Ap	537	56.5	11.3	80	7	US-11-412-325-205	Sequence 205, App
461	57.5	11.5	2026	6	US-10-505-928-831	Sequence 831, App	538	56.5	11.3	89	6	US-10-521-518-20	Sequence 20, Appl
462	57.5	11.5	2052	7	US-11-174-307B-652	Sequence 652, App	539	56.5	11.3	139	6	US-10-449-902-30417	Sequence 30417, A
463	57.5	11.5	2119	7	US-11-174-307B-4798	Sequence 4798, Ap	540	56.5	11.3	287	6	US-10-953-349-7533	Sequence 7533, Ap
464	57.5	11.5	2137	7	US-11-174-307B-4852	Sequence 4852, Ap	541	56.5	11.3	294	6	US-10-953-349-7532	Sequence 7532, Ap
465	57.5	11.5	2240	6	US-10-544-731-4	Sequence 4, Appl	542	56.5	11.3	316	6	US-10-953-349-7531	Sequence 7531, Ap
466	57.5	11.5	2258	6	US-10-544-731-3	Sequence 3, Appl	543	56.5	11.3	336	6	US-10-449-902-33585	Sequence 33585, A
467	57.5	11.5	2264	6	US-10-544-731-5	Sequence 5, Appl	544	56.5	11.3	353	7	US-11-371-354-12268	Sequence 12268, A
468	57.5	11.5	2874	7	US-11-174-307B-1990	Sequence 1990, Ap	545	56.5	11.3	353	7	US-11-371-354-55201	Sequence 55201, A
469	57.5	11.5	2871	6	US-10-574-398-390	Sequence 390, App	546	56.5	11.3	353	7	US-11-371-354-76042	Sequence 76042, A
470	57.5	11.5	3399	6	US-10-547-530-47	Sequence 47, Appl	547	56.5	11.3	401	7	US-11-303-169-4	Sequence 4, Appl
471	57.5	11.5	5109	7	US-11-174-307B-1520	Sequence 1520, Ap	548	56.5	11.3	419	7	US-11-366-965-13	Sequence 13, Appl

549	56.5	11.3	439	7	US-11-056-355B-6832	Sequence 6832, Ap	622	56	11.2	540	7	US-11-447-913-30	Sequence 30, Appl
550	56.5	11.3	462	7	US-11-056-355B-6831	Sequence 6831, Ap	623	56	11.2	565	6	US-10-669-920-663	Sequence 663, App
551	56.5	11.3	463	7	US-11-174-307B-80	Sequence 80, Appl	624	56	11.2	612	6	US-10-449-902-41558	Sequence 41558, A
552	56.5	11.3	480	7	US-11-056-355B-6830	Sequence 6830, Ap	625	56	11.2	657	7	US-11-174-307B-512	Sequence 512, App
553	56.5	11.3	540	7	US-11-392-436-18	Sequence 18, Appl	626	56	11.2	746	6	US-10-669-920-661	Sequence 661, App
554	56.5	11.3	659	7	US-11-174-307B-614	Sequence 614, App	627	56	11.2	746	6	US-10-669-920-665	Sequence 665, App
555	56.5	11.3	830	7	US-11-443-904-33	Sequence 33, Appl	628	56	11.2	746	7	US-11-371-354-12063	Sequence 12063, A
556	56.5	11.3	876	7	US-11-174-307B-144	Sequence 144, App	629	56	11.2	746	7	US-11-371-354-72055	Sequence 72055, A
557	56.5	11.3	909	7	US-11-174-307B-1506	Sequence 1506, Ap	630	56	11.2	746	7	US-11-371-354-75761	Sequence 75761, A
558	56.5	11.3	910	7	US-11-174-307B-2232	Sequence 2232, Ap	631	56	11.2	754	7	US-11-056-355B-81272	Sequence 81272, A
559	56.5	11.3	923	7	US-11-174-307B-4314	Sequence 4314, Ap	632	56	11.2	826	7	US-11-056-355B-81271	Sequence 81271, A
560	56.5	11.3	978	7	US-11-174-307B-120	Sequence 120, App	633	56	11.2	849	7	US-11-056-355B-81270	Sequence 81270, A
561	56.5	11.3	1042	7	US-11-174-307B-356	Sequence 356, App	634	56	11.2	929	7	US-11-174-307B-3988	Sequence 3988, Ap
562	56.5	11.3	1052	7	US-11-174-307B-2500	Sequence 2500, Ap	635	56	11.2	945	7	US-11-174-307B-720	Sequence 720, App
563	56.5	11.3	1042	7	US-11-174-307B-1750	Sequence 1750, Ap	636	56	11.2	1050	7	US-11-174-307B-1950	Sequence 1950, Ap
564	56.5	11.3	1068	7	US-11-054-369A-1	Sequence 1, Appl	637	56	11.2	1059	7	US-11-174-307B-2204	Sequence 2204, App
565	56.5	11.3	1093	6	US-10-449-902-41338	Sequence 41338, A	638	56	11.2	1135	7	US-11-174-307B-880	Sequence 880, App
566	56.5	11.3	1136	7	US-11-174-307B-2400	Sequence 2400, Ap	639	56	11.2	1144	7	US-11-174-307B-506	Sequence 506, App
567	56.5	11.3	1150	7	US-11-056-355B-86061	Sequence 86061, A	640	56	11.2	1194	7	US-11-045-540-2	Sequence 2, Appl
568	56.5	11.3	1170	7	US-11-056-355B-86060	Sequence 86060, A	641	56	11.2	1205	7	US-11-045-540-3	Sequence 3, Appl
569	56.5	11.3	1218	6	US-10-833-833-121	Sequence 121, App	642	56	11.2	1205	7	US-11-371-354-69641	Sequence 69641, A
570	56.5	11.3	1301	7	US-11-174-307B-2586	Sequence 2586, Ap	643	56	11.2	1220	7	US-11-174-307B-1542	Sequence 1542, Ap
571	56.5	11.3	1305	7	US-11-174-307B-2140	Sequence 2140, Ap	644	56	11.2	1237	7	US-11-045-540-4	Sequence 4, Appl
572	56.5	11.3	1337	7	US-11-174-307B-2460	Sequence 2460, Ap	645	56	11.2	1248	7	US-11-045-540-5	Sequence 5, Appl
573	56.5	11.3	1377	7	US-11-174-307B-518	Sequence 518, App	646	56	11.2	1285	7	US-11-174-307B-1124	Sequence 1124, Ap
574	56.5	11.3	1408	7	US-11-174-307B-2196	Sequence 2196, Ap	647	56	11.2	1299	7	US-11-174-307B-1524	Sequence 1524, Ap
575	56.5	11.3	1463	7	US-11-436-904-16	Sequence 16, Appl	648	56	11.2	1403	7	US-11-174-307B-738	Sequence 738, App
576	56.5	11.3	1478	7	US-11-174-307B-710	Sequence 710, App	649	56	11.2	1419	7	US-11-001-346-101	Sequence 101, App
577	56.5	11.3	1518	7	US-11-436-904-2	Sequence 2, Appl	650	56	11.2	1459	7	US-11-174-307B-1332	Sequence 1332, Ap
578	56.5	11.3	1518	7	US-11-436-904-18	Sequence 18, Appl	651	56	11.2	1482	7	US-11-174-307B-880	Sequence 880, App
579	56.5	11.3	1572	7	US-11-436-904-22	Sequence 22, Appl	652	56	11.2	1495	7	US-11-174-307B-1656	Sequence 1656, Ap
580	56.5	11.3	1573	7	US-11-436-904-20	Sequence 20, Appl	653	56	11.2	1511	7	US-11-174-307B-1120	Sequence 1120, Ap
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582	56.5	11.3	1617	7	US-11-174-307B-2448	Sequence 2448, Ap	655	56	11.2	1518	7	US-11-174-307B-1926	Sequence 1926, Ap
583	56.5	11.3	1660	7	US-11-174-307B-2908	Sequence 2908, Ap	656	56	11.2	1645	6	US-10-505-928-582	Sequence 582, App
584	56.5	11.3	1685	7	US-11-174-307B-598	Sequence 598, App	657	56	11.2	1710	7	US-11-174-307B-1588	Sequence 1588, Ap
585	56.5	11.3	1696	7	US-11-174-307B-3178	Sequence 3178, Ap	658	56	11.2	1721	7	US-11-174-307B-968	Sequence 968, App
586	56.5	11.3	1779	7	US-11-174-307B-1438	Sequence 1438, Ap	659	56	11.2	1761	7	US-11-174-307B-3708	Sequence 3708, Ap
587	56.5	11.3	1782	7	US-11-174-307B-1652	Sequence 1652, Ap	660	56	11.2	1768	7	US-11-174-307B-1220	Sequence 1220, Ap
588	56.5	11.3	1796	7	US-11-174-307B-910	Sequence 910, App	661	56	11.2	1884	7	US-11-174-307B-2588	Sequence 2588, Ap
589	56.5	11.3	1814	7	US-11-174-307B-1302	Sequence 1302, Ap	662	56	11.2	1919	7	US-11-174-307B-978	Sequence 978, App
590	56.5	11.3	1865	7	US-11-174-307B-1078	Sequence 1078, Ap	663	56	11.2	1942	7	US-11-174-307B-1296	Sequence 1296, Ap
591	56.5	11.3	1918	7	US-11-174-307B-692	Sequence 692, App	664	56	11.2	1957	7	US-11-174-307B-2192	Sequence 2192, Ap
592	56.5	11.3	1933	7	US-11-174-307B-2226	Sequence 2226, Ap	665	56	11.2	1962	7	US-11-174-307B-1446	Sequence 1446, Ap
593	56.5	11.3	2250	7	US-11-174-307B-1394	Sequence 1394, Ap	666	56	11.2	2062	7	US-11-174-307B-1454	Sequence 1454, Ap
594	56.5	11.3	2440	7	US-11-174-307B-1294	Sequence 1294, Ap	667	56	11.2	2077	7	US-11-174-307B-2340	Sequence 2340, Ap
595	56.5	11.3	2773	7	US-11-174-307B-1466	Sequence 1466, Ap	668	56	11.2	2101	7	US-11-174-307B-778	Sequence 778, App
596	56.5	11.3	2791	7	US-11-174-307B-2826	Sequence 2826, Ap	669	56	11.2	2110	7	US-11-174-307B-2010	Sequence 2010, Ap
597	56	11.2	16	7	US-11-304-129-11	Sequence 11, Appl	670	56	11.2	2415	7	US-11-174-307B-1564	Sequence 1564, Ap
598	56	11.2	64	7	US-11-350-321-8	Sequence 8, Appl	671	56	11.2	2568	7	US-11-174-307B-90	Sequence 90, Appl
599	56	11.2	65	7	US-11-377-883-12	Sequence 12, Appl	672	56	11.2	2782	7	US-11-174-307B-722	Sequence 722, App
600	56	11.2	65	7	US-11-282-519-8	Sequence 8, Appl	673	55.5	11.1	143	7	US-11-344-932-482	Sequence 482, App
601	56	11.2	76	6	US-10-449-902-39281	Sequence 39281, A	674	55.5	11.1	159	7	US-11-377-336-42	Sequence 42, Appl
602	56	11.2	124	7	US-11-056-355B-17338	Sequence 17338, A	675	55.5	11.1	173	7	US-11-303-169-31	Sequence 31, Appl
603	56	11.2	132	7	US-11-056-355B-85497	Sequence 85497, A	676	55.5	11.1	197	6	US-10-953-349-28555	Sequence 28555, A
604	56	11.2	132	7	US-11-056-355B-86353	Sequence 86353, A	677	55.5	11.1	264	7	US-11-056-355B-89430	Sequence 89430, A
605	56	11.2	156	7	US-11-404-843-122	Sequence 122, App	678	55.5	11.1	310	6	US-10-570-903-7	Sequence 7, Appl
606	56	11.2	163	7	US-11-056-355B-85496	Sequence 85496, A	679	55.5	11.1	323	7	US-11-330-403-4957	Sequence 4957, Ap
607	56	11.2	163	7	US-11-056-355B-96352	Sequence 96352, A	680	55.5	11.1	332	7	US-11-330-403-4960	Sequence 4960, Ap
608	56	11.2	208	7	US-11-056-355B-64492	Sequence 64492, A	681	55.5	11.1	332	7	US-11-330-403-4960	Sequence 4960, Ap
609	56	11.2	264	6	US-10-374-780A-58	Sequence 58, Appl	682	55.5	11.1	334	7	US-11-090-997-146	Sequence 146, App
610	56	11.2	264	7	US-11-056-355B-96351	Sequence 96351, A	683	55.5	11.1	349	7	US-11-330-403-4791	Sequence 4791, Ap
611	56	11.2	265	7	US-11-056-355B-106290	Sequence 106290, A	684	55.5	11.1	376	7	US-11-330-403-4894	Sequence 4894, Ap
612	56	11.2	285	7	US-11-056-355B-117529	Sequence 117529, A	685	55.5	11.1	376	7	US-11-330-403-4997	Sequence 4997, Ap
613	56	11.2	270	7	US-11-056-355B-106289	Sequence 106289, A	686	55.5	11.1	376	7	US-11-330-403-4911	Sequence 4911, Ap
614	56	11.2	270	7	US-11-056-355B-117528	Sequence 117528, A	687	55.5	11.1	376	7	US-11-330-403-4934	Sequence 4934, Ap
615	56	11.2	381	7	US-11-197-713-255	Sequence 255, App	688	55.5	11.1	376	7	US-11-330-403-4955	Sequence 4955, Ap
616	56	11.2	381	7	US-11-371-354-56279	Sequence 56279, A	689	55.5	11.1	376	7	US-11-330-403-4980	Sequence 4980, Ap
617	56	11.2	388	7	US-11-119-526A-41	Sequence 41, Appl	690	55.5	11.1	382	7	US-11-330-403-14854	Sequence 14854, A
618	56	11.2	408	7	US-11-119-526A-6	Sequence 6, Appl	691	55.5	11.1	382	7	US-10-570-903-118	Sequence 118, App
619	56	11.2	465	7	US-11-392-436-6	Sequence 6, Appl	692	55.5	11.1	385	6	US-10-449-902-38615	Sequence 38615, A
620	56	11.2	490	6	US-10-449-902-38615	Sequence 38615, A	693	55.5	11.1	393	7	US-11-330-403-14311	Sequence 14311, A
621	56	11.2	540	7	US-11-447-913-1	Sequence 1, Appl	694	55.5	11.1				

695	55.5	11.1	393	7	US-11-330-403-14331	Sequence 14331, A	768	55	11.0	422	6	US-10-449-902-40144	Sequence 40144, A
696	55.5	11.1	393	7	US-11-330-403-14861	Sequence 14861, A	769	55	11.0	484	7	US-11-056-355B-91092	Sequence 91092, A
697	55.5	11.1	438	7	US-11-174-307B-1434	Sequence 1434, Ap	770	55	11.0	484	7	US-11-056-355B-94848	Sequence 94848, A
698	55.5	11.1	439	7	US-11-056-355B-6544	Sequence 6544, Ap	771	55	11.0	485	7	US-11-056-355B-91091	Sequence 91091, A
699	55.5	11.1	466	6	US-10-449-902-40474	Sequence 40474, A	772	55	11.0	485	7	US-11-056-355B-94847	Sequence 94847, A
700	55.5	11.1	466	6	US-10-449-902-51623	Sequence 51623, A	773	55	11.0	486	7	US-11-056-355B-91090	Sequence 91090, A
701	55.5	11.1	466	6	US-10-449-902-51750	Sequence 51750, A	774	55	11.0	486	7	US-11-056-355B-94846	Sequence 94846, A
702	55.5	11.1	470	7	US-11-056-355B-6543	Sequence 6543, Ap	775	55	11.0	530	7	US-11-399-210-111	Sequence 111, App
703	55.5	11.1	505	7	US-11-056-355B-6542	Sequence 6542, Ap	776	55	11.0	530	7	US-11-399-210-112	Sequence 112, App
704	55.5	11.1	526	7	US-11-024-544A-12	Sequence 12, Appl	777	55	11.0	567	7	US-11-312-958-2	Sequence 2, Appl
705	55.5	11.1	526	7	US-11-024-544A-14	Sequence 14, Appl	778	55	11.0	587	7	US-11-030-653-32	Sequence 32, Appl
706	55.5	11.1	526	7	US-11-190-750-80	Sequence 80, Appl	779	55	11.0	587	7	US-11-056-355B-43888	Sequence 43888, A
707	55.5	11.1	526	7	US-11-190-750-84	Sequence 84, Appl	780	55	11.0	618	7	US-11-178-724-19	Sequence 19, Appl
708	55.5	11.1	526	7	US-11-264-784-82	Sequence 82, Appl	781	55	11.0	618	7	US-11-071-796A-18	Sequence 18, Appl
709	55.5	11.1	526	7	US-11-264-737-123	Sequence 123, App	782	55	11.0	618	7	US-11-188-417A-19	Sequence 19, Appl
710	55.5	11.1	526	7	US-11-265-761-95	Sequence 95, Appl	783	55	11.0	618	7	US-11-231-494-19	Sequence 19, Appl
711	55.5	11.1	608	6	US-10-449-902-37616	Sequence 37616, A	784	55	11.0	627	7	US-11-174-307B-522	Sequence 522, App
712	55.5	11.1	713	7	US-11-330-403-3443	Sequence 3443, Ap	785	55	11.0	619	7	US-11-317-847A-205	Sequence 205, App
713	55.5	11.1	746	6	US-10-526-572-30	Sequence 30, Appl	786	55	11.0	627	7	US-11-317-847A-211	Sequence 211, App
714	55.5	11.1	839	7	US-11-174-307B-2580	Sequence 2580, Ap	787	55	11.0	627	7	US-11-317-847A-217	Sequence 217, App
715	55.5	11.1	1005	6	US-10-449-902-53787	Sequence 53787, A	788	55	11.0	644	7	US-11-317-847A-199	Sequence 199, App
716	55.5	11.1	1005	7	US-11-174-307B-1158	Sequence 1158, Ap	789	55	11.0	672	7	US-11-317-847A-140	Sequence 140, App
717	55.5	11.1	1015	7	US-11-174-307B-330	Sequence 330, App	790	55	11.0	712	7	US-11-259-133-16	Sequence 16, Appl
718	55.5	11.1	1039	7	US-11-330-403-11260	Sequence 11260, A	791	55	11.0	726	7	US-11-317-847A-142	Sequence 142, App
719	55.5	11.1	1066	7	US-11-174-307B-624	Sequence 624, App	792	55	11.0	754	6	US-10-449-902-41136	Sequence 41136, A
720	55.5	11.1	1066	7	US-11-174-307B-1402	Sequence 1402, Ap	793	55	11.0	794	7	US-11-056-355B-45043	Sequence 45043, A
721	55.5	11.1	1098	7	US-11-174-307B-2414	Sequence 2414, Ap	794	55	11.0	794	7	US-11-056-355B-45791	Sequence 45791, A
722	55.5	11.1	1098	7	US-11-174-307B-400	Sequence 400, App	795	55	11.0	794	7	US-11-056-355B-46386	Sequence 46386, A
723	55.5	11.1	1161	7	US-11-330-403-10835	Sequence 10835, A	796	55	11.0	795	7	US-11-174-307B-1856	Sequence 1856, Ap
724	55.5	11.1	1177	7	US-11-330-403-1044	Sequence 1044, Ap	797	55	11.0	853	7	US-11-056-355B-45042	Sequence 45042, A
725	55.5	11.1	1177	7	US-11-330-403-1050	Sequence 1050, Ap	798	55	11.0	853	7	US-11-056-355B-45790	Sequence 45790, A
726	55.5	11.1	1178	7	US-11-330-403-996	Sequence 996, App	799	55	11.0	853	7	US-11-056-355B-46385	Sequence 46385, A
727	55.5	11.1	1178	7	US-11-330-403-1011	Sequence 1011, App	800	55	11.0	856	7	US-11-056-355B-45041	Sequence 45041, A
728	55.5	11.1	1178	7	US-11-330-403-1030	Sequence 1030, Ap	801	55	11.0	856	7	US-11-056-355B-45789	Sequence 45789, A
729	55.5	11.1	1178	7	US-11-330-403-1032	Sequence 1032, Ap	802	55	11.0	856	7	US-11-056-355B-46384	Sequence 46384, A
730	55.5	11.1	1178	7	US-11-330-403-1246	Sequence 1246, Ap	803	55	11.0	961	7	US-11-371-354-65039	Sequence 65039, A
731	55.5	11.1	1187	7	US-11-174-307B-1142	Sequence 1142, Ap	804	55	11.0	987	7	US-11-174-307B-236	Sequence 236, App
732	55.5	11.1	1212	7	US-11-174-307B-1696	Sequence 1696, Ap	805	55	11.0	1017	7	US-11-174-307B-3140	Sequence 3140, Ap
733	55.5	11.1	1242	7	US-11-174-307B-1968	Sequence 1968, Ap	806	55	11.0	1036	7	US-11-299-731-21	Sequence 21, Appl
734	55.5	11.1	1307	7	US-11-174-307B-4164	Sequence 4164, Ap	807	55	11.0	1036	7	US-11-399-210-113	Sequence 113, App
735	55.5	11.1	1365	7	US-11-174-307B-2318	Sequence 2318, Ap	808	55	11.0	1038	7	US-11-399-210-114	Sequence 114, App
736	55.5	11.1	1446	7	US-11-174-307B-662	Sequence 662, App	809	55	11.0	1038	7	US-11-399-210-115	Sequence 115, App
737	55.5	11.1	1463	7	US-11-174-307B-1308	Sequence 1308, Ap	810	55	11.0	1047	7	US-11-174-307B-1534	Sequence 1534, Ap
738	55.5	11.1	1481	7	US-11-174-307B-1162	Sequence 1162, Ap	811	55	11.0	1069	7	US-11-174-307B-1228	Sequence 1228, Ap
739	55.5	11.1	1487	7	US-11-174-307B-2972	Sequence 2972, Ap	812	55	11.0	1073	7	US-11-174-307B-1312	Sequence 1312, Ap
740	55.5	11.1	1516	7	US-11-174-307B-4074	Sequence 4074, Ap	813	55	11.0	1117	7	US-11-174-307B-1458	Sequence 1458, Ap
741	55.5	11.1	1698	7	US-11-174-307B-718	Sequence 718, App	815	55	11.0	1130	7	US-11-312-958-52	Sequence 52, Appl
742	55.5	11.1	1713	7	US-11-174-307B-3720	Sequence 3720, Ap	816	55	11.0	1130	7	US-11-429-599-36	Sequence 36, Appl
743	55.5	11.1	1741	7	US-11-174-307B-726	Sequence 726, App	817	55	11.0	1143	7	US-11-174-307B-492	Sequence 492, App
744	55.5	11.1	1775	7	US-11-174-307B-526	Sequence 526, App	818	55	11.0	1208	7	US-11-090-997-6	Sequence 6, Appl
745	55.5	11.1	1784	7	US-11-174-307B-2856	Sequence 2856, Ap	819	55	11.0	1263	7	US-11-174-307B-1290	Sequence 1290, Ap
746	55.5	11.1	1809	7	US-11-174-307B-2054	Sequence 2054, Ap	820	55	11.0	1268	7	US-11-174-307B-744	Sequence 744, App
747	55.5	11.1	1832	7	US-11-174-307B-2350	Sequence 2350, Ap	821	55	11.0	1287	7	US-11-343-271-35	Sequence 35, Appl
748	55.5	11.1	1847	7	US-11-174-307B-1242	Sequence 1242, Ap	822	55	11.0	1296	7	US-11-174-307B-750	Sequence 750, App
749	55.5	11.1	1951	7	US-11-174-307B-3118	Sequence 3118, Ap	823	55	11.0	1322	7	US-11-174-307B-592	Sequence 592, App
750	55.5	11.1	1962	7	US-11-174-307B-998	Sequence 998, App	824	55	11.0	1333	7	US-11-174-307B-1258	Sequence 1258, Ap
751	55.5	11.1	1973	7	US-11-174-307B-1378	Sequence 1378, Ap	825	55	11.0	1348	7	US-11-174-307B-2452	Sequence 2452, Ap
752	55.5	11.1	2325	7	US-11-174-307B-5472	Sequence 5472, Ap	826	55	11.0	1359	7	US-11-174-307B-586	Sequence 586, Ap
753	55.5	11.1	3658	7	US-11-174-307B-1668	Sequence 1668, Ap	827	55	11.0	1424	7	US-11-174-307B-504	Sequence 504, App
754	55.5	11.1	3723	7	US-11-174-307B-2802	Sequence 2802, Ap	828	55	11.0	1424	7	US-11-174-307B-2542	Sequence 2542, Ap
755	55	11.0	52	7	US-11-281-245A-98	Sequence 98, Appl	829	55	11.0	1431	7	US-11-174-307B-1112	Sequence 1112, Ap
756	55	11.0	52	7	US-11-281-256-205	Sequence 205, App	830	55	11.0	1431	7	US-11-352-664-2	Sequence 2, Appl
757	55	11.0	82	6	US-10-953-349-36789	Sequence 36789, A	831	55	11.0	1442	7	US-11-174-307B-1084	Sequence 1084, Ap
758	55	11.0	96	7	US-11-471-893-12	Sequence 12, Appl	832	55	11.0	1448	7	US-11-174-307B-2194	Sequence 2194, Ap
759	55	11.0	147	6	US-10-510-953-87	Sequence 87, Appl	833	55	11.0	1459	7	US-11-174-307B-1350	Sequence 1350, Ap
760	55	11.0	177	7	US-11-371-354-58545	Sequence 58545, A	834	55	11.0	1471	7	US-11-174-307B-2316	Sequence 2316, Ap
761	55	11.0	224	6	US-10-537-402-100	Sequence 100, App	835	55	11.0	1473	7	US-11-174-307B-1486	Sequence 1486, Ap
762	55	11.0	240	7	US-11-247-437-12	Sequence 12, Appl	836	55	11.0	1476	7	US-11-174-307B-972	Sequence 972, App
763	55	11.0	248	7	US-11-330-403-10585	Sequence 10585, A	837	55	11.0	1482	7	US-11-174-307B-1804	Sequence 1804, Ap
764	55	11.0	289	7	US-11-170-797-12	Sequence 12, Appl	838	55	11.0	1486	7	US-11-174-307B-684	Sequence 684, App
765	55	11.0	387	6	US-10-374-780A-607	Sequence 607, App	839	55	11.0	1486	7	US-11-174-307B-2236	Sequence 2236, Ap
766	55	11.0	399	7	US-11-293-112-5	Sequence 5, Appl	840	55	11.0	1523	7	US-11-174-307B-786	Sequence 786, App
767	55	11.0	420	6	US-10-449-902-49945	Sequence 49945, A	841	55	11.0	1530	7	US-11-174-307B-854	Sequence 854, App

842	55	11.0	1587	7	US-11-174-307B-2652	Sequence 2652, Ap	917	54.5	10.9	1408	7	US-11-174-307B-2510	Sequence 2510, Ap
843	55	11.0	1592	7	US-11-174-307B-5088	Sequence 5088, Ap	918	54.5	10.9	1416	7	US-11-174-307B-1480	Sequence 1480, Ap
844	55	11.0	1601	7	US-11-174-307B-2364	Sequence 2364, Ap	919	54.5	10.9	1434	7	US-11-174-307B-1194	Sequence 1194, Ap
845	55	11.0	1611	7	US-11-174-307B-2234	Sequence 2234, Ap	920	54.5	10.9	1459	7	US-11-174-307B-3196	Sequence 3196, Ap
846	55	11.0	1621	7	US-11-174-307B-2552	Sequence 2552, Ap	921	54.5	10.9	1497	7	US-11-174-307B-494	Sequence 494, App
847	55	11.0	1631	7	US-11-174-307B-2828	Sequence 2828, Ap	922	54.5	10.9	1514	7	US-11-174-307B-2476	Sequence 2476, Ap
848	55	11.0	1655	7	US-11-174-307B-962	Sequence 962, App	923	54.5	10.9	1618	7	US-11-174-307B-484	Sequence 484, App
849	55	11.0	1665	7	US-11-174-307B-1726	Sequence 1726, Ap	924	54.5	10.9	1628	7	US-11-174-307B-2748	Sequence 2748, Ap
850	55	11.0	1680	7	US-11-174-307B-712	Sequence 712, App	925	54.5	10.9	1633	7	US-11-174-307B-2406	Sequence 2406, Ap
851	55	11.0	1696	7	US-11-174-307B-1464	Sequence 1464, Ap	926	54.5	10.9	1713	7	US-11-174-307B-1752	Sequence 1752, Ap
852	55	11.0	1740	7	US-11-174-307B-1390	Sequence 1390, Ap	927	54.5	10.9	1730	7	US-11-174-307B-5198	Sequence 5198, Ap
853	55	11.0	1818	7	US-11-174-307B-2842	Sequence 2842, Ap	928	54.5	10.9	1753	7	US-11-174-307B-802	Sequence 802, App
854	55	11.0	1964	7	US-11-174-307B-4458	Sequence 4458, Ap	929	54.5	10.9	1783	7	US-11-174-307B-1440	Sequence 1440, Ap
855	55	11.0	2003	7	US-11-174-307B-5496	Sequence 5496, Ap	930	54.5	10.9	1786	7	US-11-174-307B-602	Sequence 602, App
856	55	11.0	2095	7	US-11-174-307B-954	Sequence 954, App	931	54.5	10.9	1799	6	US-10-562-469-8	Sequence 8, Appli
857	55	11.0	2384	7	US-11-174-307B-1740	Sequence 1740, Ap	932	54.5	10.9	1917	7	US-11-174-307B-2172	Sequence 2172, Ap
858	55	11.0	2505	6	US-10-669-920-15	Sequence 15, Appl	933	54.5	10.9	2148	7	US-11-174-307B-2000	Sequence 2000, Ap
859	55	11.0	2757	7	US-11-174-307B-1642	Sequence 1642, Ap	934	54.5	10.9	2337	7	US-11-174-307B-1868	Sequence 1868, Ap
860	55	11.0	3291	7	US-11-174-307B-2666	Sequence 2666, Ap	935	54.5	10.9	2433	7	US-11-174-307B-1618	Sequence 1618, Ap
861	54.5	10.9	44	7	US-11-155-989-482	Sequence 482, App	936	54.5	10.9	2494	6	US-10-669-920-22	Sequence 22, Appl
862	54.5	10.9	139	7	US-11-050-875-560	Sequence 560, App	937	54.5	10.9	2647	6	US-10-574-398-66	Sequence 66, Appl
863	54.5	10.9	173	6	US-10-449-902-43149	Sequence 43149, A	938	54.5	10.9	2647	6	US-10-525-573-87	Sequence 87, Appl
864	54.5	10.9	174	7	US-11-377-336-41	Sequence 41, Appl	939	54.5	10.9	2662	7	US-11-174-307B-2672	Sequence 2672, Ap
865	54.5	10.9	216	6	US-10-612-783-6801	Sequence 6801, Ap	940	54.5	10.9	2973	7	US-11-174-307B-1754	Sequence 1754, Ap
866	54.5	10.9	282	6	US-10-970-823-127	Sequence 127, App	941	54.5	10.9	3018	7	US-11-174-307B-1996	Sequence 1996, Ap
867	54.5	10.9	289	6	US-11-371-354-71713	Sequence 71713, A	942	54.5	10.9	3303	6	US-10-547-530-49	Sequence 49, Appl
868	54.5	10.9	299	7	US-10-533-519-1147	Sequence 1147, Ap	943	54.5	10.9	7285	7	US-11-272-521-28	Sequence 28, Appl
869	54.5	10.9	299	7	US-11-391-384-2	Sequence 2, Appli	944	54	10.8	65	6	US-10-560-918-51	Sequence 51, Appl
870	54.5	10.9	299	7	US-11-391-395-2	Sequence 2, Appli	945	54	10.8	132	6	US-10-669-920-1379	Sequence 1379, Ap
871	54.5	10.9	299	7	US-10-953-349-14084	Sequence 14084, A	946	54	10.8	132	6	US-11-365-357-4	Sequence 4, Appli
872	54.5	10.9	305	6	US-10-953-349-14084	Sequence 14084, A	947	54	10.8	132	7	US-11-050-875-625	Sequence 625, App
873	54.5	10.9	305	6	US-10-953-349-14084	Sequence 14084, A	948	54	10.8	143	7	US-11-056-355B-25639	Sequence 25639, A
874	54.5	10.9	305	6	US-10-953-349-14084	Sequence 14084, A	949	54	10.8	156	7	US-11-050-875-561	Sequence 561, App
875	54.5	10.9	356	7	US-11-056-355B-56488	Sequence 56488, A	950	54	10.8	213	7	US-11-287-573-22	Sequence 22, Appl
876	54.5	10.9	371	6	US-10-953-349-14082	Sequence 14082, A	951	54	10.8	280	7	US-11-056-355B-74373	Sequence 74373, A
877	54.5	10.9	371	6	US-10-953-349-14082	Sequence 14082, A	952	54	10.8	280	7	US-11-056-355B-107866	Sequence 107866, A
878	54.5	10.9	371	6	US-10-953-349-14082	Sequence 14082, A	953	54	10.8	280	7	US-11-056-355B-119105	Sequence 119105, A
879	54.5	10.9	376	7	US-11-330-403-4914	Sequence 4914, Ap	954	54	10.8	281	7	US-11-056-355B-74372	Sequence 74372, A
880	54.5	10.9	376	7	US-11-330-403-4917	Sequence 4917, Ap	955	54	10.8	281	7	US-11-056-355B-107865	Sequence 107865, A
881	54.5	10.9	376	7	US-11-330-403-4917	Sequence 4917, Ap	956	54	10.8	281	7	US-11-056-355B-119104	Sequence 119104, A
882	54.5	10.9	379	7	US-11-330-403-12595	Sequence 12595, A	957	54	10.8	281	7	US-11-056-355B-107864	Sequence 107864, A
883	54.5	10.9	386	7	US-11-330-403-11389	Sequence 11389, A	958	54	10.8	322	7	US-11-056-355B-119103	Sequence 119103, A
884	54.5	10.9	393	7	US-11-330-403-14363	Sequence 14363, A	959	54	10.8	322	7	US-11-056-355B-74371	Sequence 74371, A
885	54.5	10.9	535	6	US-10-553-436-355	Sequence 355, App	960	54	10.8	323	7	US-11-056-355B-4786	Sequence 4786, Ap
886	54.5	10.9	577	6	US-10-449-902-45459	Sequence 45459, A	961	54	10.8	341	7	US-11-330-403-6231	Sequence 6231, Ap
887	54.5	10.9	717	7	US-11-175-714-9	Sequence 9, Appli	962	54	10.8	375	7	US-11-330-403-6231	Sequence 53, Appl
888	54.5	10.9	802	7	US-11-174-307B-5486	Sequence 5486, Ap	963	54	10.8	401	7	US-11-377-336-53	Sequence 50, Appl
889	54.5	10.9	879	7	US-11-174-307B-1938	Sequence 1938, Ap	964	54	10.8	440	6	US-10-530-539A-1	Sequence 1, Appli
890	54.5	10.9	880	6	US-10-449-902-41499	Sequence 41499, A	965	54	10.8	516	7	US-11-174-307B-2272	Sequence 2272, Ap
891	54.5	10.9	891	7	US-11-174-307B-1484	Sequence 1484, Ap	966	54	10.8	732	7	US-11-300-928-58	Sequence 58, Appl
892	54.5	10.9	902	6	US-10-449-902-41556	Sequence 41556, A	967	54	10.8	737	7	US-11-330-403-6842	Sequence 6842, Ap
893	54.5	10.9	976	7	US-11-259-133-2	Sequence 2, Appli	968	54	10.8	738	7	US-11-408-441-1	Sequence 1, Appli
894	54.5	10.9	976	7	US-11-365-989-148	Sequence 148, App	969	54	10.8	770	7	US-11-056-355B-75253	Sequence 75253, A
895	54.5	10.9	984	6	US-10-541-749-138	Sequence 138, App	970	54	10.8	770	7	US-11-056-355B-103525	Sequence 103525, A
896	54.5	10.9	1061	7	US-11-174-307B-328	Sequence 328, App	971	54	10.8	770	7	US-11-056-355B-114764	Sequence 114764, A
897	54.5	10.9	1067	7	US-11-054-369A-3	Sequence 3, Appli	972	54	10.8	770	7	US-11-056-355B-10069	Sequence 10069, A
898	54.5	10.9	1151	7	US-11-174-307B-556	Sequence 556, App	973	54	10.8	911	6	US-10-822-303-10069	Sequence 2082, Ap
899	54.5	10.9	1170	7	US-11-174-307B-1300	Sequence 1300, Ap	974	54	10.8	931	7	US-11-174-307B-2082	Sequence 4702, Ap
900	54.5	10.9	1177	7	US-11-174-307B-884	Sequence 884, App	975	54	10.8	936	7	US-11-174-307B-470	Sequence 1470, Ap
901	54.5	10.9	1195	7	US-11-174-307B-2420	Sequence 2420, Ap	976	54	10.8	936	7	US-11-174-307B-470	Sequence 75252, A
902	54.5	10.9	1199	7	US-11-174-307B-392	Sequence 392, App	977	54	10.8	1039	7	US-11-056-355B-75252	Sequence 4, Appli
903	54.5	10.9	1201	7	US-11-174-307B-2186	Sequence 2186, Ap	978	54	10.8	1042	6	US-10-543-003-4	Sequence 75251, A
904	54.5	10.9	1218	6	US-10-833-833-124	Sequence 124, App	979	54	10.8	1044	7	US-11-056-355B-75251	Sequence 103524, A
905	54.5	10.9	1218	7	US-11-178-724-21	Sequence 21, Appl	980	54	10.8	1044	7	US-11-056-355B-114763	Sequence 114763, A
906	54.5	10.9	1218	7	US-11-071-796A-20	Sequence 20, Appl	981	54	10.8	1044	7	US-11-056-355B-103523	Sequence 103523, A
907	54.5	10.9	1218	7	US-11-108-417A-21	Sequence 21, Appl	982	54	10.8	1049	7	US-11-056-355B-114762	Sequence 114762, A
908	54.5	10.9	1218	7	US-11-231-494-21	Sequence 21, Appl	983	54	10.8	1049	7	US-11-174-307B-1630	Sequence 1630, Ap
909	54.5	10.9	1224	7	US-11-174-307B-1958	Sequence 1958, Ap	984	54	10.8	1077	7	US-11-174-307B-1122	Sequence 1122, Ap
910	54.5	10.9	1242	7	US-11-174-307B-1616	Sequence 1616, Ap	985	54	10.8	1108	7	US-11-174-307B-4504	Sequence 2504, Ap
911	54.5	10.9	1244	7	US-11-174-307B-488	Sequence 488, App	986	54	10.8	1136	7	US-11-174-307B-84	Sequence 84, Appl
912	54.5	10.9	1270	7	US-11-174-307B-364	Sequence 364, App	987	54	10.8	1146	7	US-11-174-307B-2372	Sequence 2372, Ap
913	54.5	10.9	1287	7	US-11-174-307B-444	Sequence 444, App	988	54	10.8	1167	7	US-11-174-307B-2734	Sequence 2734, Ap
914	54.5	10.9	1362	7	US-11-174-307B-1772	Sequence 1772, Ap	989	54	10.8				
915	54.5	10.9	1403	7	US-11-174-307B-448	Sequence 448, App	990	54	10.8				
916	54.5	10.9	1407	7	US-11-174-307B-464	Sequence 464, App							

991	54	10.8	1206	7	US-11-174-307B-316	Sequence 916, App	1064	53.5	10.7	309	7	US-11-056-355B-55598	Sequence 55598, A
992	54	10.8	1209	7	US-11-174-307B-360	Sequence 360, App	1065	53.5	10.7	309	7	US-11-395-706-7	Sequence 7, Appli
993	54	10.8	1209	7	US-11-174-307B-3564	Sequence 2544, Ap	1066	53.5	10.7	353	6	US-10-970-823-2	Sequence 2, Appli
994	54	10.8	1217	7	US-11-174-307B-4324	Sequence 4324, Ap	1068	53.5	10.7	353	6	US-11-355-441-2	Sequence 2, Appli
995	54	10.8	1220	7	US-11-174-307B-1044	Sequence 1044, Ap	1069	53.5	10.7	356	7	US-11-371-354-12182	Sequence 12182, A
996	54	10.8	1221	7	US-11-174-307B-1260	Sequence 1260, Ap	1070	53.5	10.7	356	7	US-11-371-354-75925	Sequence 75925, A
997	54	10.8	1220	7	US-11-174-307B-1888	Sequence 1888, Ap	1071	53.5	10.7	404	6	US-10-540-847-3	Sequence 3, Appli
998	54	10.8	1251	7	US-11-174-307B-426	Sequence 426, App	1072	53.5	10.7	406	6	US-10-540-847-2	Sequence 2, Appli
999	54	10.8	1280	6	US-10-669-920-1139	Sequence 1139, Ap	1073	53.5	10.7	412	6	US-10-540-847-4	Sequence 4, Appli
1000	54	10.8	1292	7	US-11-174-307B-1736	Sequence 1736, Ap	1074	53.5	10.7	429	7	US-11-505-151-16	Sequence 16, Appl
1001	54	10.8	1293	7	US-11-174-307B-824	Sequence 824, App	1075	53.5	10.7	430	6	US-10-540-847-15	Sequence 15, Appl
1002	54	10.8	1296	7	US-11-174-307B-2080	Sequence 2080, Ap	1076	53.5	10.7	430	6	US-10-540-847-16	Sequence 16, Appl
1003	54	10.8	1303	7	US-11-174-307B-1570	Sequence 1570, Ap	1077	53.5	10.7	432	6	US-10-540-847-13	Sequence 13, Appl
1004	54	10.8	1314	7	US-11-174-307B-736	Sequence 736, App	1078	53.5	10.7	432	6	US-10-540-847-14	Sequence 14, Appl
1005	54	10.8	1324	7	US-11-174-307B-1210	Sequence 1210, Ap	1079	53.5	10.7	438	6	US-10-540-847-17	Sequence 17, Appl
1006	54	10.8	1326	7	US-11-174-307B-1514	Sequence 1514, Ap	1080	53.5	10.7	438	6	US-10-540-847-18	Sequence 18, Appl
1007	54	10.8	1335	7	US-11-174-307B-3964	Sequence 3964, Ap	1081	53.5	10.7	440	6	US-10-533-519-297	Sequence 297, App
1008	54	10.8	1346	7	US-11-174-307B-3122	Sequence 3122, Ap	1082	53.5	10.7	440	7	US-11-371-354-13168	Sequence 13168, A
1009	54	10.8	1367	7	US-11-174-307B-510	Sequence 510, App	1083	53.5	10.7	440	7	US-11-371-354-72755	Sequence 72755, A
1010	54	10.8	1370	7	US-11-174-307B-858	Sequence 858, App	1084	53.5	10.7	440	7	US-11-371-354-77635	Sequence 77635, A
1011	54	10.8	1370	7	US-11-174-307B-2124	Sequence 2124, Ap	1085	53.5	10.7	459	6	US-10-540-847-8	Sequence 8, Appli
1012	54	10.8	1388	7	US-11-174-307B-1842	Sequence 1842, Ap	1086	53.5	10.7	459	6	US-10-540-847-9	Sequence 9, Appli
1013	54	10.8	1391	7	US-11-174-307B-566	Sequence 566, App	1087	53.5	10.7	461	6	US-10-540-847-6	Sequence 6, Appli
1014	54	10.8	1393	7	US-11-174-307B-606	Sequence 606, App	1088	53.5	10.7	461	6	US-10-540-847-7	Sequence 7, Appli
1015	54	10.8	1439	7	US-11-174-307B-3364	Sequence 3364, Ap	1089	53.5	10.7	467	6	US-10-540-847-10	Sequence 10, Appl
1016	54	10.8	1452	7	US-11-174-307B-38	Sequence 38, Appl	1090	53.5	10.7	467	6	US-10-540-847-11	Sequence 11, Appl
1017	54	10.8	1480	7	US-11-174-307B-752	Sequence 752, App	1091	53.5	10.7	481	7	US-11-477-982-5	Sequence 5, Appli
1018	54	10.8	1522	7	US-11-174-307B-3906	Sequence 3906, Ap	1094	53.5	10.7	509	6	US-10-970-823-315	Sequence 315, App
1019	54	10.8	1524	7	US-11-174-307B-2656	Sequence 2656, Ap	1095	53.5	10.7	513	7	US-11-174-307B-3284	Sequence 3284, Ap
1020	54	10.8	1532	7	US-11-174-307B-2324	Sequence 2324, Ap	1096	53.5	10.7	578	7	US-11-174-307B-4104	Sequence 4104, Ap
1021	54	10.8	1538	7	US-11-174-307B-2654	Sequence 2654, Ap	1097	53.5	10.7	582	7	US-11-293-697-3683	Sequence 3683, Ap
1022	54	10.8	1605	7	US-11-174-307B-1410	Sequence 1410, Ap	1098	53.5	10.7	688	7	US-11-330-403-5573	Sequence 5573, Ap
1023	54	10.8	1610	7	US-11-174-307B-1472	Sequence 1472, Ap	1099	53.5	10.7	753	6	US-10-525-573-438	Sequence 438, App
1024	54	10.8	1648	7	US-11-174-307B-670	Sequence 670, App	1100	53.5	10.7	788	7	US-11-188-417A-30	Sequence 30, Appl
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1028	54	10.8	1753	7	US-11-174-307B-1222	Sequence 1222, Ap	1104	53.5	10.7	864	7	US-11-090-997-1584	Sequence 1584, Ap
1029	54	10.8	1761	7	US-11-174-307B-1306	Sequence 1306, Ap	1105	53.5	10.7	870	7	US-11-090-997-1582	Sequence 1582, Ap
1030	54	10.8	1762	7	US-11-174-307B-2674	Sequence 2674, Ap	1106	53.5	10.7	873	7	US-11-174-307B-1072	Sequence 1072, Ap
1031	54	10.8	1763	7	US-11-174-307B-2112	Sequence 2112, Ap	1107	53.5	10.7	907	7	US-11-174-307B-1040	Sequence 1040, Ap
1032	54	10.8	1766	7	US-11-174-307B-5194	Sequence 5194, Ap	1108	53.5	10.7	1003	7	US-11-174-307B-2592	Sequence 2592, Ap
1033	54	10.8	1771	7	US-11-174-307B-1944	Sequence 1944, Ap	1109	53.5	10.7	1101	7	US-11-371-354-67173	Sequence 67173, A
1034	54	10.8	1771	7	US-11-174-307B-928	Sequence 928, App	1110	53.5	10.7	1124	7	US-11-365-989-190	Sequence 190, App
1035	54	10.8	1782	7	US-11-174-307B-780	Sequence 780, App	1111	53.5	10.7	1124	7	US-11-401-340-42	Sequence 42, Appl
1036	54	10.8	1785	7	US-11-174-307B-1774	Sequence 1774, Ap	1112	53.5	10.7	1125	7	US-11-174-307B-650	Sequence 650, App
1037	54	10.8	1792	7	US-11-174-307B-1192	Sequence 1192, Ap	1113	53.5	10.7	1143	7	US-11-174-307B-1918	Sequence 1918, Ap
1038	54	10.8	1818	7	US-11-174-307B-586	Sequence 586, App	1114	53.5	10.7	1164	7	US-11-174-307B-2218	Sequence 2218, Ap
1039	54	10.8	1818	7	US-11-174-307B-732	Sequence 732, App	1115	53.5	10.7	1182	6	US-10-449-902-41231	Sequence 41231, A
1040	54	10.8	1861	7	US-11-174-307B-1744	Sequence 1744, Ap	1116	53.5	10.7	1193	6	US-10-505-928-537	Sequence 537, App
1041	54	10.8	1868	7	US-11-174-307B-4320	Sequence 4320, Ap	1117	53.5	10.7	1220	7	US-11-174-307B-2404	Sequence 2404, Ap
1042	54	10.8	1873	7	US-11-174-307B-846	Sequence 846, App	1118	53.5	10.7	1221	7	US-11-174-307B-362	Sequence 362, App
1043	54	10.8	2010	7	US-11-174-307B-1358	Sequence 1358, Ap	1119	53.5	10.7	1289	7	US-11-174-307B-434	Sequence 434, App
1044	54	10.8	2118	7	US-11-192-046-1325	Sequence 125, App	1120	53.5	10.7	1329	7	US-11-174-307B-914	Sequence 914, App
1045	54	10.8	2180	7	US-11-174-307B-530	Sequence 530, App	1121	53.5	10.7	1346	7	US-11-174-307B-676	Sequence 676, App
1046	54	10.8	4243	7	US-11-174-307B-1722	Sequence 1722, Ap	1122	53.5	10.7	1373	7	US-11-105-233-187	Sequence 187, App
1047	54	10.8	6629	6	US-10-822-303-9905	Sequence 9905, Ap	1123	53.5	10.7	1413	7	US-11-174-307B-654	Sequence 654, App
1048	53.5	10.7	58	7	US-11-265-762-134	Sequence 134, App	1124	53.5	10.7	1413	7	US-11-174-307B-936	Sequence 936, App
1049	53.5	10.7	92	6	US-10-474-647B-2	Sequence 2, Appli	1125	53.5	10.7	1456	7	US-11-174-307B-1164	Sequence 1164, Ap
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1054	53.5	10.7	173	7	US-11-303-169-23	Sequence 23, Appl	1130	53.5	10.7	1493	7	US-11-174-307B-4196	Sequence 4196, Ap
1055	53.5	10.7	173	7	US-11-303-169-36	Sequence 36, Appl	1131	53.5	10.7	1521	7	US-11-174-307B-1956	Sequence 1956, Ap
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1140	53.5	10.7	1659	7	US-11-174-307B-1436	Sequence 1436, Ap	1213	53	10.6	796	6	US-10-612-783-3679	Sequence 3679, Ap
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1143	53.5	10.7	1746	7	US-11-174-307B-2742	Sequence 2742, Ap	1216	53	10.6	945	7	US-11-174-307B-1700	Sequence 1700, Ap
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1145	53.5	10.7	1831	7	US-11-174-307B-1034	Sequence 1034, Ap	1218	53	10.6	994	7	US-11-303-935-12	Sequence 12, Appl
1146	53.5	10.7	1848	7	US-11-174-307B-1372	Sequence 1372, Ap	1219	53	10.6	998	7	US-11-174-307B-918	Sequence 918, App
1147	53.5	10.7	1880	7	US-11-174-307B-2102	Sequence 2102, Ap	1220	53	10.6	998	7	US-11-303-935-2	Sequence 2, Appl
1148	53.5	10.7	2013	7	US-11-174-307B-1326	Sequence 1326, Ap	1221	53	10.6	1035	7	US-11-174-307B-1704	Sequence 1704, Ap
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1150	53.5	10.7	2411	7	US-11-174-307B-4618	Sequence 4618, Ap	1223	53	10.6	1053	7	US-11-174-307B-596	Sequence 596, App
1151	53.5	10.7	2598	7	US-11-174-307B-1888	Sequence 1888, Ap	1224	53	10.6	1055	7	US-11-174-307B-3194	Sequence 3194, Ap
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1157	53	10.6	52	6	US-10-953-349-36790	Sequence 36790, A	1230	53	10.6	1148	7	US-11-174-307B-2150	Sequence 2150, Ap
1158	53	10.6	187	6	US-10-953-349-1282	Sequence 1282, Ap	1231	53	10.6	1152	7	US-11-174-307B-2712	Sequence 2712, Ap
1159	53	10.6	187	7	US-11-056-355B-38622	Sequence 38622, A	1232	53	10.6	1159	7	US-11-174-307B-1666	Sequence 1666, Ap
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1161	53	10.6	220	6	US-10-953-349-1281	Sequence 1281, A	1234	53	10.6	1162	7	US-11-174-307B-2244	Sequence 2244, Ap
1162	53	10.6	220	7	US-11-056-355B-38621	Sequence 38621, A	1235	53	10.6	1164	7	US-11-174-307B-338	Sequence 338, App
1163	53	10.6	228	7	US-11-056-355B-77611	Sequence 77611, A	1236	53	10.6	1182	7	US-11-174-307B-1872	Sequence 1872, Ap
1164	53	10.6	228	7	US-11-351-617-6	Sequence 6, Appl	1237	53	10.6	1192	7	US-11-174-307B-2814	Sequence 2814, Ap
1165	53	10.6	232	7	US-11-351-617-7	Sequence 7, Appl	1238	53	10.6	1194	7	US-11-174-307B-5030	Sequence 5030, Ap
1166	53	10.6	241	7	US-11-351-617-4	Sequence 4, Appl	1239	53	10.6	1209	7	US-11-174-307B-4384	Sequence 4384, Ap
1167	53	10.6	241	7	US-11-315-825-3	Sequence 3, Appl	1240	53	10.6	1220	7	US-11-174-307B-2330	Sequence 2330, Ap
1168	53	10.6	250	7	US-11-056-355B-77610	Sequence 77610, A	1241	53	10.6	1250	7	US-11-174-307B-1204	Sequence 1204, Ap
1169	53	10.6	251	6	US-10-953-349-1280	Sequence 1280, Ap	1242	53	10.6	1257	7	US-11-174-307B-24	Sequence 24, Appl
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1171	53	10.6	264	7	US-11-265-762-82	Sequence 82, Appl	1244	53	10.6	1270	7	US-11-174-307B-2730	Sequence 2730, Ap
1172	53	10.6	310	7	US-11-232-404-1	Sequence 1, Appl	1245	53	10.6	1282	7	US-11-174-307B-1140	Sequence 1140, Ap
1173	53	10.6	310	7	US-11-231-494-1	Sequence 1, Appl	1246	53	10.6	1283	7	US-11-174-307B-578	Sequence 578, App
1174	53	10.6	311	7	US-11-351-617-8	Sequence 8, Appl	1247	53	10.6	1315	7	US-11-174-307B-610	Sequence 610, App
1175	53	10.6	314	6	US-10-953-349-34590	Sequence 34590, A	1248	53	10.6	1323	7	US-11-174-307B-1734	Sequence 1734, Ap
1176	53	10.6	314	7	US-11-056-355B-13298	Sequence 13298, A	1249	53	10.6	1325	7	US-11-174-307B-450	Sequence 450, App
1177	53	10.6	317	7	US-11-315-825-26	Sequence 26, Appl	1250	53	10.6	1336	7	US-11-174-307B-532	Sequence 532, App
1178	53	10.6	322	6	US-10-953-349-18839	Sequence 18839, A	1251	53	10.6	1343	7	US-11-174-307B-1146	Sequence 1146, Ap
1179	53	10.6	322	7	US-11-056-355B-54922	Sequence 54922, A	1252	53	10.6	1345	7	US-11-174-307B-2572	Sequence 2572, Ap
1180	53	10.6	331	7	US-11-231-494-46	Sequence 46, Appl	1253	53	10.6	1351	7	US-11-174-307B-354	Sequence 354, App
1181	53	10.6	332	7	US-11-178-724-1	Sequence 1, Appl	1254	53	10.6	1351	7	US-11-174-307B-2808	Sequence 2808, Ap
1182	53	10.6	332	7	US-11-188-417A-1	Sequence 1, Appl	1255	53	10.6	1368	7	US-11-174-307B-116	Sequence 116, App
1183	53	10.6	332	7	US-11-188-417A-103	Sequence 103, App	1256	53	10.6	1375	7	US-11-174-307B-2276	Sequence 2276, Ap
1184	53	10.6	332	7	US-11-231-494-60	Sequence 60, Appl	1257	53	10.6	1394	7	US-11-174-307B-640	Sequence 640, App
1185	53	10.6	333	7	US-11-056-355B-10931	Sequence 10931, A	1258	53	10.6	1400	7	US-11-174-307B-446	Sequence 446, App
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1482	52	10.4	271	7	US-11-429-276-438	Sequence 438, Ap
1483	52	10.4	271	7	US-11-429-276-440	Sequence 440, Ap
1484	52	10.4	271	7	US-11-429-276-443	Sequence 443, Ap
1485	52	10.4	271	7	US-11-429-276-449	Sequence 449, Ap
1486	52	10.4	271	7	US-11-429-276-450	Sequence 450, Ap
1487	52	10.4	271	7	US-11-429-276-451	Sequence 451, Ap
1488	52	10.4	271	7	US-11-429-276-490	Sequence 490, Ap
1489	52	10.4	271	7	US-11-429-276-495	Sequence 495, Ap
1490	52	10.4	271	7	US-11-429-373-433	Sequence 433, Ap
1491	52	10.4	271	7	US-11-429-373-434	Sequence 434, Ap
1492	52	10.4	271	7	US-11-429-373-435	Sequence 435, Ap
1493	52	10.4	271	7	US-11-429-373-436	Sequence 436, Ap
1494	52	10.4	271	7	US-11-429-373-437	Sequence 437, Ap
1495	52	10.4	271	7	US-11-429-373-438	Sequence 438, Ap
1496	52	10.4	271	7	US-11-429-373-440	Sequence 440, Ap
1497	52	10.4	271	7	US-11-429-373-443	Sequence 443, Ap
1498	52	10.4	271	7	US-11-429-373-449	Sequence 449, Ap
1499	52	10.4	271	7	US-11-429-373-450	Sequence 450, Ap
1500	52	10.4	271	7	US-11-429-373-451	Sequence 451, Ap

Search completed: December 14, 2006, 14:37:44
Job time : 28.7644 secs

Image Blank (uspto)

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 14, 2006, 14:06:11 ; Search time 22.0628 Seconds
(without alignments)
375.049 Million cell updates/sec

Title: US-10-692-299-2_COPY_20_105

Perfect score: 498
Sequence: 1 AVITGACERDVQAGATCCA.....CSRFPDGRYRCSDMLKNINF 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 80.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.5	20.2	350	JC7188	REIC protein - hum
2	88.5	17.8	640	T08179	LRG5 protein - chl
3	81	16.3	1964	T09059	notch4 - mouse
4	77.5	15.6	473	A56175	adhesive plaque pr
5	75	15.1	2531	T31070	notch homolog - se
6	73	14.7	112	XLHU	collipase precursor
7	72.5	14.6	461	A35356	tumor necrosis fac
8	71.5	14.4	1178	A39804	thrombospondin pre
9	71.5	14.4	1574	T13954	MEGF6 protein - ra
10	71.5	14.4	1854	T13576	hypothetical prote
11	71	14.3	112	IS1909	collipase precursor
12	71	14.3	286	S34665	collagen, cuticula
13	71	14.3	593	GYHU	granulin precursor
14	70.5	14.2	591	I48141	acroganin - guine
15	70.5	14.2	1101	T16840	hypothetical prote
16	70.5	14.2	2318	S45306	notch 3 protein -
17	70	14.1	251	A55035	cysteine-rich prot
18	69	13.9	601	B36346	fibulin 1 precursor
19	69	13.9	683	C36346	fibulin 1 precursor
20	68.5	13.8	850	T14450	serine/threonine k
21	68.5	13.8	1172	A42587	thrombospondin 2 p
22	68.5	13.8	1639	MMF5B2	laminin gamma-1 ch
23	68	13.7	112	A46717	collipase precursor
24	68	13.7	427	GOHUN	nerve growth facto
25	68	13.7	547	A33901	mannosyl-oligosac
26	68	13.7	586	WMBE01	65K early nonstruc
27	68	13.7	1150	A41641	mannosyl-oligosac
28	68	13.7	2215	T00348	LR11 protein - mou
29	68	13.7	5147	IJFPTM	cadherin-related t

protein F21H11.4 [proble membrane
mouse developmenta
hypothetical prote
notch3 protein - h
epithelin/granulin
epithelin/granulin
osteonidogen - hum
alpha-2-macroglobu
thrombospondin 2 p
probable ocsB prot
laminin alpha-1 ch
laminin alpha-1 ch
DELTA-like 1 - mou
hypothetical prote
hypothetical prote
probable vitellog
hemocytin - silkw
hypothetical prote
protein Fl1C7.4 [i
laminin alpha 5 ch
hypothetical prote
probable transpos
nerve growth facto
65K early nonstruc
hypothetical prote
probable vitellog
C-Delta-1 - chicke
heparan sulfate pr
collipase II precu
high cysteine chor
gene murine tumour
Doc4 protein, stre
fibillin I - bovi
fructose-bisphosph
hypothetical prote
EP-cadherin precu
mucin 2 precursor,
high-cysteine chor
hypothetical prote
protein-tyrosine k
low-density lipopr
thrombospondin 1 p
thrombospondin 1 p
fibulin-2 precursor
transmembrane prot
notch protein homo
hypothetical prote
OX40 homolog - hum
hypothetical prote
EGF repeat transme
hypothetical prote
cell-fate determin
hypothetical prote
zonadhesin - mouse
pancreatic colipas
collipase - nutria
triacylglycerol li
fibulin, splice fo
fibulin, splice fo
integrin beta-3 ch
latent transformat
hypothetical prote
zonadhesin - pig
hypothetical prote
hypothetical prote
hypothetical prote
transcription fac
norch protein - fr
perlecan homolog 2
fertilin beta cha
fertilin beta - cr

103	60	12.0	1295	2	A32901	glp1 protein precu	176	57	11.4	419	2	A59414
104	60	12.0	1522	2	H88380	protein T22F7.3 [i	177	57	11.4	468	2	T48686
105	60	12.0	1547	2	UQ0096	hypothetical 176K	178	57	11.4	514	2	T10559
106	60	12.0	1680	2	A43434	furin (EC 3.4.21.7	179	57	11.4	917	2	JC7799
107	60	12.0	1955	1	AGCH	agrin precursor -	180	57	11.4	984	2	T00326
108	60	12.0	2318	2	A54105	fibrillin-2 precu	181	57	11.4	1522	2	T00028
109	60	12.0	4006	2	T09070	probable tenascin	182	57	11.4	1548	2	S34583
110	59.5	11.9	128	2	S32936	sporulation initia	183	57	11.4	2265	1	FNBO
111	59.5	11.9	589	2	T43210	fibulin-1D precu	184	57	11.4	2386	1	FNHU
112	59.5	11.9	689	2	T42760	fibulin-1, splice fo	185	57	11.4	2481	2	A43908
113	59.5	11.9	712	2	T42990	fibulin 1, splice	186	56.5	11.3	99	2	S60231
114	59.5	11.9	886	2	A57172	probable hormone r	187	56.5	11.3	113	2	S11532
115	59.5	11.9	925	2	T37475	lipoprotein recept	188	56.5	11.3	130	1	KRSH3A
116	59.5	11.9	2823	2	F87908	protein T22A3.8 [i	189	56.5	11.3	258	2	T32542
117	59.5	11.9	2823	2	T23064	hypothetical prote	190	56.5	11.3	383	2	D88633
118	59.5	11.9	3102	2	T43291	laminin alpha chai	191	56.5	11.3	443	2	T08905
119	59.5	11.9	4135	2	T46229	tenascin-X - bovin	192	56.5	11.3	682	2	T12968
120	59.5	11.9	4544	1	S02392	alpha-2-macroglobu	193	56.5	11.3	905	2	T02205
121	59	11.8	96	2	S14018	hypothetical prote	194	56.5	11.3	1106	2	T44598
122	59	11.8	186	2	A28401	agglutinin isolect	195	56.5	11.3	1106	2	T13938
123	59	11.8	269	2	T28957	hypothetical prote	196	56.5	11.3	1220	2	A56136
124	59	11.8	283	2	E88597	protein Y47DJB.6 [197	56.5	11.3	1458	2	A45685
125	59	11.8	315	2	B84654	probable CCH-type	198	56.5	11.3	1490	2	JC5145
126	59	11.8	419	2	S41607	atrolysin A (EC 3.	199	56.5	11.3	1495	2	S22610
127	59	11.8	474	2	B38634	tumor necrosis fac	200	56.5	11.3	1537	2	JC4172
128	59	11.8	616	2	T29234	hypothetical prote	201	56.5	11.3	1572	2	T00027
129	59	11.8	907	2	T27317	hypothetical prote	202	56.5	11.3	1612	2	JC5210
130	59	11.8	930	2	T34334	hypothetical prote	203	56.5	11.3	1622	2	JC50378
131	59	11.8	1119	2	A89481	protein C16A3.6 [i	204	56.5	11.3	2767	1	UIHU
132	59	11.8	1203	2	A49175	Motch B protein -	205	56.5	11.3	4753	1	A47437
133	59	11.8	2871	2	A55624	fibrillin-1 precu	206	56	11.2	254	2	T48603
134	58.5	11.7	308	2	JC7125	epidermal growth f	207	56	11.2	264	2	T52104
135	58.5	11.7	325	2	B43692	T2 protein - rabbi	208	56	11.2	265	2	H84857
136	58.5	11.7	358	2	S12100	hypothetical prote	209	56	11.2	320	2	T14624
137	58.5	11.7	717	2	S12100	transferrin precu	210	56	11.2	377	2	T52606
138	58.5	11.7	782	2	A61625	tenascin-like prot	211	56	11.2	478	2	S47040
139	58.5	11.7	884	2	T18649	hypothetical prote	212	56	11.2	491	2	S52920
140	58.5	11.7	895	2	T49010	hypothetical prote	213	56	11.2	643	2	T25473
141	58.5	11.7	962	1	TVB814	106.6K protein kin	214	56	11.2	801	2	T52605
142	58.5	11.7	1712	2	A38261	masking protein pr	215	56	11.2	849	1	T05181
143	58.5	11.7	2195	2	T34264	hypothetical prote	216	56	11.2	1136	1	S57845
144	58.5	11.7	4391	2	A38096	perlecan precursor	217	56	11.2	1170	2	A53612
145	58	11.6	46	2	A44794	antimicrobial pept	218	56	11.2	1194	2	T03818
146	58	11.6	170	2	H83404	probable ferredoxi	219	56	11.2	1661	2	T43260
147	58	11.6	387	2	B43175	Motch A protein -	220	56	11.2	1797	2	A55677
148	58	11.6	574	2	B88465	protein B0244.8 [i	221	55.5	11.1	106	2	A72581
149	58	11.6	755	2	A44315	cartilage oligomer	222	55.5	11.1	264	2	A84868
150	58	11.6	798	2	T27993	hypothetical prote	223	55.5	11.1	309	2	T28708
151	58	11.6	869	1	JC4858	VLDL receptor prec	224	55.5	11.1	383	2	S53716
152	58	11.6	891	2	H86306	F20D23.20 protein	225	55.5	11.1	385	2	S53718
153	58	11.6	998	2	T14764	hypothetical prote	226	55.5	11.1	385	2	A54785
154	58	11.6	1184	2	A55184	fibulin-2 precu	227	55.5	11.1	471	1	KHRZOB
155	58	11.6	1217	1	EGMSMG	epidermal growth f	228	55.5	11.1	503	2	T070926
156	58	11.6	1311	2	T33757	hypothetical prote	229	55.5	11.1	569	2	T50711
157	58	11.6	1428	2	T08852	lustrin A - Califo	230	55.5	11.1	674	2	T15524
158	58	11.6	1790	1	MMFEB1	laminin beta-1 cha	231	55.5	11.1	680	2	T39858
159	58	11.6	2531	2	A46019	notch-1 protein -	232	55.5	11.1	1039	2	T14802
160	58	11.6	2907	2	A57278	fibrillin-2 precu	233	55.5	11.1	1296	2	T16859
161	57.5	11.5	458	2	AF0631	probable 4-hydroxy	234	55.5	11.1	3570	2	T45025
162	57.5	11.5	680	2	PN0510	integrin beta-3 ch	235	55	11.0	171	2	S66858
163	57.5	11.5	710	2	T46589	ropv-2 protein (im	236	55	11.0	268	2	S25311
164	57.5	11.5	810	2	T10756	Nel-homolog protei	237	55	11.0	305	2	A46476
165	57.5	11.5	1356	2	JC1402	protein-tyrosine k	238	55	11.0	323	2	A99211
166	57.5	11.5	1469	2	B36665	slit protein 2 pre	239	55	11.0	343	2	S45321
167	57.5	11.5	1480	2	A35665	slit protein 1 pre	240	55	11.0	531	2	T06713
168	57.5	11.5	2139	2	A35672	crumbs protein - f	241	55	11.0	512	2	B83422
169	57.5	11.5	2352	2	T30201	Notch homolog prot	242	55	11.0	599	2	JC8009
170	57.5	11.5	3002	2	A47221	fibrillin 1 precu	243	55	11.0	853	2	B85429
171	57	11.4	92	1	S36658	proteinase inhibit	244	55	11.0	961	1	TSHP4
172	57	11.4	175	2	C82686	lactoylglycathione	245	55	11.0	996	2	JE0237
173	57	11.4	212	2	T05936	agglutinin isolect	246	55	11.0	1038	2	I38935
174	57	11.4	250	1	A49053	CD27 antigen precu	247	55	11.0	1038	2	JC5527
175	57	11.4	414	2	T24563	hypothetical prote	248	55	11.0	1192	2	S69000

metalloproteinase
hypothetical prote
hypothetical prote
PARIS-1 protein -
hypothetical prote
brain-specific ang
serine proteinase
fibronectin - bovi
fibronectin precu
fibronectin - Afri
glibberellin-regula
colicin E1 immunit
keratin high-sulfu
hypothetical prote
protein P56B3.2 [i
hypothetical prote
Lu-ECAM-1 protein
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gene shuttle craft
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adult-specific bru
DNA (cytosine-5-)-
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thyroglobulin prec
LDL-receptor-relat
insulin-like growt
GATA-binding trans
probable endochiti
hypothetical prote
squamosa promoter
gene Tt52 protein
disintegrin (EC 3.
hypothetical prote
squamosa promoter
S-receptor kinase
protein-tyrosine k
laminin B1k chain
apoptotic proteina
RNA polymerase (EC
laminin beta-2 cha
hypothetical prote
probable endochiti
hypothetical prote
delta-like homeoti
homeotic protein d
preadipocyte facto
oryzain (EC 3.4.22
hypothetical prote
urease (EC 3.5.1.5
hypothetical prote
hypothetical prote
phytochrome B - so
hypothetical prote
mucin MUC5B, trach
probable membrane
chitinase (EC 3.2.
B cell-associated
follistatin - mous
probable cytochrom
probable serine/th
choline dehydrogen
beta-galactosidase
thrombospondin 4 p
apolipoprotein B r
bone morphogenetic
bone morphogenetic
laminin gamma 2 ch

249	55	11.0	1357	2	T16860	hypothetical prote	322	53.5	10.7	109	2	S67091	probable membrane
250	55	11.0	1743	2	T26859	hypothetical prote	323	53.5	10.7	202	1	A44247	C4b-binding protei
251	55	11.0	2052	2	T18290	FVVE finger-contai	324	53.5	10.7	232	2	H69315	cytochrome-c3 hydr
252	55	11.0	2477	2	S14428	fibronectin precu	325	53.5	10.7	266	2	B72532	hypothetical prote
253	55	11.0	2616	2	A57096	nudel protein prec	326	53.5	10.7	273	2	F63199	conserved hypothet
254	55	11.0	3225	2	I52300	giantin - human	327	53.5	10.7	280	2	T33519	hypothetical prote
255	55	11.0	3259	1	A56539	giantin - human	328	53.5	10.7	314	2	T32985	hypothetical prote
256	55	11.0	4660	2	T42737	gp330 protein prec	329	53.5	10.7	346	2	JA0159	cysteine proteinase
257	54.5	10.9	57	2	C46654	growth modulatory	330	53.5	10.7	370	2	AB0289	conserved hypothet
258	54.5	10.9	92	2	D37057	epithelial cell gl	331	53.5	10.7	390	2	S46540	methionine adenosy
259	54.5	10.9	220	2	A95956	hypothetical prote	332	53.5	10.7	424	2	S11676	spore coat protein
260	54.5	10.9	221	2	C34768	ORF2 protein - Orf	333	53.5	10.7	466	2	T06416	cysteine proteinase
261	54.5	10.9	226	2	JC4868	ribonuclease S2 [E	334	53.5	10.7	509	2	T02864	probable Zn finger
262	54.5	10.9	248	2	T19913	hypothetical prote	335	53.5	10.7	568	2	F86291	hypothetical prote
263	54.5	10.9	263	2	T27641	hypothetical prote	336	53.5	10.7	575	2	A49667	interleukin-10 rec
264	54.5	10.9	279	2	C70458	diaminopimelate ep	337	53.5	10.7	584	2	I50419	s-glycerin precurs
265	54.5	10.9	292	2	C88072	protein ZK1240.8 [338	53.5	10.7	753	2	B36268	platelet glycoprot
266	54.5	10.9	310	2	A60967	insulin-like growt	339	53.5	10.7	753	2	G02173	semaphorin III fam
267	54.5	10.9	317	2	I46916	insulin-like growt	340	53.5	10.7	768	2	B41029	integrin beta-8 ch
268	54.5	10.9	318	2	E87929	protein T22H2.6 [i	341	53.5	10.7	773	2	JQ2187	p87 protein - Card
269	54.5	10.9	358	2	T25137	hypothetical prote	342	53.5	10.7	775	2	A61228	collagen alpha 2(I
270	54.5	10.9	386	2	S52035	hypothetical prote	343	53.5	10.7	778	2	A60798	platelet glycoprot
271	54.5	10.9	419	2	E71519	probable alcohol d	344	53.5	10.7	788	2	I77349	platelet glycoprot
272	54.5	10.9	442	2	JC4978	probable ATPase -	345	53.5	10.7	850	2	S56015	gastric mucin MUC5
273	54.5	10.9	530	2	C95334	oxidative stress p	346	53.5	10.7	863	1	S51789	VLDL receptor prec
274	54.5	10.9	644	2	A36325	epidermal growth f	347	53.5	10.7	952	2	T18900	disintegrin and me
275	54.5	10.9	711	2	S43464	ecdysteroid-induce	348	53.5	10.7	957	2	T15976	hypothetical prote
276	54.5	10.9	761	2	JC5759	brain-specific ser	349	53.5	10.7	1036	2	T17405	scavenger receptor
277	54.5	10.9	788	2	I51530	integrin beta-3 su	350	53.5	10.7	1107	2	T15884	hypothetical prote
278	54.5	10.9	837	1	A29512	LDL receptor precu	351	53.5	10.7	1124	1	I58388	protein-tyrosine k
279	54.5	10.9	938	2	I49071	protein kinase - m	352	53.5	10.7	1193	2	A44018	laminin B2t chain
280	54.5	10.9	948	2	S51605	receptor-like tyro	353	53.5	10.7	1201	2	A57369	anillin - fruit fl
281	54.5	10.9	955	2	A45441	thrombospondin 4 -	354	53.5	10.7	1245	1	MMMSND	nidogen precursor
282	54.5	10.9	984	1	A34076	protein-tyrosine k	355	53.5	10.7	1394	2	A35626	transforming growt
283	54.5	10.9	1143	2	T10636	hypothetical prote	356	53.5	10.7	1678	2	D86481	189.6K hypothetica
284	54.5	10.9	1237	2	A34598	ecdysone-induced p	357	53.5	10.7	1959	1	AGRT	agrin - rat
285	54.5	10.9	1332	2	T23024	hypothetical prote	358	53.5	10.7	2813	1	VMHU	von Willebrand fac
286	54.5	10.9	1386	2	T00257	hypothetical prote	359	53.5	10.7	3507	2	T34513	hypothetical prote
287	54.5	10.9	1443	2	S05979	steroid hormone re	360	53	10.6	47	2	B58319	gamma-zeathionin 2
288	54.5	10.9	2647	2	A37098	gelation factor AB	361	53	10.6	77	2	S29563	endothelin 2 precu
289	54.5	10.9	7562	2	I38346	elastic titin - hu	362	53	10.6	141	2	T08790	hypothetical prote
290	54	10.8	63	2	S08572	chymotrypsin/elast	363	53	10.6	177	2	B71682	probable ubiquinol
291	54	10.8	132	1	T1HUSP	antileukoproteinas	364	53	10.6	216	2	JX0265	platelet aggregati
292	54	10.8	148	2	G82223	pilB-related prote	365	53	10.6	309	2	T22402	hypothetical prote
293	54	10.8	212	2	S09623	agglutinin isolect	366	53	10.6	343	2	I49067	zinc finger protei
294	54	10.8	213	1	AEWT2	agglutinin isolect	367	53	10.6	396	1	KXBOZ	plasma protein Z -
295	54	10.8	236	2	T05695	pathogenesis-relat	368	53	10.6	424	2	T39524	hypothetical prote
296	54	10.8	287	2	A41257	apoptosis protein	369	53	10.6	502	2	T20130	hypothetical prote
297	54	10.8	335	2	S03212	hypothetical prote	370	53	10.6	551	2	S51941	prunin 1 precursor
298	54	10.8	341	2	AE2445	hypothetical prote	371	53	10.6	578	2	S50446	VAC8 protein - yea
299	54	10.8	496	1	ALPGP	alpha-amylase (EC	372	53	10.6	605	2	JC5673	receptor tyrosine
300	54	10.8	496	2	AL7230	alpha-amylase (EC	373	53	10.6	610	2	I48612	developmental kina
301	54	10.8	571	2	S24789	jararhagin C precu	374	53	10.6	613	2	A88448	protein C45G9.6 [i
302	54	10.8	609	2	S55270	catrocollastatin p	375	53	10.6	626	2	I48614	developmental kina
303	54	10.8	732	2	JC4194	lanosterol synthas	376	53	10.6	636	2	H64429	DNA-directed RNA p
304	54	10.8	737	2	S65758	nitrate reductase	377	53	10.6	670	2	T49510	fibroin-3 related
305	54	10.8	748	2	S66129	disintegrin (EC 3,	378	53	10.6	686	2	S43562	KOAP5.3 protein -
306	54	10.8	790	2	A38627	protein-tyrosine k	379	53	10.6	711	1	A47135	macrophage-stimula
307	54	10.8	794	2	F88508	protein H4A12.6 [380	53	10.6	738	2	S40992	hypothetical prote
308	54	10.8	823	2	S18968	cytatestin precurs	381	53	10.6	739	2	B88553	protein K04H4.2b [
309	54	10.8	977	2	T00014	DAP-1-alpha protei	382	53	10.6	838	2	T20125	hypothetical prote
310	54	10.8	1052	2	B49120	protein-tyrosine k	383	53	10.6	874	2	B70914	probable dnaB prot
311	54	10.8	1142	2	T30272	hypothetical prote	384	53	10.6	964	2	JC5545	integrin beta-4 pr
312	54	10.8	1364	2	T51920	probable xanthine	385	53	10.6	998	2	JC5672	receptor tyrosine
313	54	10.8	1364	2	T00250	MEGF2 protein - hu	386	53	10.6	1360	2	T33922	hypothetical prote
314	54	10.8	1429	2	S06434	homeotic protein l	387	53	10.6	1875	2	A36429	integrin beta-4 ch
315	54	10.8	1584	2	T22674	hypothetical prote	388	53	10.6	2017	1	A36014	myosin heavy chain
316	54	10.8	2531	2	S18188	notch protein homo	389	53	10.6	2057	2	S61477	myosin II heavy ch
317	54	10.8	2652	1	VF1HB2	genome polyprotein	390	52.5	10.5	70	2	A55824	drosomycin precurs
318	54	10.8	3051	2	S42373	hypothetical prote	391	52.5	10.5	154	2	A86086	hypothetical prote
319	54	10.8	3175	1	RRWVEV	genome polyprotein	392	52.5	10.5	163	2	E91238	hypothetical prote
320	54	10.8	4351	2	T00252	MEGF1 protein - ra	393	52.5	10.5	203	2	T02696	probable disease r
321	53.5	10.7	57	2	A46654	growth modulatory	394	52.5	10.5	250	2	T01779	trypsin (EC 3.4.21

395	52.5	10.5	250	2	S31384	trypsin (EC 3.4.21	468	51.5	10.3	252	2	T46247	hypothetical prote
396	52.5	10.5	255	2	T44991	oxidoreductase [im	469	51.5	10.3	261	2	A55242	MHC class II hieso
397	52.5	10.5	261	2	S17889	class II histocomp	470	51.5	10.3	282	2	A48516	sulfatant protein
398	52.5	10.5	268	2	AF0195	4-amino-4-deoxycho	471	51.5	10.3	284	2	JC7686	activator of CAMP-
399	52.5	10.5	280	2	D82017	hypothetical prote	472	51.5	10.3	287	1	S75925	DNA-formamidopyrim
400	52.5	10.5	287	2	T09303	hypothetical prote	473	51.5	10.3	289	2	A84812	probable aquaporin
401	52.5	10.5	288	2	D81002	conserved hypothet	474	51.5	10.3	297	2	H69609	hypothetical prote
402	52.5	10.5	288	1	A41927	insulin-like growt	475	51.5	10.3	317	2	AF2129	hypothetical prote
403	52.5	10.5	329	2	S47093	hypothetical prote	476	51.5	10.3	323	2	T27450	hypothetical prote
404	52.5	10.5	354	2	T22274	hypothetical prote	477	51.5	10.3	384	2	AF0295	conserved hypothte
405	52.5	10.5	362	2	G96735	hypothetical prote	478	51.5	10.3	394	2	T24860	hypothetical prote
406	52.5	10.5	370	2	AE3479	probable prolina-r	479	51.5	10.3	409	2	A86240	protein F20B24.10
407	52.5	10.5	373	2	T34126	alcohol dehydrogen	480	51.5	10.3	410	2	T47926	hypothetical prote
408	52.5	10.5	387	2	I38449	hypothetical prote	481	51.5	10.3	435	2	S40933	hypothetical prote
409	52.5	10.5	397	2	S26731	extracellular prot	482	51.5	10.3	485	2	S36772	E-selectin - bovin
410	52.5	10.5	403	2	T26326	neuro-D4 protein -	483	51.5	10.3	488	2	T47697	Regulator of chrom
411	52.5	10.5	431	2	T37621	hypothetical prote	484	51.5	10.3	497	2	T27012	hypothetical prote
412	52.5	10.5	431	2	C85073	hypothetical prote	485	51.5	10.3	518	2	T23120	hypothetical prote
413	52.5	10.5	559	2	T39744	probable transposo	486	51.5	10.3	523	2	F71302	asparagine-tRNA li
414	52.5	10.5	747	2	T39744	conserved hypothet	487	51.5	10.3	562	2	T49386	hypothetical prote
415	52.5	10.5	788	2	A28547	platelet glycoprot	488	51.5	10.3	585	2	S43572	CUGB5.5 protein (C
416	52.5	10.5	788	2	A37057	integrin beta-6 ch	489	51.5	10.3	585	2	E88571	protein C05B5.5 [i
417	52.5	10.5	941	1	A55195	chordin precursor	490	51.5	10.3	591	2	T48596	ankyrin-like prote
418	52.5	10.5	1106	2	T04015	hypothetical prote	491	51.5	10.3	592	2	T21536	hypothetical prote
419	52.5	10.5	1373	2	JE0095	gastric mucin MUC5	492	51.5	10.3	685	2	C56591	E75 B steroid rece
420	52.5	10.5	1531	2	T42218	slit-1 protein hom	493	51.5	10.3	765	2	T15447	hypothetical prote
421	52.5	10.5	1607	2	T43212	insulin-like growt	494	51.5	10.3	865	2	B69074	probable formate d
422	52.5	10.5	1650	2	S53457	dominant autoantig	495	51.5	10.3	899	2	G02428	subtilisin-like pr
423	52.5	10.5	1712	1	CGHU2B	collagen alpha 2(I	496	51.5	10.3	915	2	JC6148	mineralocorticoid
424	52.5	10.5	1737	2	T00209	MEGF8 protein - hu	497	51.5	10.3	981	2	A41401	mineralocorticoid
425	52.5	10.5	1801	1	MRP7S	laminin beta-2 cha	498	51.5	10.3	984	2	A29513	mineralocorticoid
426	52.5	10.5	3566	1	A40701	tenascin-X precurs	499	51.5	10.3	1165	2	S27809	GNPase-activating
427	52.5	10.4	77	2	S47158	metallothionein II	500	51.5	10.3	1299	2	T43251	furin (EC 3.4.21.7
428	52.5	10.4	107	2	T49527	hypothetical prote	501	51.5	10.3	1321	2	JE0352	mucin MUC5B, trach
429	52.5	10.4	151	2	T20071	hypothetical prote	502	51.5	10.3	1786	1	MMMSB1	laminin beta-1 cha
430	52.5	10.4	181	1	MXRRD	nonstructural prot	503	51.5	10.3	2023	2	T13154	polycomb protein e
431	52.5	10.4	189	2	JC6064	RNA-binding protei	504	51	10.2	84	2	JN0469	85K MKK-2 recogni
432	52.5	10.4	191	2	T50306	hypothetical prote	505	51	10.2	87	2	JN0670	Na+-channel-blocki
433	52.5	10.4	213	1	D70416	phosphoglycolate p	506	51	10.2	102	2	S26409	protein 108 precur
434	52.5	10.4	221	2	G69420	hydrogenase expres	507	51	10.2	120	2	JQ1740	hypothetical prote
435	52.5	10.4	227	1	LNKZ	lectin precursor -	508	51	10.2	142	2	A71097	probable cytochrom
436	52.5	10.4	281	2	I39199	C2H2-150 - human	509	51	10.2	169	2	T03033	5-formyltetrahydro
437	52.5	10.4	289	2	A12128	ATP-binding protei	510	51	10.2	187	2	H69956	probable phosphogl
438	52.5	10.4	302	1	S65021	chitinase (EC 3.2.	511	51	10.2	205	2	T27278	hypothetical prote
439	52.5	10.4	375	1	S62640	alcohol dehydrogen	512	51	10.2	226	2	E71478	probable phosphogl
440	52.5	10.4	393	2	D86168	hypothetical prote	513	51	10.2	229	2	T34325	hypothetical prote
441	52.5	10.4	435	2	I54182	tumor necrosis fac	514	51	10.2	233	2	B69202	endonuclease III -
442	52.5	10.4	456	1	KXBO	protein C (activat	515	51	10.2	240	2	T47864	GATA transcription
443	52.5	10.4	467	2	D86485	protein F28J9.13 [516	51	10.2	243	2	T31144	hypothetical prote
444	52.5	10.4	513	2	D88991	protein apx-1 [imp	517	51	10.2	260	2	S11562	probable MASH-1 pr
445	52.5	10.4	541	2	T48811	hypothetical prote	518	51	10.2	261	2	S11678	chitinase (EC 3.2.
446	52.5	10.4	601	2	D89711	protein F40E10.4 [519	51	10.2	284	2	A28008	troponin T, cardia
447	52.5	10.4	601	2	T22025	hypothetical prote	520	51	10.2	319	2	D97081	ketopantoate reduc
448	52.5	10.4	610	2	T16761	hypothetical prote	521	51	10.2	353	2	T27800	hypothetical prote
449	52.5	10.4	635	2	C81861	hypothetical prote	522	51	10.2	374	1	A53142	alcohol dehydrogen
450	52.5	10.4	656	2	S49745	probable membrane	523	51	10.2	374	1	S35669	alcohol dehydrogen
451	52.5	10.4	716	1	JC5061	macrophage-stimula	524	51	10.2	375	1	DEHOAL	cystathionine gamm
452	52.5	10.4	737	2	PQ0219	RNA-2 polypeptid	525	51	10.2	388	2	A82045	hypothetical prote
453	52.5	10.4	786	2	T31793	hypothetical prote	526	51	10.2	413	2	T34123	hypothetical prote
454	52.5	10.4	893	2	H95953	probable bifunctio	527	51	10.2	417	2	T45857	hypothetical prote
455	52.5	10.4	961	2	A55380	faciogonital dyspl	528	51	10.2	429	2	T21113	coagulation factor
456	52.5	10.4	1064	2	A40136	fibropellin ia - g	529	51	10.2	452	1	A30351	hypothetical prote
457	52.5	10.4	1106	2	T18739	hypothetical prote	530	51	10.2	525	2	T35084	hypothetical prote
458	52.5	10.4	1300	2	A36502	insulin receptor-r	531	51	10.2	548	2	T16642	hypothetical prote
459	52.5	10.4	1358	1	XOCHDH	xanthine dehydroge	532	51	10.2	651	2	JC7705	death receptor-6 -
460	52.5	10.4	1513	2	A54895	mucin 2, intestina	533	51	10.2	675	1	KXMS	plasma protein S p
461	52.5	10.4	1557	2	T28811	hypothetical prote	534	51	10.2	714	2	S77385	nitrate reductase
462	51.5	10.3	77	2	AF2564	hypothetical prote	535	51	10.2	736	2	S57961	dimethylamine dehy
463	51.5	10.3	103	4	SR5331	hypothetical prote	536	51	10.2	780	2	A34102	von Willebrand fac
464	51.5	10.3	131	1	KRSHA3	keratin high-sulfu	537	51	10.2	873	1	I48952	VLDR receptor prec
465	51.5	10.3	132	1	KRGT37	keratin high-sulfu	538	51	10.2	934	1	A34372	complement C6 prec
466	51.5	10.3	135	2	AH2100	hypothetical prote	539	51	10.2	1345	2	B71608	DNA-directed RNA p
467	51.5	10.3	221	2	S59832	hypothetical prote	540	51	10.2	1379	2	T37752	hypothetical serin
467	51.5	10.3	251	2	G96006	probable SUR1-like							

541	51	10.2	1408	2	S16148	gene serrate prote	614	50	10.0	249	2	E69546	conserved hypothet
542	51	10.2	1700	2	S08167	Balbani ring 3 pr	615	50	10.0	256	2	T06649	hypothetical prote
543	51	10.2	1798	2	S53869	laminin beta-2 ch	616	50	10.0	268	1	G71271	probable ABC trans
544	51	10.2	1820	2	A55494	latent transformin	617	50	10.0	281	2	AE0671	N-hydroxyarylamine
545	51	10.2	3106	1	S53868	laminin alpha-2 ch	618	50	10.0	281	2	A38090	N-hydroxyarylamine
546	51	10.2	3191	2	T22945	hypothetical prote	619	50	10.0	282	1	YP00D1	prestalk D11 prote
547	51	10.2	4543	1	A53102	alpha-2-macroglobu	620	50	10.0	288	2	S46536	chitinase (EC 3.2.
548	51	10.2	13288	2	T03099	mucin, submaxillar	621	50	10.0	294	2	T23916	hypothetical prote
549	50.5	10.1	47	2	S69145	gamma-thionin SI-a	622	50	10.0	297	2	T46590	probable regulator
550	50.5	10.1	118	2	S38491	Ig heavy chain - h	623	50	10.0	298	2	T33046	hypothetical prote
551	50.5	10.1	122	2	T28977	hypothetical prote	624	50	10.0	302	1	TPCHTC	troponin T, cardia
552	50.5	10.1	151	2	T32445	hypothetical prote	625	50	10.0	306	2	S38251	folliculin-relate
553	50.5	10.1	154	2	E87530	isoquinoline 1-oxi	626	50	10.0	306	2	S51361	folliculin-relate
554	50.5	10.1	201	2	T07011	proteinase inhibit	627	50	10.0	308	2	S51362	folliculin-relate
555	50.5	10.1	214	2	T19930	hypothetical prote	628	50	10.0	345	2	T25138	hypothetical prote
556	50.5	10.1	230	2	T34854	hypothetical prote	629	50	10.0	353	2	D96596	hypothetical prote
557	50.5	10.1	247	2	D75027	dihydroorotate deh	630	50	10.0	356	2	A25918	thrombomodulin - b
558	50.5	10.1	260	1	A46517	CD27 antigen precu	631	50	10.0	359	2	T02833	threonine aldolase
559	50.5	10.1	272	2	H95314	probable transposa	632	50	10.0	372	2	AE3184	alcohol dehydrogen
560	50.5	10.1	283	2	T23785	hypothetical prote	633	50	10.0	384	2	T19513	hypothetical prote
561	50.5	10.1	284	2	T29715	hypothetical prote	634	50	10.0	393	1	A48357	nonstructural prot
562	50.5	10.1	308	2	T37286	collagen 40 - Caen	635	50	10.0	415	2	T32467	hypothetical prote
563	50.5	10.1	323	1	SYECAC	cysteine synthase	636	50	10.0	427	2	E84966	serine-tRNA ligase
564	50.5	10.1	323	2	F91039	cysteine synthase	637	50	10.0	449	2	B82802	conserved hypothet
565	50.5	10.1	323	2	A85884	cysteine synthase	638	50	10.0	450	2	T14352	WD-repeat protein
566	50.5	10.1	334	2	T25154	hypothetical prote	639	50	10.0	460	2	B87455	DNA repair protein
567	50.5	10.1	348	1	S32484	L-iditol 2-dehydro	640	50	10.0	481	2	JC4342	fibinolytic prote
568	50.5	10.1	372	2	A42778	agglutinin precurs	641	50	10.0	481	2	S43125	trimucin precursor
569	50.5	10.1	390	2	S49491	methionine adenosy	642	50	10.0	503	2	A49431	activin/TGF-beta-1
570	50.5	10.1	390	2	G84785	probable s-adenosy	643	50	10.0	558	2	T17324	hypothetical prote
571	50.5	10.1	398	2	A35281	integumentary muc	644	50	10.0	573	2	JC4335	anti-mullerian hor
572	50.5	10.1	428	2	S45361	LRR47 protein - fr	645	50	10.0	581	2	BS4665	netrin-2 precursor
573	50.5	10.1	473	2	H84550	probable obtusifol	646	50	10.0	604	2	D71377	phenylalanine-tRNA
574	50.5	10.1	484	2	T25944	hypothetical prote	647	50	10.0	642	2	D69085	transcription cont
575	50.5	10.1	533	1	RGBYC6	cell division cont	648	50	10.0	647	2	T43952	hypothetical prote
576	50.5	10.1	538	2	E84863	hypothetical prote	649	50	10.0	666	2	F71310	probable periplasm
577	50.5	10.1	603	2	JC5063	prostaglandin-endo	650	50	10.0	669	2	T06702	hypothetical prote
578	50.5	10.1	604	2	F87936	protein M01G12.12	651	50	10.0	684	2	I39595	phospholipase C -
579	50.5	10.1	604	2	T23669	hypothetical prote	652	50	10.0	686	2	B75267	prolyl endopeptida
580	50.5	10.1	618	2	D71055	probable indolepyr	653	50	10.0	686	2	T25987	hypothetical prote
581	50.5	10.1	657	2	D71351	probable primoema	654	50	10.0	704	2	T03478	probable DNA-direc
582	50.5	10.1	664	1	JX0336	succinate dehydrog	655	50	10.0	759	2	T44142	DRI protein [impor
583	50.5	10.1	686	2	JC7569	Delta-4 protein -	656	50	10.0	775	2	S28284	hypothetical prote
584	50.5	10.1	758	2	S51748	lethal(2)denticlel	657	50	10.0	780	2	T27941	hypothetical prote
585	50.5	10.1	769	1	IJHULM	leukocyte adhesion	658	50	10.0	782	2	E88556	protein B0464.5c [
586	50.5	10.1	769	2	A41029	integrin beta-8 ch	659	50	10.0	792	2	T42963	hypothetical prote
587	50.5	10.1	814	2	A95206	glycosyl transfera	660	50	10.0	887	2	S57430	probable formate d
588	50.5	10.1	856	2	T52415	polycarb protein E	661	50	10.0	889	2	T23299	hypothetical prote
589	50.5	10.1	898	2	T01503	hypothetical prote	662	50	10.0	962	2	JC5571	subtilisin-like pr
590	50.5	10.1	955	2	S56649	pyruvate, phosphat	663	50	10.0	975	2	JC5570	probable complemen
591	50.5	10.1	1019	1	A56318	enteropeptidase (E	664	50	10.0	1053	2	S46199	probable calcium t
592	50.5	10.1	1087	2	S28282	hypothetical prote	665	50	10.0	1054	2	A61221	hypothetical prote
593	50.5	10.1	1164	2	T06144	disease resistance	666	50	10.0	1069	2	T42681	hypothetical prote
594	50.5	10.1	1237	2	T46609	calcium-activated	667	50	10.0	1093	2	F88556	protein B0464.5a [
595	50.5	10.1	1297	2	T30274	proteoliasin - se	668	50	10.0	1108	2	JC4037	alpha-mannosidase
596	50.5	10.1	1384	2	T02748	hypothetical prote	669	50	10.0	1391	2	S73652	RNA polymerase bet
597	50.5	10.1	1551	1	A43364	M polypeptide prec	670	50	10.0	1481	1	O2D0P3	pyrimidine synthes
598	50.5	10.1	1627	2	S65464	pregnancy-associat	671	50	10.0	2027	2	S60123	hypothetical prote
599	50.5	10.1	1746	1	S19694	tenascin precursor	672	50	10.0	2056	2	G88564	protein R10E11.1 [
600	50.5	10.1	1761	2	T13990	collagen type IV a	673	50	10.0	2120	2	T30243	alpha tectorin - c
601	50.5	10.1	2180	2	T29764	hypothetical prote	674	50	10.0	2910	2	T42214	otogelin - mouse
602	50.5	10.1	2225	2	T26063	hypothetical prote	675	50	10.0	3005	2	T08841	hypothetical prote
603	50.5	10.1	2599	2	A96616	unknown protein F1	676	49.5	9.9	61	2	C81079	polypeptide - dour
604	50.5	10.1	3084	1	MMMSA	laminin alpha-1 ch	677	49.5	9.9	74	2	S05594	hypothetical prote
605	50.5	10.1	4307	2	T20721	hypothetical prote	678	49.5	9.9	142	2	H72600	hypothetical prote
606	50	10.0	87	2	JN0669	Na+-channel-blocki	679	49.5	9.9	156	2	T43957	hypothetical prote
607	50	10.0	96	1	XLHOB	collipase B precurs	680	49.5	9.9	163	2	B83445	probable oxidoredu
608	50	10.0	98	2	AG3416	hypothetical prote	681	49.5	9.9	170	2	T51042	hypothetical prote
609	50	10.0	103	2	T25294	hypothetical prote	682	49.5	9.9	176	2	T48699	hypothetical prote
610	50	10.0	136	2	T31796	hypothetical prote	683	49.5	9.9	213	2	E71212	hypothetical prote
611	50	10.0	193	2	T16566	hypothetical prote	684	49.5	9.9	256	2	JC4627	fibroblast growth
612	50	10.0	204	2	T35410	probable DNA-bind	685	49.5	9.9	274	2	G84353	hypothetical prote
613	50	10.0	233	2	T47136	hypothetical prote	686	49.5	9.9	291	1	JN0064	insulin-like growt

687	49.5	9.9	305	2	I48601	insulin-like growth	760	49	9.8	415	2	S60078	Runt domain contai
688	49.5	9.9	322	1	S37344	chitinase (EC 3.2.	761	49	9.8	468	2	B40228	neurexin I-beta pr
689	49.5	9.9	349	2	A85303	probable transcrip	762	49	9.8	469	2	G86638	cationic amino aci
690	49.5	9.9	349	2	T04272	hypothetical prote	763	49	9.8	474	2	T27297	hypothetical prote
691	49.5	9.9	357	2	F72022	UDP-N-acetylglucos	764	49	9.8	490	2	T06714	membrane glycoprot
692	49.5	9.9	357	2	F86603	peptidoglycan tran	765	49	9.8	493	2	JC5486	hypothetical prote
693	49.5	9.9	357	2	T32881	hypothetical prote	766	49	9.8	500	2	H96570	hypothetical prote
694	49.5	9.9	369	2	S72734	DNA-binding protei	767	49	9.8	524	2	T44889	probable aminopept
695	49.5	9.9	375	1	DEMSAA	alcohol dehydrogen	768	49	9.8	525	2	T41683	probable transcrip
696	49.5	9.9	379	1	F64633	site-specific DNA-	769	49	9.8	527	2	T04329	importin alpha - t
697	49.5	9.9	381	2	A71882	type II DNA modifi	770	49	9.8	568	2	JC5629	mullerian-inhibiti
698	49.5	9.9	397	2	T22932	hypothetical prote	771	49	9.8	573	2	H96744	probable cytosolic
699	49.5	9.9	416	2	T32458	hypothetical prote	772	49	9.8	592	2	B83231	probable short-cha
700	49.5	9.9	416	2	T25101	hypothetical prote	773	49	9.8	593	2	S45281	coagulation factor
701	49.5	9.9	483	2	T06712	probable cytochrom	774	49	9.8	606	2	A38630	prostaglandin-endo
702	49.5	9.9	490	2	T06711	probable cytochrom	775	49	9.8	603	2	A54665	netrin-1 precursor
703	49.5	9.9	554	2	B85072	hypothetical prote	776	49	9.8	640	1	A30452	uromodulin precurs
704	49.5	9.9	608	2	T02684	MYB-related trans	777	49	9.8	642	2	S53433	plasma protein S p
705	49.5	9.9	642	1	S52111	uromodulin precurs	778	49	9.8	663	1	A38283	arachidonate 12-li
706	49.5	9.9	646	2	JN0473	p-selectin precurs	779	49	9.8	685	2	JC7570	Delta-4 protein -
707	49.5	9.9	661	2	T42754	hypothetical prote	780	49	9.8	699	2	T12170	NADH2 dehydrogenas
708	49.5	9.9	689	2	T52060	protein MEDEA [imp	781	49	9.8	715	2	JC2222	major surface glyc
709	49.5	9.9	741	2	T13042	NADH2 dehydrogenas	782	49	9.8	727	2	E84847	probable CCH-type
710	49.5	9.9	741	2	T13658	NADH2 dehydrogenas	783	49	9.8	736	2	A99279	hypothetical prote
711	49.5	9.9	744	2	T13757	NADH2 dehydrogenas	784	49	9.8	739	2	H85245	VPI like protein l
712	49.5	9.9	756	2	S60966	probable protein k	785	49	9.8	739	2	T05163	hypothetical prote
713	49.5	9.9	853	2	T04600	probable beta-gala	786	49	9.8	754	2	AH3004	vgrG protein [impo
714	49.5	9.9	861	2	A48825	Notch homolog Motc	787	49	9.8	774	1	RRVETC	RNA-directed RNA p
715	49.5	9.9	874	2	T30398	late expression fa	788	49	9.8	790	2	H71509	phenylalanine-tRNA
716	49.5	9.9	915	1	A48225	subtilisin-like pr	789	49	9.8	816	2	B98196	hypothetical prote
717	49.5	9.9	926	1	A35905	endopeptidase Clp	790	49	9.8	816	2	AH3090	vgrG protein [impo
718	49.5	9.9	1188	2	T05846	DNA-directed RNA p	791	49	9.8	854	1	QRHYLD	LDL receptor precu
719	49.5	9.9	1191	2	S65068	DNA-directed RNA p	792	49	9.8	862	1	QRMSLD	LDL receptor precu
720	49.5	9.9	1221	2	T23472	hypothetical prote	793	49	9.8	873	1	A49729	VLDL receptor prec
721	49.5	9.9	1255	1	B44213	structural polypro	794	49	9.8	873	1	QRRBYD	VLDL receptor prec
722	49.5	9.9	1367	2	A14228	protein-tyrosine k	795	49	9.8	875	2	F96027	probable maltoolig
723	49.5	9.9	1523	2	T13953	MEGF5 protein - ra	796	49	9.8	910	2	A34721	androgen receptor
724	49.5	9.9	1607	1	MMMSB2	laminin gamma-1 ch	797	49	9.8	911	2	B34721	androgen receptor
725	49.5	9.9	1614	2	T29861	hypothetical prote	798	49	9.8	925	2	JC2033	G protein-coupled
726	49.5	9.9	1707	2	A33526	collagen alpha 2(I	799	49	9.8	949	2	T44577	hypothetical prote
727	49.5	9.9	1745	2	A46431	tight junction-ass	800	49	9.8	951	2	T45726	hypothetical prote
728	49.5	9.9	1748	1	JN0786	integrin beta-4 ch	801	49	9.8	973	2	T01862	hypothetical prote
729	49.5	9.9	1807	2	JC6319	integrin beta-4 ch	802	49	9.8	976	2	A36355	protein-tyrosine k
730	49.5	9.9	2025	2	T03884	hypothetical prote	803	49	9.8	998	2	I58351	receptor protein-t
731	49.5	9.9	2156	1	RRVUNE	genome polyprotein	804	49	9.8	1019	2	T13039	tyrosine kinase re
732	49.5	9.9	2406	2	A54148	odz protein - frui	805	49	9.8	1081	2	T15692	hypothetical prote
733	49.5	9.9	2415	1	A39086	aggreacan precursor	806	49	9.8	1133	1	EGRT	G protein-coupled
734	49.5	9.9	2515	2	S47008	tenascin-like prot	807	49	9.8	1135	2	S40241	epidermal growth f
735	49.5	9.9	3229	2	S27852	probable cell-surf	808	49	9.8	1176	2	C26427	period clock prote
736	49.5	9.9	3512	2	T17121	CPV protein - midg	809	49	9.8	1176	2	S40899	VPS8 protein - yea
737	49.5	9.9	3562	2	A47171	chondroitin sulfat	810	49	9.8	1292	2	T09229	galactose binding
738	49	9.8	62	2	I51538	metallothionein -	811	49	9.8	1343	2	T20718	hypothetical prote
739	49	9.8	65	2	S03858	carboxypeptidase A	812	49	9.8	1353	1	JQ2168	E2 glycoprotein pr
740	49	9.8	67	2	PC4008	hypothetical prote	813	49	9.8	1361	2	S29998	G glycoprotein pr
741	49	9.8	72	2	A42325	orf 5' to pheC - p	814	49	9.8	1362	2	A37474	surface protein -
742	49	9.8	93	2	S72363	pancreatic ribonuc	815	49	9.8	1363	2	VGIHQV	surface glycoprote
743	49	9.8	93	2	JE0159	gibberellin-stimul	816	49	9.8	1363	1	VGIHVA	E2 glycoprotein pr
744	49	9.8	96	2	S43910	gibberellin-regula	817	49	9.8	1363	1	VGIHF1	E2 glycoprotein pr
745	49	9.8	117	2	A24178	Whey acidic protei	818	49	9.8	1363	1	VGIHLY	E2 glycoprotein pr
746	49	9.8	127	1	NRBOK2	pancreatic-type ri	819	49	9.8	1363	1	VGIHNM	E2 glycoprotein pr
747	49	9.8	145	2	PSKF2U	phospholipase A2 (820	49	9.8	1363	2	S44241	surface protein -
748	49	9.8	193	2	PQ0503	surface protein -	821	49	9.8	1363	2	S44240	surface protein -
749	49	9.8	193	2	PQ0504	conserved hypothet	822	49	9.8	1526	2	T19473	hypothetical prote
750	49	9.8	239	2	F83366	keratin-like prote	823	49	9.8	1645	2	T31339	carbamoyl-phosphat
751	49	9.8	257	2	I38025	hypothetical prote	824	49	9.8	1711	2	AD1842	WD-40 repeat prote
752	49	9.8	278	2	H95611	hypothetical prote	825	49	9.8	1770	2	S56221	hypothetical prote
753	49	9.8	300	2	T49748	hypothetical prote	826	49	9.8	1786	1	MMHUB1	laminin beta-1 cha
754	49	9.8	302	2	T26513	hypothetical prote	827	49	9.8	2019	1	JQ1322	tenascin precursor
755	49	9.8	329	2	T07000	chitinase (EC 3.2.	828	49	9.8	2524	2	A35844	Xotrch protein - Af
756	49	9.8	329	2	T06999	chitinase (EC 3.2.	829	49	9.8	2588	2	T14342	NSDI protein - mou
757	49	9.8	375	2	S05390	fibromodulin precu	830	49	9.8	4302	2	A38971	polycystic kidney
758	49	9.8	386	2	JC7508	45K WW domain-cont	831	48.5	9.7	54	1	S23075	protein PMP-01 - m
759	49	9.8	388	2	JQ0189	oligogalacturonide	832	48.5	9.7	79	2	T06381	proteinase inhibit

833	48.5	9.7	99	2	S60230	gibberellin-regula	906	48	9.6	67	2	B69830	hypothetical prote
834	48.5	9.7	112	1	S54832	gipi protein - gar	907	48	9.6	74	2	AF3436	hypothetical prote
835	48.5	9.7	118	2	PSKFT2	phospholipase A2 (908	48	9.6	107	1	WMBEL2	latency-related pr
836	48.5	9.7	120	2	PH1650	ig heavy chain V r	909	48	9.6	134	1	WTBO	seminal fluid prot
837	48.5	9.7	135	2	G83671	hypothetical prote	910	48	9.6	147	2	T30616	hypothetical prote
838	48.5	9.7	150	2	T46301	hypothetical prote	911	48	9.6	170	2	A64347	conserved hypotet
839	48.5	9.7	155	2	I39626	nicotine denydroge	912	48	9.6	192	2	AF2851	hypothetical prote
840	48.5	9.7	177	1	CYDFAA	vascular endotheli	913	48	9.6	197	2	S66662	protease inhibit
841	48.5	9.7	190	2	S22130	hypothetical prote	914	48	9.6	201	2	T31492	hypothetical prote
842	48.5	9.7	202	2	T24524	nitrite hydratase	915	48	9.6	204	2	S63145	probable membrane
843	48.5	9.7	203	2	S54800	nitrite hydratase	916	48	9.6	229	2	D97628	ubiquinol-cytochro
844	48.5	9.7	203	2	S19714	hypothetical prote	917	48	9.6	237	2	I47031	insulin-like growt
845	48.5	9.7	207	2	B83523	hypothetical prote	918	48	9.6	237	2	S08073	cyclic nucleotide
846	48.5	9.7	232	2	A41551	vascular endotheli	919	48	9.6	240	2	A39842	insulin-like growt
847	48.5	9.7	250	2	T30124	hypothetical prote	920	48	9.6	245	2	T49889	zinc finger transc
848	48.5	9.7	267	2	F87665	hypothetical prote	921	48	9.6	250	2	S30157	osmotin precursor
849	48.5	9.7	274	2	T18768	hypothetical prote	922	48	9.6	251	2	B71298	hypothetical prote
850	48.5	9.7	297	2	T45705	hypothetical prote	923	48	9.6	260	2	T47391	hypothetical prote
851	48.5	9.7	298	2	T27644	hypothetical prote	924	48	9.6	268	2	B42424	chitinase (EC 3.2.
852	48.5	9.7	304	2	A33274	insulin-like growt	925	48	9.6	272	1	G69587	L-arabinose operon
853	48.5	9.7	305	2	JN0508	insulin-like growt	926	48	9.6	302	2	T39146	hypothetical prote
854	48.5	9.7	306	2	E97471	hypothetical prote	927	48	9.6	303	2	T46715	hypothetical prote
855	48.5	9.7	307	2	F71294	hypothetical prote	928	48	9.6	326	2	S14266	uracil-DNA glycosy
856	48.5	9.7	317	2	A36066	trans-activator of	929	48	9.6	332	2	T19150	hypothetical prote
857	48.5	9.7	317	2	D86070	regulator for metE	930	48	9.6	334	2	H69076	hypothetical prote
858	48.5	9.7	317	2	F91223	regulator for metE	931	48	9.6	334	2	D70918	hypothetical prote
859	48.5	9.7	346	2	T34129	hypothetical prote	932	48	9.6	335	2	H75518	probable cytochrom
860	48.5	9.7	350	2	T37511	probable phosphopr	933	48	9.6	344	2	I57698	folliculin - rat
861	48.5	9.7	354	1	S04243	proteoglycan link	934	48	9.6	348	2	A34705	collagen - Caenorh
862	48.5	9.7	355	1	LKCH	proteoglycan link	935	48	9.6	356	2	C70398	hypothetical prote
863	48.5	9.7	357	2	S09267	ig alpha chain C r	936	48	9.6	363	2	G82070	3-isopropylmalate
864	48.5	9.7	369	2	T48612	hypothetical prote	937	48	9.6	369	2	S41971	3-beta-hydroxy-Delt
865	48.5	9.7	396	1	WZBB8	dutp diphosphatase	938	48	9.6	374	2	A95960	probable cytochrom
866	48.5	9.7	400	2	T46383	hypothetical prote	939	48	9.6	375	1	A60004	matrix protein - m
867	48.5	9.7	433	2	B82365	hypothetical prote	940	48	9.6	375	1	MENZMS	matrix protein - m
868	48.5	9.7	448	2	S41725	integrase - Saccha	941	48	9.6	390	2	S52036	probable alcohol d
869	48.5	9.7	455	2	S33033	hypothetical prote	942	48	9.6	404	2	C86396	hypothetical prote
870	48.5	9.7	462	2	T40420	probable acid phos	943	48	9.6	414	2	H95843	hypothetical prote
871	48.5	9.7	470	2	A12188	hypothetical prote	944	48	9.6	431	2	S56228	alpha-factor recep
872	48.5	9.7	476	2	S57963	methyl CpG binding	945	48	9.6	442	2	S50062	cell wall glycopro
873	48.5	9.7	489	2	T06715	probable cytochrom	946	48	9.6	455	1	GQHUT1	tumor necrosis fac
874	48.5	9.7	521	2	I51693	XpPolcomb - Africa	947	48	9.6	457	2	S20662	glycine receptor a
875	48.5	9.7	559	1	C9HU	complement 'C9 prec	948	48	9.6	487	2	C47080	copper resistance
876	48.5	9.7	605	2	H69581	transcription acti	949	48	9.6	495	2	S32179	tniQ protein homol
877	48.5	9.7	614	2	S42526	finger protein unk	950	48	9.6	512	2	S28358	prespore vesicle p
878	48.5	9.7	634	1	S35574	transcription fact	951	48	9.6	532	2	E70731	probable pitB prot
879	48.5	9.7	640	2	T19346	hypothetical prote	952	48	9.6	551	2	E70610	hypothetical prote
880	48.5	9.7	702	2	E72775	probable helicase	953	48	9.6	580	2	D84772	probable sugar tra
881	48.5	9.7	726	2	H82774	phage-related DNA	954	48	9.6	594	1	A46758	glutamate decarbox
882	48.5	9.7	779	2	H71301	probable membrane-	955	48	9.6	600	2	JC4065	glutamate decarbox
883	48.5	9.7	796	2	AG2375	WD-40 repeat-prote	956	48	9.6	621	2	I49281	fertilin alpha pre
884	48.5	9.7	809	2	S55344	outer envelope mem	957	48	9.6	606	2	D86443	probable pPR-repea
885	48.5	9.7	810	2	B30848	plasmin (EC 3.4.21	958	48	9.6	615	1	KFHU12	coagulation factor
886	48.5	9.7	860	2	T39502	hypothetical prote	959	48	9.6	616	2	T32131	hypothetical prote
887	48.5	9.7	917	2	I48950	telencephalin prec	960	48	9.6	624	2	I38467	low density lipopr
888	48.5	9.7	932	2	T45894	hypothetical prote	961	48	9.6	624	2	T00044	vacuolar sorting r
889	48.5	9.7	958	2	H84783	probable PHD-type	962	48	9.6	634	2	T02594	hypothetical prote
890	48.5	9.7	977	2	S49004	tyrosine kinase Mp	963	48	9.6	651	2	A39372	potassium channel
891	48.5	9.7	1021	2	T05108	hypothetical prote	964	48	9.6	690	2	G84638	hypothetical prote
892	48.5	9.7	1162	2	T21557	hypothetical prote	965	48	9.6	698	2	T23469	hypothetical prote
893	48.5	9.7	1207	1	EGHU	epidermal growth f	966	48	9.6	706	2	T49899	zinc finger transc
894	48.5	9.7	1247	1	MMHUND	nidogen precursor	967	48	9.6	724	2	B71404	hypothetical prote
895	48.5	9.7	1328	2	T43060	agrin - electric r	968	48	9.6	729	2	AH2857	anthranilate synth
896	48.5	9.7	1391	2	T20406	hypothetical prote	969	48	9.6	729	2	F97634	hypothetical prote
897	48.5	9.7	1490	2	S72351	nonstructural poly	970	48	9.6	739	2	T21431	fibroblast growth
898	48.5	9.7	1508	2	E87696	glutamate synthase	971	48	9.6	748	2	S41050	fibroblast growth
899	48.5	9.7	1895	2	T15881	hypothetical prote	972	48	9.6	750	2	S41051	fibroblast growth
900	48.5	9.7	2182	2	T14320	calcineurin inhibi	973	48	9.6	786	2	A35466	progesterone recep
901	48.5	9.7	2643	2	T29149	hypothetical prote	974	48	9.6	818	2	T32154	hypothetical prote
902	48.5	9.7	3005	1	GNVSTV	genome polypeptin	975	48	9.6	822	2	T25866	hypothetical prote
903	48.5	9.7	3672	2	T23433	hypothetical prote	976	48	9.6	824	2	T23923	hypothetical prote
904	48.5	9.7	3704	2	T73116	probable laminin a	977	48	9.6	834	2	S13442	hemocyanin type A
905	48	9.6	66	2	S59621	metallothionein is	978	48	9.6	840	2	AG0526	penicillin-binding

979	48	9.6	892	2	F87325	hypothetical prote	1052	47.5	9.5	416	1	JN0006	nerve growth facto
980	48	9.6	923	2	A39596	progesterone recep	1053	47.5	9.5	418	2	E50925	probable enzyme EC
981	48	9.6	923	2	I53280	progesterone recep	1054	47.5	9.5	418	2	A85774	probable enzyme Z2
982	48	9.6	930	2	A25923	progesterone recep	1055	47.5	9.5	418	2	B64924	hypothetical prote
983	48	9.6	933	1	QRHUP	progesterone recep	1056	47.5	9.5	419	2	S69207	vascular endotheli
984	48	9.6	948	2	AD0790	sensor protein Rcs	1057	47.5	9.5	429	1	VHVUVH	nucleocapsid prote
985	48	9.6	965	2	S62935	hypothetical prote	1058	47.5	9.5	451	2	T20798	hypothetical prote
986	48	9.6	972	2	A30363	glycoprotein GP330	1059	47.5	9.5	451	2	A37048	similar to phospho
987	48	9.6	1013	2	I50615	receptor-type prot	1060	47.5	9.5	454	2	A37048	zinc finger protei
988	48	9.6	1019	2	A38738	coagulation factor	1061	47.5	9.5	455	2	T32189	probable lipopolya
989	48	9.6	1068	2	T04112	pol protein homolo	1062	47.5	9.5	473	2	C81984	probable udp-n-ace
990	48	9.6	1076	2	F96831	hypothetical prote	1063	47.5	9.5	475	2	T39359	4-carboxy-2-hydrox
991	48	9.6	1100	2	G83376	probable trehalase	1064	47.5	9.5	484	2	JC5779	4-carboxy-2-hydrox
992	48	9.6	1146	2	A38587	collagen, cornea-s	1065	47.5	9.5	505	2	T31272	thioglycosidase (E
993	48	9.6	1193	2	A86193	hypothetical prote	1066	47.5	9.5	524	2	S57621	protein-tyrosine k
994	48	9.6	1352	2	G84473	hypothetical prote	1067	47.5	9.5	527	2	S13763	amine oxidase (fla
995	48	9.6	1416	2	E88550	protein ZC84.1 [im	1068	47.5	9.5	527	2	S03974	hypothetical prote
996	48	9.6	1433	2	A46053	bullous pemphigoid	1069	47.5	9.5	535	2	D62437	hypothetical prote
997	48	9.6	1532	2	A61262	collagen alpha 1(X	1070	47.5	9.5	537	2	D86299	hypothetical prote
998	48	9.6	1609	1	MMHUB2	laminin gamma-1 ch	1071	47.5	9.5	558	2	S57953	C48p protein alpha
999	48	9.6	1767	2	T00458	hypothetical prote	1072	47.5	9.5	587	2	AG3169	conserved hypothet
1000	48	9.6	1808	2	T15099	hypothetical prote	1073	47.5	9.5	602	2	JU0215	protein-tyrosine k
1001	48	9.6	1959	1	A33977	myosin heavy chain	1074	47.5	9.5	611	2	A54086	calnexin-t - mouse
1002	48	9.6	2214	2	T16305	hypothetical prote	1075	47.5	9.5	630	1	T01380	protein-tyrosine k
1003	48	9.6	2319	2	A45597	DNA-directed RNA p	1076	47.5	9.5	631	2	E71933	hypothetical prote
1004	48	9.6	2470	2	I50726	cation-independent	1077	47.5	9.5	665	1	A42792	succinate dehydrog
1005	48	9.6	2610	2	T20968	hypothetical prote	1078	47.5	9.5	817	2	T21336	hypothetical prote
1006	48	9.6	2809	2	S20213	G-cadherin - sea u	1079	47.5	9.5	900	2	S70630	xeroderma pigmento
1007	48	9.6	2844	2	S28291	hypothetical prote	1080	47.5	9.5	919	2	A96812	protein F3F9.18 [i
1008	48	9.6	2896	2	T30939	hemocyanin G-type	1081	47.5	9.5	922	2	T23573	hypothetical prote
1009	48	9.6	3391	2	JS0219	polyprotein - deng	1082	47.5	9.5	987	2	T50850	receptor protein k
1010	47.5	9.5	64	2	A25775	metallothionein A	1083	47.5	9.5	1042	2	T26644	hypothetical prote
1011	47.5	9.5	65	1	NTSR3C	neurotoxin 3 - bar	1084	47.5	9.5	1045	2	S55253	sucrose-phosphate
1012	47.5	9.5	97	2	S26890	Ig heavy chain V r	1085	47.5	9.5	1119	2	T16720	hypothetical prote
1013	47.5	9.5	100	2	T17962	hypothetical prote	1086	47.5	9.5	1158	2	T50454	probable rho1 GDP-
1014	47.5	9.5	108	2	PH1651	Ig heavy chain V r	1087	47.5	9.5	1210	2	S35548	DNA-directed RNA p
1015	47.5	9.5	113	2	D75583	hypothetical prote	1088	47.5	9.5	1224	2	A25884	DNA-directed RNA p
1016	47.5	9.5	120	2	T31000	cysteine-rich prot	1089	47.5	9.5	2492	1	A44213	nonstructural poly
1017	47.5	9.5	125	2	S24831	hypothetical prote	1090	47.5	9.5	2492	1	MNVVTD	nonstructural poly
1018	47.5	9.5	143	2	B84128	cell wall hydrolas	1091	47.5	9.5	2567	2	A49551	filamin, Muller ce
1019	47.5	9.5	152	2	A56939	isoquinoline 1-oxi	1092	47.5	9.5	3034	2	T14119	seven-pass transme
1020	47.5	9.5	172	1	KRSHHA	keratin high-sulfu	1093	47.5	9.5	3228	2	T21381	hypothetical prote
1021	47.5	9.5	186	2	T32656	hypothetical prote	1094	47.5	9.5	3759	2	A35085	trithorax protein
1022	47.5	9.5	207	2	F95966	probable aldehyde	1095	47.5	9.5	3766	2	T29185	hypothetical prote
1023	47.5	9.5	209	2	T02394	hypothetical prote	1096	47.5	9.5	5825	2	T12117	polyprotein - fava
1024	47.5	9.5	220	2	T21730	hypothetical prote	1097	47	9.4	88	2	T36927	probable small sec
1025	47.5	9.5	230	2	JC7972	spermatogenesis-re	1098	47	9.4	97	2	S71371	gibberellin-regula
1026	47.5	9.5	231	2	B90691	hypothetical prote	1099	47	9.4	114	2	T38286	T cell leukemia/ly
1027	47.5	9.5	231	2	D64774	ybax protein - Esc	1100	47	9.4	114	2	T19716	hypothetical prote
1028	47.5	9.5	231	2	F85541	hypothetical prote	1101	47	9.4	131	1	ZYSMN	metalloproteinase
1029	47.5	9.5	236	2	H71287	conserved hypothet	1102	47	9.4	131	1	KRG73M	keratin high-sulfu
1030	47.5	9.5	255	2	I38426	lymphocyte activat	1103	47	9.4	138	2	A05215	hypothetical prote
1031	47.5	9.5	264	2	T16271	hypothetical prote	1104	47	9.4	144	2	C71252	hypothetical prote
1032	47.5	9.5	281	2	C88638	protein F58F6.1 [i	1105	47	9.4	150	2	D87652	hypothetical prote
1033	47.5	9.5	304	2	T30716	hypothetical prote	1106	47	9.4	155	2	T25845	hypothetical prote
1034	47.5	9.5	308	2	T05297	hypothetical prote	1107	47	9.4	157	2	C87659	conserved hypothet
1035	47.5	9.5	312	2	T25048	hypothetical prote	1108	47	9.4	158	2	AB1045	FxaA protein [limp
1036	47.5	9.5	317	2	AD0461	lysR-family transac	1109	47	9.4	158	2	T42700	hypothetical prote
1037	47.5	9.5	323	1	SYEBAC	cysteine synthase	1110	47	9.4	158	2	AG0223	conserved hypothet
1038	47.5	9.5	323	2	AD0810	cysteine synthase	1111	47	9.4	167	1	JC1102	endothelin 3 precu
1039	47.5	9.5	324	2	S20981	chitinase (EC 3.2.	1112	47	9.4	168	2	S78110	thi protein - Rhiz
1040	47.5	9.5	324	2	JC2395	Fas antigen precu	1113	47	9.4	169	2	JQ1599	dUTP diphosphatase
1041	47.5	9.5	325	2	T02455	hypothetical prote	1114	47	9.4	176	2	B85355	hypothetical prote
1042	47.5	9.5	329	2	T32783	hypothetical prote	1115	47	9.4	176	2	T22273	hypothetical prote
1043	47.5	9.5	333	2	T20436	hypothetical prote	1116	47	9.4	180	2	AE1010	conserved hypothet
1044	47.5	9.5	342	2	T18993	hypothetical prote	1117	47	9.4	200	2	F69047	hypothetical prote
1045	47.5	9.5	347	2	T34131	hypothetical prote	1118	47	9.4	208	2	P97570	GTP cyclohydrolase
1046	47.5	9.5	354	2	T19856	hypothetical prote	1119	47	9.4	208	2	Ar2791	GTP cyclohydrolase
1047	47.5	9.5	370	2	F86236	conserved hypothet	1120	47	9.4	219	2	H85358	hypothetical prote
1048	47.5	9.5	375	2	A81227	probable integral	1121	47	9.4	230	2	S25964	ribosomal protein
1049	47.5	9.5	375	2	F81999	hypothetical prote	1122	47	9.4	233	2	T22977	hypothetical prote
1050	47.5	9.5	397	2	A32370	cyclin B1 - Africa	1123	47	9.4	235	2	A53853	apolipoprotein B m
1051	47.5	9.5	411	2	T19728	hypothetical prote	1124	47	9.4	242	2	T31174	hypothetical prote

1125	47	9.4	250	2	E70104	1-acylglycerol-3-P	1198	47	9.4	788	1	JDLVHH	DNA-directed DNA p
1126	47	9.4	258	2	D85550	glyoxylate-induced	1199	47	9.4	861	2	I39714	cellulose synthase
1127	47	9.4	258	2	A90700	hydroxypruvate is	1200	47	9.4	907	2	B75182	DNA-directed RNA p
1128	47	9.4	266	2	T08059	alcohol dehydrogen	1201	47	9.4	916	2	G75417	SNP/Rad54 helicas
1129	47	9.4	271	2	S12783	OX40 antigen precu	1202	47	9.4	969	1	A39490	subtilisin-like pr
1130	47	9.4	271	2	JC4584	insulin-like growt	1203	47	9.4	988	2	I50611	protein-tyrosine k
1131	47	9.4	274	2	T36489	hypothetical prote	1204	47	9.4	1086	2	T05407	hypothetical prote
1132	47	9.4	279	2	C75538	hypothetical prote	1205	47	9.4	1168	2	I56985	kalinin B1 - mouse
1133	47	9.4	280	2	A42424	chitinase (EC 3.2.	1206	47	9.4	1219	2	H84464	probable helicase
1134	47	9.4	283	2	JC6531	avermectin B 5-O-m	1207	47	9.4	1324	2	S06187	RNA2 polypeptide -
1135	47	9.4	309	2	B49878	coagulation factor	1208	47	9.4	1354	2	T13363	phosphoribosylform
1136	47	9.4	332	2	D70605	probable nh0A prot	1209	47	9.4	1356	2	A54445	janusin precursor,
1137	47	9.4	338	2	AB1816	hypothetical prote	1210	47	9.4	1372	2	T25933	hypothetical prote
1138	47	9.4	350	2	T39795	probable ubiquitin	1211	47	9.4	1375	2	T18961	FAB1 protein homol
1139	47	9.4	350	2	S00337	legumin B legk pre	1212	47	9.4	1474	2	D88550	protein ZC94.6 [im
1140	47	9.4	351	2	S20078	NOV protein - chic	1213	47	9.4	1545	2	T14288	DNA (cytosine-5-) -
1141	47	9.4	353	1	ROECA	recombination prot	1214	47	9.4	1611	2	G84493	probable retroelem
1142	47	9.4	353	2	H85917	hypothetical prote	1215	47	9.4	1961	1	A61231	myosin heavy chain
1143	47	9.4	353	2	AH0843	RecA protein (impo	1216	47	9.4	2201	2	A32160	tenascin-C - human
1144	47	9.4	353	2	D91073	RecA protein (impo	1217	47	9.4	4151	2	T13734	groovin gene prote
1145	47	9.4	354	2	S31481	recombination prot	1218	46.5	9.3	58	2	AD0841	hypothetical prote
1146	47	9.4	356	2	S37586	recombination prot	1219	46.5	9.3	65	1	NTSR1C	neurotoxin 1 - bar
1147	47	9.4	356	2	AG0401	RecA protein (impo	1220	46.5	9.3	98	2	I47086	BIIB4 high-sulfur
1148	47	9.4	358	2	T26281	hypothetical prote	1221	46.5	9.3	118	1	PSKFT3	phospholipase A2 (
1149	47	9.4	367	1	S24935	choline-phosphate	1222	46.5	9.3	130	2	T08584	hypothetical prote
1150	47	9.4	369	2	A34614	placental protein	1223	46.5	9.3	137	2	T15609	hypothetical prote
1151	47	9.4	380	2	G01639	transmembrane prot	1224	46.5	9.3	141	2	A64751	hypothetical prote
1152	47	9.4	387	2	B38302	pepsin (EC 3.4.23.	1225	46.5	9.3	147	2	G83586	hypothetical prote
1153	47	9.4	404	2	H84593	hypothetical prote	1226	46.5	9.3	162	2	QJ1551	V3 protein - panic
1154	47	9.4	410	2	S26669	retinoic acid rece	1227	46.5	9.3	182	1	KRSHHD	keratin high-sulfu
1155	47	9.4	434	2	T19205	hypothetical prote	1228	46.5	9.3	188	1	S53524	adrenodoxin precu
1156	47	9.4	438	2	E86924	probable glycosyl	1229	46.5	9.3	198	2	S56510	hypothetical prote
1157	47	9.4	444	2	T27234	hypothetical prote	1230	46.5	9.3	202	2	JC1358	thiol-endopeptidas
1158	47	9.4	446	2	A34418	H-2 region II bind	1231	46.5	9.3	210	2	T10590	hypothetical prote
1159	47	9.4	448	2	D41727	retinoid X recepto	1232	46.5	9.3	235	2	S43513	hemoglobin linker
1160	47	9.4	448	2	T36114	probable transfera	1233	46.5	9.3	252	2	H82574	phage-related prot
1161	47	9.4	451	2	A41651	retinoic acid rece	1234	46.5	9.3	259	1	PMMSBM	bisphosphoglycerat
1162	47	9.4	461	1	KXHU	protein C (activat	1235	46.5	9.3	262	2	E70548	probable bpoC prot
1163	47	9.4	478	2	JQ1301	hemorrhagic protei	1236	46.5	9.3	274	2	T52103	GATA-binding trans
1164	47	9.4	479	2	T16130	hypothetical prote	1237	46.5	9.3	277	2	JC7903	collectin liver 1
1165	47	9.4	486	2	T06770	cellulase (EC 3.2.	1238	46.5	9.3	282	1	HLHMSG	class II histocomp
1166	47	9.4	490	2	T06710	probable cytochrom	1239	46.5	9.3	282	2	S27769	NAD glycohydrolase
1167	47	9.4	493	2	JC5621	epidermal growth f	1240	46.5	9.3	292	2	T50710	hypothetical prote
1168	47	9.4	499	2	A86468	probable zinc fing	1241	46.5	9.3	305	2	S76401	hypothetical prote
1169	47	9.4	500	2	S26688	legumin K - garden	1242	46.5	9.3	312	2	D97552	lipid A biosynthes
1170	47	9.4	520	2	I84718	RXR-beta1 isoform	1243	46.5	9.3	312	2	A52772	lipid A biosynthes
1171	47	9.4	522	2	D96764	unknown protein F2	1244	46.5	9.3	313	2	T22828	hypothetical prote
1172	47	9.4	527	2	JE0373	low density lipopr	1245	46.5	9.3	316	2	S65020	chitinase (EC 3.2.
1173	47	9.4	533	2	S37781	retinoid X recepto	1246	46.5	9.3	316	2	AB0669	probable virulence
1174	47	9.4	541	2	T47290	hypothetical prote	1247	46.5	9.3	320	2	S22450	cell adhesion glyco
1175	47	9.4	551	1	VGNZPG	cell fusion glycop	1248	46.5	9.3	320	2	A53119	conserved hypotet
1176	47	9.4	555	2	I53869	zinc finger protei	1249	46.5	9.3	328	2	B81724	hypothetical prote
1177	47	9.4	555	2	T40294	hypothetical prote	1250	46.5	9.3	332	2	F85058	hypothetical prote
1178	47	9.4	581	2	F82723	single-stranded DN	1251	46.5	9.3	342	2	A83263	dihydroorotate den
1179	47	9.4	585	2	T47364	hypothetical prote	1252	46.5	9.3	347	2	T32768	hypothetical prote
1180	47	9.4	606	2	S43118	finger protein - m	1253	46.5	9.3	356	2	T32827	hypothetical prote
1181	47	9.4	612	2	JH0799	laminin-related pr	1254	46.5	9.3	359	2	A43532	B-cell surface ant
1182	47	9.4	621	2	JC1346	dopamine beta-mono	1255	46.5	9.3	367	2	G71076	probable hydrogena
1183	47	9.4	635	2	S36718	phosphoprotein pho	1256	46.5	9.3	369	1	TVCHTB	thyroid hormone re
1184	47	9.4	647	2	E82579	acetyl coenzyme A	1257	46.5	9.3	369	2	S58211	beta-thyroid hormo
1185	47	9.4	651	2	E85024	probable CHP-rich	1258	46.5	9.3	371	2	T32692	hypothetical prote
1186	47	9.4	676	2	A40363	DNA ligase-(NAD) (1259	46.5	9.3	377	2	C83372	hypothetical prote
1187	47	9.4	693	2	JN0573	ubiquitin-like fus	1260	46.5	9.3	390	2	D70849	probable aminotran
1188	47	9.4	704	2	B84685	hypothetical prote	1261	46.5	9.3	391	2	H70640	probable pqqE prot
1189	47	9.4	716	1	A40332	macrophage-stimula	1262	46.5	9.3	394	2	T21013	hypothetical prote
1190	47	9.4	724	2	C49423	semaphorin II prec	1263	46.5	9.3	394	2	C75405	streptomycin biosy
1191	47	9.4	735	2	T08140	1-deoxy-D-xylulose	1264	46.5	9.3	419	2	JQ2254	farnesyl-diphospha
1192	47	9.4	735	2	AE1858	anthranilate synth	1265	46.5	9.3	421	2	E86184	hypothetical prote
1193	47	9.4	743	2	B84639	probable ubiquitin	1266	46.5	9.3	437	2	B70540	probable adenosylm
1194	47	9.4	756	2	S47656	tMDC II protein -	1267	46.5	9.3	446	2	T31644	hypothetical prote
1195	47	9.4	759	2	T43031	DNA topoisomerase	1268	46.5	9.3	449	2	C84458	hypothetical prote
1196	47	9.4	763	2	E86326	hypothetical prote	1269	46.5	9.3	459	2	T19991	hypothetical prote
1197	47	9.4	775	2	A48644	polypeptide - deng	1270	46.5	9.3	465	2	H86482	protein P5J5.11 [i

1271	46.5	9.3	469	1	NMTV27	exo-alpha-sialidas	1344	46	9.2	62	2	H81791	hypothetical prote
1272	46.5	9.3	473	2	C81039	lipopolysaccharide	1345	46	9.2	66	2	A55869	crustacean-specifi
1273	46.5	9.3	476	2	T46067	hypothetical prote	1346	46	9.2	81	4	B49316	hypothetical prote
1274	46.5	9.3	476	2	S09489	carboxypeptidase E	1347	46	9.2	95	2	T42112	hypothetical prote
1275	46.5	9.3	476	2	JC7189	tubulointerstitial	1348	46	9.2	98	1	KRSHH4	keratin high-sulfu
1276	46.5	9.3	476	2	I80182	activin type I rec	1349	46	9.2	113	2	SS6647	trypsin inhibitor
1277	46.5	9.3	485	2	JM0056	2-hydroxyuconic s	1350	46	9.2	123	2	S18470	wnt protein homolo
1278	46.5	9.3	485	2	T19990	hypothetical prote	1351	46	9.2	124	2	AE2874	hypothetical prote
1279	46.5	9.3	486	2	S10772	2-hydroxyuconic s	1352	46	9.2	125	2	E72716	hypothetical prote
1280	46.5	9.3	486	2	E42902	2-hydroxyuconic s	1353	46	9.2	127	2	T44119	hypothetical prote
1281	46.5	9.3	487	2	I80183	activin type I rec	1354	46	9.2	132	2	H72531	hypothetical prote
1282	46.5	9.3	492	2	A41907	methyl-CpG-binding	1355	46	9.2	137	2	AI0575	conserved hypothe
1283	46.5	9.3	496	2	S51668	tyrosine kinase -	1356	46	9.2	143	2	JQ1448	hypothetical 16K p
1284	46.5	9.3	503	2	S00336	legumin B LegJ pre	1357	46	9.2	150	1	OKBY51	cell diviaion cont
1285	46.5	9.3	523	2	T23003	hypothetical prote	1358	46	9.2	151	2	AE2352	hypothetical prote
1286	46.5	9.3	530	2	T38558	Mi-2 autoantigen 2	1359	46	9.2	156	2	H69455	tungsten formylmet
1287	46.5	9.3	565	2	T16408	hypothetical prote	1360	46	9.2	160	2	C86458	unknown protein, 6
1288	46.5	9.3	617	2	G70366	glucose inhibited	1361	46	9.2	163	1	H83499	ferredoxin protein
1289	46.5	9.3	639	2	A32545	protein kinase C (1362	46	9.2	174	2	T15176	hypothetical prote
1290	46.5	9.3	657	2	T00859	hypothetical prote	1363	46	9.2	180	2	AG0796	NADH2 dehydrogen
1291	46.5	9.3	662	2	T23271	hypothetical prote	1364	46	9.2	180	2	F85868	NADH dehydrogen
1292	46.5	9.3	668	2	T18635	hypothetical prote	1365	46	9.2	180	2	G64939	NADH dehydrogen
1293	46.5	9.3	677	2	C42125	trophozoite cystei	1366	46	9.2	180	2	E91034	NADH dehydrogen
1294	46.5	9.3	680	2	T30620	hypothetical prote	1367	46	9.2	180	2	AB0311	NADH2 dehydrogen
1295	46.5	9.3	680	2	G95964	probable iron upta	1368	46	9.2	184	2	AC3427	transposase BME114
1296	46.5	9.3	684	2	T71379	probable phosphotr	1369	46	9.2	188	2	G95889	probable oxidoredu
1297	46.5	9.3	700	2	B06088	hypothetical prote	1370	46	9.2	191	2	G90088	40S ribosomal prot
1298	46.5	9.3	707	2	S52390	D-hordein precursor	1371	46	9.2	193	2	T35847	probable carbonic
1299	46.5	9.3	726	2	C82548	phage-related DNA	1372	46	9.2	193	2	D97157	stage III sporulat
1300	46.5	9.3	729	2	JC7501	oligopeptide trans	1373	46	9.2	203	2	T17972	hypothetical prote
1301	46.5	9.3	736	2	B71972	DNA topoisomerase	1374	46	9.2	204	2	E84443	probable disease r
1302	46.5	9.3	736	2	D64534	DNA topoisomerase	1375	46	9.2	205	2	G82563	autolytic lysozyme
1303	46.5	9.3	740	2	A71141	hypothetical prote	1376	46	9.2	207	2	S28510	E6 protein - multi
1304	46.5	9.3	744	2	T12627	NADH2 dehydrogen	1377	46	9.2	209	2	T30638	hypothetical prote
1305	46.5	9.3	744	2	T13585	NADH2 dehydrogen	1378	46	9.2	210	1	OQZMCA	hypothetical prote
1306	46.5	9.3	751	2	F87789	protein C34G6.2 [i	1379	46	9.2	210	2	I40540	varD protein - Pee
1307	46.5	9.3	772	2	S32659	integrin beta 2 ch	1380	46	9.2	214	2	AF0779	glutathione-S-tran
1308	46.5	9.3	786	2	S28084	env polypeptin -	1381	46	9.2	215	2	A29318	ubiquinol-cytochro
1309	46.5	9.3	787	2	E82227	DNA polymerase II	1382	46	9.2	219	2	E82825	hypothetical prote
1310	46.5	9.3	797	2	A36811	hypothetical prote	1383	46	9.2	220	2	S44808	hypothetical prote
1311	46.5	9.3	812	2	T52569	squamosa-promoter	1384	46	9.2	223	2	D81741	glutamate decarbox
1312	46.5	9.3	905	2	S43064	cadherin - African	1385	46	9.2	226	2	D81741	phosphoglycerate m
1313	46.5	9.3	909	1	ORXL2	LDL receptor 2 pre	1386	46	9.2	231	1	RDCUF	ubiquinol-cytochro
1314	46.5	9.3	920	2	T40771	hypothetical prote	1387	46	9.2	243	2	D97237	phosphoglycerate m
1315	46.5	9.3	979	2	G90459	formate dehydrogen	1388	46	9.2	249	2	T24604	hypothetical prote
1316	46.5	9.3	995	2	AB1398	formate dehydrogen	1389	46	9.2	254	2	I48539	insulin-like growt
1317	46.5	9.3	995	2	AE1773	formate dehydrogen	1390	46	9.2	254	2	JC1464	insulin-like growt
1318	46.5	9.3	1023	2	T30257	IGF Fc binding pro	1391	46	9.2	256	2	T28106	hypothetical prote
1319	46.5	9.3	1034	1	A53663	enteropeptidase (E	1392	46	9.2	257	2	T12961	hypothetical prote
1320	46.5	9.3	1035	2	G83342	hypothetical prote	1393	46	9.2	269	2	T36639	probable substrate
1321	46.5	9.3	1046	2	A28638	prestalk protein p	1394	46	9.2	269	2	S75243	hypothetical prote
1322	46.5	9.3	1108	2	D96798	hypothetical prote	1395	46	9.2	270	2	T16868	hypothetical prote
1323	46.5	9.3	1148	2	S51855	hypothetical prote	1396	46	9.2	286	2	S61199	hypothetical prote
1324	46.5	9.3	1182	2	I48378	hairless protein -	1397	46	9.2	287	2	B72387	deoxyribonuclease
1325	46.5	9.3	1186	2	T33754	O/E-1-associated z	1398	46	9.2	289	2	AH3113	shikimate 5-dehydr
1326	46.5	9.3	1188	2	D82636	protein F4AN23.5 [1399	46	9.2	289	2	E98173	hypothetical prote
1327	46.5	9.3	1210	2	A53183	epidermal growth f	1400	46	9.2	289	2	T46026	hypothetical prote
1328	46.5	9.3	1254	1	JQ1978	structural polyprio	1401	46	9.2	312	2	AE3083	alcohol dehydrogen
1329	46.5	9.3	1254	1	JQ1979	structural polyprio	1402	46	9.2	312	2	C98203	probable adhE prot
1330	46.5	9.3	1254	1	VHVVE	structural polyprio	1403	46	9.2	319	2	A53502	folliatin - Afri
1331	46.5	9.3	1254	1	VHVVT	structural polyprio	1404	46	9.2	320	1	G72061	probable phosphoe
1332	46.5	9.3	1255	1	D44213	structural polyprio	1405	46	9.2	320	1	G86562	probable phosphoe
1333	46.5	9.3	1353	1	JH0675	restrictin precurs	1406	46	9.2	325	2	VNUT17	VSG expression sit
1334	46.5	9.3	1414	2	T33236	hypothetical prote	1407	46	9.2	334	2	C70673	probable gpd2 pro
1335	46.5	9.3	1414	2	T33236	hypothetical prote	1408	46	9.2	334	2	D83788	UDP-glucose 4-epim
1336	46.5	9.3	2163	2	T15276	genome polypeptin	1409	46	9.2	334	2	E95279	probable [imported
1337	46.5	9.3	2531	2	T16743	hypothetical prote	1410	46	9.2	338	2	S75089	UDP-glucose 4-epim
1338	46.5	9.3	3461	2	S58870	hypothetical prote	1411	46	9.2	343	2	S55369	folliatin - chic
1339	46	9.2	43	2	JC2554	reelin precursor -	1412	46	9.2	346	2	A64448	hypothetical prote
1340	46	9.2	44	2	I48942	holotricin 1 - Hol	1413	46	9.2	361	2	T30743	hypothetical prote
1341	46	9.2	48	2	S68952	cellular disintegr	1414	46	9.2	366	1	A46704	aryl-alcohol dehyd
1342	46	9.2	60	2	B27490	omega-hordothionin	1415	46	9.2	366	1	D70351	probable hexosyltr
1343	46	9.2	60	2	AE3099	metallothionein B	1416	46	9.2	367	2	T29752	hypothetical prote

hypothetical prote	hypothetical prote	crustacean-specific	hypothetical prote	hypothetical prote	keratin high-sulfu	trypsin inhibitor	wnt protein homolo	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothe	hypothetical 16K p	cell diviaion cont	hypothetical prote	tungsten formylmet	unknown protein, 6	ferredoxin protein	hypothetical prote	NADH2 dehydrogen	NADH dehydrogen	NADH dehydrogen	NADH dehydrogen	NADH dehydrogen	NADH2 dehydrogen	transposase BME114	probable oxidoredu	40S ribosomal prot	probable carbonic	stage III sporulat	hypothetical prote	probable disease r	autolytic lysozyme	E6 protein - multi	hypothetical prote	hypothetical prote	varD protein - Pee	glutathione-S-tran	ubiquinol-cytochro	hypothetical prote	hypothetical prote	glutamate decarbox	phosphoglycerate m	ubiquinol-cytochro	phosphoglycerate m	hypothetical prote	insulin-like growt	insulin-like growt	hypothetical prote	hypothetical prote	probable substrate	hypothetical prote	hypothetical prote	hypothetical prote	deoxyribonucle	shikimate 5-dehydry	hypothetical prote	hypothetical prote	alcohol dehydrogen	probable adhE prot	foliastatin - Afri	probable phosphose	probable phosphose	vsg expression sit	probable gp42 pro	UNP-glucose 4-epim	probable [importe	UNP-glucose 4-epim	foliastatin - chic	hypothetical prote	hypothetical prote	aryl-alcohol dehydry	probable hexosyltr	hypothetical prote
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Db 488 CTAGRCC-----WM-----TCLPWWGSGGTWPRPLMTF-----SRTACALPTPCCSRWL 533

Qy 71 -----PDGRYRCSM 79

Db 534 RWRGWPAGGRWRCSL 549

RESULT 3

notch4 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09059

R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Schmitt, L.; et al. 1997. The mouse major histocompatibility locus class III region. Submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.

A:Reference number: Z16543

A:Accession: T09059

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1964 <ROW>

A:Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:g2564945;

C:Genetics:

A:Gene: notch4

A:Map position: 17

A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 671/1; 729/1; 761/1; 761/3

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

C:Keywords: receptor; signal transduction

F:514-545/Domain: EGF homology <EGF>

Query Match 16.3%; Score 81; DB 2; Length 1964;

Best Local Similarity 30.4%; Pred. No. 1.8;

Matches 24; Conservative 7; Mismatches 22; Indels 26; Gaps 5;

Qy 7 CBRDQV-----CGAGTCCALSLWLRGRLWC-TPLGREGECHPGSHKVPFRKRKH 57

Db 188 CBRDINECFLEPGCPQGTSCHNTL---GSYCLCPVGQEGPQC-----KLKRG 233

Qy 58 TCP---CLPNLLCSRPDQ 73

Db 234 ACPGSGCLNGTCLQVPEG 252

RESULT 4

A56175

adhesive plaque protein Mgf2 precursor - Mediterranean mussel

C:Species: Mytilus galloprovincialis (Mediterranean mussel)

C:Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C:Accession: A56175

R:Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.

J. Biol. Chem. 270, 6698-6701, 1995

A:Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth factor family

A:Reference number: A56175; MUID:95204464; PMID:7896812

A:Accession: A56175

A:Molecule type: mRNA

A:Residues: 1-473 <INO>

A:Cross-references: UNIPROT:Q25464; UNIPARC:UPI000012AB7B; GB:D43794; NID:g602767; PIDN:

C:Keywords: duplication

F:1-17/Domain: signal homology #status predicted <SIG>

F:387-419/Domain: EGF homology <EGF>

F:429-460/Domain: EGF homology <EGF>

F:23.36, 43.55, 75.382, 424.455, 468.473/Modified site: 3', 4'-dihydroxyphenylalanine (Tyr) #

Query Match 15.6%; Score 77.5; DB 2; Length 473;

Best Local Similarity 31.2%; Pred. No. 1.2;

Matches 24; Conservative 11; Mismatches 23; Indels 19; Gaps 7;

Qy 7 CBRDVOCGAGTCCALSLWLRGLRMCCTPLGREGECH-PGSHKVPFRKRKH 62

Db 117 CEKNV-CSPNPC-----KNGKCSPLKTKYKCTCGGYTGP---RCEVHACKPNPK 165

Qy 63 PNLLCSRPDGR--YRC 77

Db 166 NKGRC--FPDGKTYKC 180

RESULT 5

T31070

notch homolog - sea urchin (Lytechinus variegatus)

C:Species: Lytechinus variegatus (variegated urchin)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000

C:Accession: T31070

R:Sherwood, D.R.; McClay, D.R.

Development 124, 3363-3374, 1997

A:Title: Identification and localization of a sea urchin Notch homologue: insights into the role of the Notch signaling pathway in the development of the sea urchin

A:Reference number: Z20986; MUID:97454256; PMID:9310331

A:Accession: T31070

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2531 <SHE>

A:Cross-references: UNIPARC:UPI000007E31C; EMBL:AF000634; NID:g2570350; PID:g2570351; P31

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 15.1%; Score 75; DB 2; Length 2531;

Best Local Similarity 29.9%; Pred. No. 9.4;

Matches 23; Conservative 8; Mismatches 32; Indels 14; Gaps 5;

Qy 3 ITGACERDVQCGAGTCCAI--SLWLRGLRMCCTPLGREGECHPGSHKVPFRKRKH 60

Db 120 VDNVCKLEEPQCGTCTRLTSLWDYEC-FCTP-ANTGENCTDDNHCV-----SNP 168

Qy 61 CLPNLLCSRPDGRYRC 77

Db 169 CLNGAVCTSSSDG-YSC 184

RESULT 6

XLHU

colipase precursor [validated] - human

N:Alternate names: procolipase

C:Species: Homo sapiens (man)

C:Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004

C:Accession: A42568; A33949; A03163

R:Sims, H.F.; Lowe, M.E.

Biochemistry 31, 7120-7125, 1992

A:Title: The human colipase gene: isolation, chromosomal location, and tissue-specific expression

A:Reference number: A42568; MUID:92353041; PMID:1643046

A:Accession: A42568

A:Molecule type: DNA

A:Residues: 1-112 <SIM>

A:Cross-references: UNIPROT:P04118; UNIPARC:UPI0000127E78; GB:M95529; NID:g180842; PIDN:

A:Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBIP:110580)

R:Lowe, M.E.; Rosenblum, J.L.; McEwen, P.; Strauss, A.W.

Biochemistry 29, 823-828, 1990

A:Title: Cloning and characterization of the human colipase cDNA.

A:Reference number: A33949; MUID:90248429; PMID:2337598

A:Accession: A33949

A:Molecule type: mRNA

A:Residues: 1-112 <LOW>

A:Cross-references: UNIPARC:UPI0000127E78; GB:J02883; NID:g180885; PIDN:AAA52054.1; PID:

A:Note: evidence of partial N-glycosylation, possibly at Asn-43

R:Strom, B.; Engstrom, A.; Hellman, U.; Vihert, A.M.; Sternby, N.H.; Borgstrom, B.

Biochim. Biophys. Acta 784, 75-80, 1984

A:Title: The primary sequence of human pancreatic colipase.

A:Reference number: A90652; MUID:84104937; PMID:6691986

A:Accession: A03163

A:Molecule type: protein

A:Residues: 23-108 <STE>

A:Cross-references: UNIPARC:UPI0000174141

C:Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 stoichiometric complex with the enzyme which are known to have an inhibitory effect on the enzyme is washed off by bile salts, which are known to have an inhibitory effect on the enzyme

C:Genetics:

A:Gene: GDB:CLPS

A:Cross-references: GDB:127277; OMIM:120105

A;Map position: 6pter-6p21.1
 A;Introns: 28/3; 69/3
 C;Superfamily: colipase
 C;Keywords: lipid digestion; lipid hydrolysis; pancreas
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-22/Domain: amino-terminal propeptide #status predicted <APP>
 F;23-108/Product: colipase #status experimental <MAT>
 F;109-112/Domain: carboxyl-terminal propeptide #status predicted <CPP>
 F;34-104,40-56,44-80,45-78,66-86/Disulfide bonds: #status predicted
 F;69,72,75,76/Binding site: micellar substrate (Lys, Tyr, Tyr) #status predicted

Query Match 14.7%; Score 73; DB 1; Length 112;
 Best Local Similarity 31.2%; Pred. No. 1;
 Matches 25; Conservative 6; Mismatches 37; Indels 12; Gaps 5;

QY 7 CERDVCGAGTCAISLWLRGLRMCTPLGRGEGCHPGSHKVPFRKRKHHTCPCLPPLL 66
 DB 34 CWNASQC-KSNCOHSAL-GLARCTSMASENSEC---SVKTLF---GIYKPCBGRGLT 85

QY 67 CSRFDPDGRYCSMDLKNINF 86
 DB 86 C---EGDKTIVGSINTNF 101

RESULT 7
 A35356
 tumor necrosis factor receptor 2 precursor [validated] - human
 N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
 C;Species: Homo sapiens (man)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A35356; A48416; A36007; A23666; B35010; I38094
 R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
 Science 248, 1019-1023, 1990
 A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
 A;Reference number: A35356; MUID:90260639; PMID:2160731
 A;Accession: A35356
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-461 <SMI>
 A;Cross-references: UNIPROT:P20333; UNIPARC:UPI000002FAEL; GB:M32315; NID:G189185; PIDN:
 R;Kohn, T.; Brewer, M.T.; Baker, S.B.; Schwart, P.E.; King, M.W.; Hale, K.K.; Squires,
 Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A;Reference number: A36475; MUID:91045991; PMID:2172983
 A;Accession: A36475
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-195,'R',197-461 <KOH>
 A;Cross-references: UNIPARC:UPI000003475F; GB:M55994; GB:M38549; NID:G339757; PIDN:AAA36
 R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
 Cytokine 2, 231-237, 1990
 A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
 A;Reference number: A48416; MUID:91370690; PMID:1966549
 A;Accession: A48416
 A;Status: preliminary
 A;Molecule type: mRNA; protein
 A;Residues: 23-461 <DEW>
 A;Cross-references: UNIPARC:UPI00001736E6; GB:S63368; NID:G235648; PIDN:AAB19824.1; PID:
 A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIPI:63371)
 R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
 A;Reference number: A36007; MUID:90349572; PMID:2166946
 A;Accession: A36007
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
 A;Cross-references: UNIPARC:UPI000016B4D8; GB:M35857; NID:G339751; PIDN:AAA63262.1; PID:
 R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
 J. Biol. Chem. 265, 20131-20138, 1990
 A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
 A;Reference number: A23666; MUID:91056048; PMID:2173696
 A;Accession: A23666

A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 23-40;65-69;136-141;300-306 <LOE>
 A;Cross-references: UNIPARC:UPI000002D39D; UNIPARC:UPI00001736E7; UNIPARC:UPI00001736E8
 R;Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A;Reference number: A35010; MUID:90110215; PMID:2153136
 A;Accession: B35010
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 27-31 <ENG>
 A;Cross-references: UNIPARC:UPI00001736EA
 R;Kuhnert, P.; Kemper, O.; Wallach, D.
 Gene 150, 381-386, 1994
 A;Title: Cloning, sequencing and partial functional characterization of the 5' region o
 A;Reference number: I38094; MUID:95121934; PMID:7821811
 A;Accession: I38094
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-37 <RES>
 A;Cross-references: UNIPARC:UPI00000006D8; EMBL:X80021; NID:G666044; PIDN:CAA56324.1; P
 C;Genetics:
 A;Gene: GDB:TNFR2
 A;Cross-references: GDB:125914; OMIM:191191
 A;Map position: 1p36.2-1p36.2
 A;Introns: 26/3
 A;Note: the list of introns is incomplete
 C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homol
 C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F;40-76/Domain: NGF receptor repeat homology <NG1>
 F;78-119/Domain: NGF receptor repeat homology <NG2>
 F;120-162/Domain: NGF receptor repeat homology <NG3>
 F;164-201/Domain: NGF receptor repeat homology <NG4>
 F;262-279/Domain: transmembrane #status predicted <TMN>
 F;280-461/Domain: intracellular #status predicted <INT>
 F;171,193/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 14.6%; Score 72.5; DB 1; Length 461;
 Best Local Similarity 29.5%; Pred. No. 3.9;
 Matches 26; Conservative 7; Mismatches 28; Indels 27; Gaps 5;

QY 2 VITGACERD---VCGAGTCCCAISLWLRGLRMCTPL-----GREGE----- 40
 DB 105 VETQACTREQNRICTRCPGWYCALSK-QEGCLCAPLRKCRPGFGVARGPTETSDVVCKP 163

QY 41 CHFGSHKVPFRKRKHHTCPCLPPLLCS 68
 DB 164 CAPGT-----FSNTTSSTDICRPHQICN 186

RESULT 8
 A39804
 thrombospondin precursor - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A39804
 R;Lawler, J.; Duquette, M.; Ferro, P.
 J. Biol. Chem. 266, 8039-8043, 1991
 A;Title: Cloning and sequencing of chicken thrombospondin.
 A;Reference number: A39804; MUID:91217026; PMID:2022631
 A;Accession: A39804
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1178 <LAW>
 A;Cross-references: UNIPROT:P35440; UNIPARC:UPI000013776D; GB:M60853; NID:G212763; PIDN:
 C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
 F;325-383/Domain: von Willebrand factor type C repeat homology <VWC>
 F;386-437/Domain: thrombospondin type 1 repeat homology <THR1>
 F;442-498/Domain: thrombospondin type 1 repeat homology <THR2>
 F;499-555/Domain: thrombospondin type 1 repeat homology <THR3>

F:658-697/Domain: EGF homology <EGF>

Query Match 14.4%; Score 71.5; DB 1; Length 1178;
Best Local Similarity 21.8%; Pred. No. 11;
Matches 27; Conservative 8; Mismatches 32; Indels 57; Gaps 5;

QY 11 VCGAGTCCASISLW-----LRGLRMCTPLGREGECHPGSHKV-----PF----- 50
DB 457 VTGCVGNITRIILCNSPIPMGKGNKGVNGRTEKCEKAPCPVNGWGPSPWSACTVTC 516

QY 51 ----FRKR-----KHHTC-----PCLPNLLCSRFPDG 73
DB 517 GGIIRSRSLNSPEPYGKPCVGTQKQHDNCKNEDCFIDGCLSNFPCPGAECNSYPDG 576

QY 74 RYRC 77
DB 577 SWSC 580

RESULT 9
T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:G3449293;
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match 14.4%; Score 71.5; DB 2; Length 1574;
Best Local Similarity 28.4%; Pred. No. 14;
Matches 23; Conservative 6; Mismatches 31; Indels 21; Gaps 4;

QY 3 ITGAC-----ERDVCGAGTCCASISLWLRGLRMCTPLGREGECHPGSHKVFFRKRKH 57
DB 758 VTGELCPPEKGTGDCGAD--CPGKRWGLGCGEICPACGHCSCNP-----ETG 804

QY 58 TCCPLPNLLCSRFPDGRYRCS 78
DB 805 TCLCLPFGVGSRCQD---TCS 822

RESULT 10
T13576
hypothetical protein S2C10.5 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13576
R:Benois, P.
submitted to the EMBL Data Library, February 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17690
A:Accession: T13576
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1854 <BEN>
A:Cross-references: UNIPROT:O96838; UNIPARC:UPI000008354E; EMBL:AL035311; NID:e1373062;
C:Genetics:
A:Cross-references: FlyBase:FBgn0026309
A:Introns: 4/3; 53/3; 209/3; 962/1; 1632/1; 1686/2; 1739/1; 1793/1
A>Note: EG:S2C10.5

Query Match 14.4%; Score 71.5; DB 2; Length 1854;
Best Local Similarity 36.4%; Pred. No. 17;

Matches 20; Conservative 6; Mismatches 22; Indels 7; Gaps 3;
QY 37 EGEECHPGSHKVFFRKRKHHTCPCLPNLLCSR-----FPDGRYRCSMDLKNINF 86
DB 228 KAKCYDCSQRFSTFR-RKHH-CRLCGQIFCSKCCNQQVVPGMIRCDGDLKVCNY 280

RESULT 11

I51909
collipase precursor - rat
N:Alternate names: procollipase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I51909; A34623
R:Payne, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.
Am. J. Physiol. 266, G914-G921, 1994
A:Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA
A:Reference number: I51909; MUID:94262798; PMID:8203536
A:Accession: I51909
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-112 <PAY>
A:Cross-references: UNIPROT:P17084; UNIPARC:UPI0000127E7C; GB:M58370; NID:G203504; PIDN:
R:Wicker, C.; Puigserver, A.
Biochem. Biophys. Res. Commun. 167, 130-136, 1990
A:Title: Rat pancreatic collipase mRNA: nucleotide sequence of a cDNA clone and nutrition
A:Reference number: A34623; MUID:90179738; PMID:2129524
A:Accession: A34623
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17, 'V', 19-112 <WIC>
A:Cross-references: UNIPARC:UPI0000170BE5; GB:M33333; NID:G203502; PIDN:AAA40943.1; PID:
C:Superfamily: collipase
C:Keywords: lipid digestion; lipid hydrolysis; pancreas
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-112/Product: collipase #status predicted <MAT>

Query Match 14.3%; Score 71; DB 2; Length 112;
Best Local Similarity 31.1%; Pred. No. 1.6; Mismatches 5; Indels 8; Gaps 3;
Matches 19; Conservative 5; Mismatches 20; Indels 20; Gaps 0;
QY 7 CERDVCGAGTCCASISLWLRGLRMCTPLGREGECHPGSHKVFFRKRKHHTCPCLPNLL 66
DB 34 CVNSNQC-KSRCCQHDITL-GIARCTHKAMENSECSPTLVGIYYR-----CPCERGLT 85
QY 67 C 67
DB 86 C 86

RESULT 12
S34665
collagen, cuticular - root-knot nematode (Meloidogyne incognita)
C:Species: Meloidogyne incognita
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34665
R:van der Eycken, W.V.; de Almeida Engler, J.; van Montagu, M.; Gheysen, G.
submitted to the EMBL Data Library, July 1993
A:Description: Identification and analysis of a cuticular collagen gene from the plant-
A:Reference number: S34665
A:Accession: S34665
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-286 <VAN>
A:Cross-references: UNIPROT:Q25467; UNIPARC:UPI000016BF3F; EMBL:Z24734; NID:G395144; PI:

Query Match 14.3%; Score 71; DB 2; Length 286;
Best Local Similarity 40.5%; Pred. No. 3.7; Mismatches 2; Indels 20; Gaps 0;
Matches 15; Conservative 2; Mismatches 20; Indels 20; Gaps 0;
QY 33 PLGREGECHPGSHKVFFRKRKHHTCPCLPNLLCSR 69
DB 234 PSGKGPAPQPGPHGPPGQDQAQYCPGPRSLCSR 270

granulin precursor [validated] - human

N; Alternate names: epithelin
N; Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin F; granulin G; Species: Homo sapiens (man)
C; Date: 30-Sep-1992 #sequence revision 03-May-1996 #text change 31-Dec-2004
C; Accession: JCI284; J38128; A38118; A36698; B36698; C36698; D36698; A56873
R; Bhandari, V.; Bateman, A.
Biochem. Biophys. Res. Commun. 188, 57-63, 1992
A; Title: Structure and chromosomal location of the human granulin gene.
A; Reference number: JCI284; MUID:93038704; PMID:1417868
A; Accession: JCI284
A; Molecule type: DNA
A; Residues: 1-593 <BHA>
A; Cross-references: UNIPROT:P28799; UNIPROT:Q9UCH0; UNIPARC:UPI00000015E0
R; J. Polman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.
J. Biol. Chem. 267, 13073-13078, 1992
A; Title: The epithelin precursor encodes two proteins with opposing activities on epithelial cells.
A; Reference number: A38128; MUID:92317004; PMID:1618805
A; Accession: A38128
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-593 <PLO>
A; Cross-references: UNIPARC:UPI00000015E0; GB:X62320; NID:G31192; PIDN:CAA44196.1; PID:G31192
R; Bhandari, V.; Palfree, R.G.E.; Bateman, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992
A; Title: Isolation and sequence of the granulin precursor cDNA from human bone marrow rederived cells.
A; Reference number: A38118; MUID:92179253; PMID:1542665
A; Accession: A38118
A; Molecule type: mRNA
A; Residues: 1-406, 'R', 408-433, 'G', 435-453, 'G', 455-459, 'O', 461-546, 'A', 548-566, 'R', 568-599
A; Cross-references: UNIPARC:UPI0000151BF; GB:M75161; NID:G183612; PIDN:AAA58617.1; PID:G183612
A; Note: this sequence has been revised in reference JCI284
R; Bateman, A.; Balcourt, D.; Bennett, H.; Lazure, C.; Solomon, S.
Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990
A; Title: Granulins, a novel class of peptide from leukocytes.
A; Reference number: A36698; MUID:91097544; PMID:2268320
A; Accession: A36698
A; Molecule type: protein
A; Residues: 364-367, 'X', 369-385, 'H', 387-396 <BA3>
A; Cross-references: UNIPARC:UPI00001744F2
A; Note: this protein was purified and characterized as granulin A
A; Accession: B36698
A; Molecule type: protein
A; Residues: 206-218, 'H', 220-233 <BA2>
A; Cross-references: UNIPARC:UPI00001744F3
A; Note: this protein was purified and characterized as granulin B
A; Accession: C36698
A; Molecule type: protein
A; Residues: 442-446, 'XDTSS', 456-458, 'DG', <BA4>
A; Cross-references: UNIPARC:UPI00001744F5
R; Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
Br. J. Cancer 67, 686-692, 1993
A; Title: Characterisation of UGP and its relationship with beta-core fragment.
A; Reference number: A56873; MUID:93229246; PMID:8471426
A; Accession: A56873
A; Molecule type: protein
A; Residues: 281-283, 'X', 285-289, 'S', 291-295 <KAR>
A; Cross-references: UNIPARC:UPI0000070B1E
A; Experimental source: urine
A; Note: sequence extracted from NCBI backbone (NCBIP:129524)
C; Genetics: GRN
A; Gene: GDB:GRN
A; Cross-references: GDB:136006; OMIM:138945
A; Map position: 17pter-17qter

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1101 <GEI>
A;Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:g1049339; PI
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:T10E10.4
A;introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 14.2%; Score 70.5; DB 2; Length 1101;
Best Local Similarity 22.9%; Pred. No. 13;
Matches 27; Conservative 6; Mismatches 36; Indels 49; Gaps 5;
QY 7 CERDVQCGAGTCCATSLMURG-----LMCTPLGR-- 36
Db 761 CPPGNQCENGVCPPMCMSSGSIASSVCGMANSCPIGYICEGRGCCLEPLPLCPNGGRAS 820
QY 37 ----EGECHPG-----SHKVPPFRKRKHTCPCLPNLCSRPDPGRYRCSM 79
Db 821 MRCYRGAECPGYGCTPLGGCCLLSMEPVCPTRSNVAVQCSPNNVC---PSGA-SCTM 874

Search completed: December 14, 2006, 14:13:51
Job time : 29.0628 secs

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: December 14, 2006, 14:05:27 ; Search time 175.602 Seconds
(without alignments)
453.020 Million cell updates/sec

Title: US-10-692-299-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVCGAGTCCA.....CSRFPDGRYCRSMDLKNINF 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	105	1	PROK1_HUMAN
2	498	100.0	105	2	Q5VMD4_HUMAN
3	497	99.8	105	2	Q8TC69_HUMAN
4	473	95.0	105	1	PROK1_RAT
5	432	86.7	81	2	Q8K457_MOUSE
6	417	83.7	81	2	Q3ZF12_BOVIN
7	345	69.3	104	2	Q2XXR8_VARVA
8	340	68.3	104	2	Q2XXR7_VARVA
9	315	63.3	81	1	VPRA_DENPO
10	311	62.4	106	2	Q4RVU3_TETNG
11	304	61.0	108	2	Q863H4_BOVIN
12	291	58.4	108	2	Q6TSR0_HUMAN
13	286	57.4	107	1	PROK2_RAT
14	286	57.4	107	2	Q50E37_9MURI
15	286	57.4	107	2	Q50E38_9MURI
16	285	57.2	102	2	Q4SR12_TETNG
17	284	57.0	128	2	Q863H5_BOVIN
18	278.5	55.9	96	2	Q8JFQ0_BOMMX
19	273.5	54.9	96	2	Q5W280_BOMMX
20	270.5	54.3	129	1	PROK2_HUMAN
21	270.5	54.3	129	2	Q53279_HUMAN
22	267.5	53.7	96	1	BV8_BOVVA
23	265.5	53.3	128	1	PROK2_MOUSE
24	265.5	53.3	128	2	Q50E33_9MURI
25	265.5	53.3	128	2	Q50E34_9MURI
26	265.5	53.3	128	2	Q6V8J7_RAT
27	254.5	51.1	96	2	Q8JFE6_BOMMX
28	253.5	50.9	96	2	Q8JFX8_BOMMX
29	253.5	50.9	96	2	Q8JFY1_BOMMX
30	249.5	50.1	96	2	Q8JFX9_BOMMX
31	249.5	50.1	96	2	Q8JFY0_BOMMX

32	246.5	49.5	96	2	Q8JFY2_BOMMX
33	193	38.8	39	2	Q50E61_9MURI
34	191	38.4	82	2	Q2TBS7_BOVIN
35	188	37.8	86	2	Q50E35_9MURI
36	188	37.8	86	2	Q50E36_9MURI
37	121.5	24.4	124	2	Q56R10_PENMO
38	112	22.5	96	2	Q8UUX3_CHICK
39	108.5	21.8	221	1	DKK4_MOUSE
40	107.5	21.6	224	1	DKK4_HUMAN
41	107.5	21.6	224	2	Q3KNX0_HUMAN
42	107.5	21.6	350	1	DKK3_CHICK
43	104	20.9	255	1	Q9DDA4_XENLA
44	102	20.5	180	2	Q4RJF1_TETNG
45	102	20.5	259	1	DKK2_HUMAN
46	101.5	20.4	256	1	Q5EHU6_GECJA
47	101	20.3	259	1	DKK2_MOUSE
48	101	20.3	259	2	Q8BFW0_MOUSE
49	101	20.3	272	1	DKK1_MOUSE
50	101	20.3	272	2	Q80UL5_MOUSE
51	100.5	20.2	171	2	Q43532_HUMAN
52	100.5	20.2	215	2	Q8N294_HUMAN
53	100.5	20.2	341	2	Q5R8T0_PONPY
54	100.5	20.2	350	1	DKK3_HUMAN
55	100.5	20.2	350	2	Q4R4I7_MACFA
56	100.5	20.2	350	2	Q5R4Q2_PONPY
57	99.5	20.0	277	2	Q5ES33_RAT
58	99.5	20.0	348	2	Q5RKL1_RAT
59	98.5	19.8	349	1	DKK3_MOUSE
60	97	19.5	266	1	DKK1_HUMAN
61	96.5	19.4	268	2	Q6PVU5_RABIT
62	95.5	19.2	259	2	Q57464_XENLA
63	95	19.1	177	2	Q4SL69_TETNG
64	94.5	19.0	350	2	Q6PQ81_HUMAN
65	94	18.9	240	2	Q6PMH3_BRARE
66	90.5	18.2	104	2	Q56R11_PACLE
67	88.5	17.8	640	2	Q96397_CHLRE
68	88	17.7	88	2	Q5D229_HADSP
69	87	17.5	88	2	Q5D228_HADSP
70	86	17.3	241	2	Q9W6D9_BRARE
71	84.5	17.0	102	2	Q3UW21_MOUSE
72	84	16.9	102	2	Q5D230_HADSP
73	83.5	16.8	110	2	Q4PML0_IKOSC
74	82.5	16.6	400	2	Q3U1Z8_MOUSE
75	82.5	16.6	425	1	CNI30_MOUSE
76	82.5	16.6	425	2	Q52KC0_MOUSE
77	82.5	16.6	425	2	Q642A8_RAT
78	82	16.5	1165	2	Q5BKFS_XENTR
79	81.5	16.4	446	2	Q8NB03_HUMAN
80	81	16.3	1964	1	NOTC4_MOUSE
81	80.5	16.2	1193	2	Q4S758_TETNG
82	80	16.1	412	2	Q86HY9_DICDI
83	79.5	16.0	191	2	Q6ZQM6_HUMAN
84	79.5	16.0	404	2	Q6ZQR7_HUMAN
85	79.5	16.0	418	2	Q4T860_TETNG
86	79.5	16.0	446	2	Q8N1N5_HUMAN
87	79.5	16.0	870	2	Q8IQG6_DROME
88	79.5	16.0	1233	2	Q4S163_TETNG
89	79.5	16.0	1331	2	Q4S572_TETNG
90	79.5	16.0	1353	2	Q4UGZ9_THEAN
91	79	15.9	107	1	COL_RABIT
92	79	15.9	224	2	Q4H3Q2_CIOIN
93	79	15.9	225	2	Q4H3Q3_CIOIN
94	79	15.9	704	1	FBLN1_CHICK
95	79	15.9	2447	2	O13149_FUGRU
96	78.5	15.8	162	2	Q5UHV8_PYKRO
97	78	15.7	593	2	Q5R5T2_PONPY
98	77.5	15.6	350	2	Q54EN7_DICDI
99	77.5	15.6	473	1	FP2_MVTGA
100	77	15.5	5533	2	Q5BTP6_BRARE
101	76	15.3	113	2	Q9D2R7_MOUSE
102	76	15.3	264	2	Q5H2W5_RAT
103	76	15.3	496	2	Q54L19_DICDI
104	76	15.3	496	2	Q6TMJ0_DICDI

Q8jfy2	bombina max
Q50e61	arvicanthis
Q2tbs7	bos taurus
Q50e35	arvicanthis
Q50e36	arvicanthis
Q56r10	penaeus mon
Q8uux3	gallus gall
Q8vuj3	mus musculus
Q3ubt3	homo sapien
Q3knx0	homo sapien
Q90d39	gallus gall
Q9ddaa	xenopus lae
Q4rjfi	tetraodon n
Q9ubt2	homo sapien
Q9ubt2	gecko japon
Q9qyz8	mus musculus
Q8bfw0	m 10, 11 da
Q54908	mus musculus
Q80ul5	m dickkopf
Q43532	homo sapien
Q8n294	homo sapien
Q5r8t0	pongo pygma
Q9ubp4	homo sapien
Q4r4i7	macaca fasc
Q5r4q2	pongo pygma
Q9e333	rattus norv
Q5rkl1	rattus norv
Q9qun9	mus musculus
Q94907	homo sapien
Q6pru5	oryctolagus
Q57464	xenopus lae
Q4sl69	tetraodon n
Q6pq81	homo sapien
Q9pwh3	brachydanio
Q56r11	pacifastacu
Q96397	chlamydomon
Q5d229	hadronyche
Q5d228	hadronyche
Q9w6d9	brachydanio
Q3uw21	mus musculus
Q5d230	hadronyche
Q4pml0	ixodes scap
Q8u1z8	mus musculus
Q8bn04	mus musculus
Q52kc0	m hypotheri
Q642a8	rattus norv
Q5bkf5	xenopus tro
Q8nb03	homo sapien
P31595	mus musculus
Q86hy9	dictyosteli
Q6zqw6	homo sapien
Q6zqr7	homo sapien
Q4t860	tetraodon n
Q8n1n5	homo sapien
Q8iqg6	drosophila
Q4s163	tetraodon n
Q4s572	tetraodon n
Q4ugz9	theileria a
P42890	oryctolagus
Q4h3q2	ciona intes
Q4h3q3	ciona intes
Q73775	gallus gall
O13149	fugu rubrip
Q5jhv8	pyrococcus
Q5r5t2	pongo pygma
Q54en7	dictyosteli
Q2s464	mytilus gal
Q5rip6	brachydanio
Q9d2r7	mus musculus
Q5h2w5	rattus norv
Q54l19	dictyosteli
Q6tmj0	dictyosteli

105	75.5	15.2	1259	2	Q385C6	trypanosoma	178	70	14.1	251	2	Q70LQ4	ENCHBU	Q70LQ4	enchytraeus
106	75.5	15.2	1651	2	Q9TVQ2	caenorhabdi	179	70	14.1	387	2	Q4KLX7	XENLA	Q4KLX7	xenopus lae
107	75	15.1	130	2	Q4PMW2	ixodes scap	180	70	14.1	387	2	Q9PVD4	XENLA	Q9PVD4	xenopus lae
108	75	15.1	425	2	Q53RA0	homo sapien	181	70	14.1	392	2	Q6NUF1	XENLA	Q6NUF1	xenopus lae
109	75	15.1	647	2	Q6P3V5	homo sapien	182	70	14.1	406	2	Q920K3	RAT	Q920K3	rattus norv
110	75	15.1	762	2	Q8ML23	drosophila	183	70	14.1	706	2	Q4H3Q7	CIOIN	Q4H3Q7	ciona intes
111	75	15.1	1581	1	LAMC3	mouse	184	70	14.1	729	2	Q7T3M4	BRARE	Q7T3M4	brachydanio
112	75	15.1	1581	1	Q4VAI3	mouse	185	70	14.1	729	2	Q4V9K5	BRARE	Q4V9K5	brachydanio
113	75	15.1	1957	2	Q4SU28	tetraodon n	186	70	14.1	950	2	Q802C1	XENLA	Q802C1	xenopus lae
114	75	15.1	1961	2	Q6MG89	rattus norv	187	69.5	14.0	111	2	Q4PN79	IXOSC	Q4PN79	ixodes scap
115	75	15.1	2003	1	NOTC4	human	188	69.5	14.0	123	2	Q3XNW9	SPROT	Q3XNW9	magnetococc
116	75	15.1	2003	2	Q5SP11	homo sapien	189	69.5	14.0	818	2	Q4V7B3	RAT	Q4V7B3	rattus norv
117	75	15.1	2003	2	Q5SSY7	homo sapien	190	69.5	14.0	1099	2	Q6OV58	CAEBR	Q6OV58	caenorhabdi
118	75	15.1	2005	2	Q5STG5	homo sapien	191	69.5	14.0	1147	2	Q3TLU3	MOUSE	Q3TLU3	mus musculus
119	75	15.1	2531	2	Q16004	lytechinus	192	69	13.9	413	2	Q9H8S1	HUMAN	Q9H8S1	homo sapien
120	75	15.1	4599	1	LRP1B	human	193	69	13.9	638	2	Q8NBH6	HUMAN	Q8NBH6	homo sapien
121	74.5	15.0	190	2	Q47E9	tetraodon n	194	69	13.9	703	1	PBLN1	HUMAN	PBLN1	homo sapien
122	74.5	15.0	194	2	Q4SIA7	tetraodon n	195	69	13.9	835	2	Q692Y6	MOUSE	Q692Y6	mus musculus
123	74.5	15.0	274	2	Q5RCC3	pongo pygma	196	68.5	13.8	143	2	Q330K5	TRIMU	Q330K5	trimeresuru
124	74.5	15.0	286	2	Q7F5C8	giardia lam	197	68.5	13.8	333	2	Q3HTT8	CANFA	Q3HTT8	canis faml
125	74.5	15.0	425	1	CN130	human	198	68.5	13.8	425	2	Q4R222	MACFA	Q4R222	macaca faec
126	74.5	15.0	1426	2	Q4RTA6	tetraodon n	199	68.5	13.8	708	2	Q7F803	ORYSA	Q7F803	oryza sativ
127	74	14.9	623	2	Q4P8A3	ustilago ma	200	68.5	13.8	850	2	O04384	BRAOL	O04384	brassica ol
128	74	14.9	693	2	Q505M8	xenopus lae	201	68.5	13.8	909	2	Q5ZEL8	ORYSA	Q5ZEL8	oryza sativ
129	74	14.9	708	2	P87363	gallus gall	202	68.5	13.8	1172	1	TSP2	MOUSE	Q03350	mus musculus
130	74	14.9	1171	2	Q4RLR5	tetraodon n	203	68.5	13.8	1172	2	Q7TMT3	MOUSE	Q7TMT3	mus musculus
131	74	14.9	4680	2	Q7PV66	anopheles g	204	68.5	13.8	1172	2	Q8CG21	MOUSE	Q8CG21	mus musculus
132	73.5	14.8	701	2	Q8AVE8	xenopus lae	205	68.5	13.8	1639	1	LAMC1	DROME	P15215	drosophila
133	73.5	14.8	2327	2	Q1BG7	xenopus lae	206	68.5	13.8	1639	2	Q5BI30	DROME	Q5BI30	drosophila
134	73	14.7	64	1	TX16	PHORI	207	68.5	13.8	1801	2	Q8WSJ2	BOMMO	Q8WSJ2	bombyx mori
135	73	14.7	109	2	Q5U809	homo sapien	208	68.5	13.8	1952	2	Q95SN5	DROME	Q95SN5	drosophila
136	73	14.7	112	1	COL	HUMAN	209	68.5	13.8	2559	1	STAB2	MOUSE	Q84TU0	mus musculus
137	73	14.7	112	2	Q5T9G7	human	210	68.5	13.8	4547	2	Q9W343	DROME	Q9W343	drosophila
138	73	14.7	172	2	Q8RU50	oryza sativ	211	68	13.7	112	1	COL	CANFA	P19090	canis faml
139	73	14.7	229	2	Q3FKI4	rhodoferax	212	68	13.7	113	2	Q5T9G1	HUMAN	Q5T9G1	homo sapien
140	73	14.7	417	1	TNR16	mouse	213	68	13.7	314	2	Q5XTR8	NACMU	Q5XTR8	macaca mula
141	73	14.7	417	2	Q8BYI1	mouse	214	68	13.7	427	1	TNR15	HUMAN	P08138	homo sapien
142	73	14.7	427	2	Q8CFT3	mouse	215	68	13.7	489	1	MA2A1	RAT	P28494	rattus norv
143	73	14.7	7302	2	Q9RH03	azospirillu	216	68	13.7	490	2	Q6P7D7	RAT	P16727	rattus norv
144	73	14.7	1408	2	Q4RX38	tetraodon n	217	68	13.7	586	1	UL84	HCNVA	P16727	human cytom
145	72.5	14.6	103	2	Q62331	oryza sativ	218	68	13.7	587	2	Q6RFX3	HCNV	Q6RFX3	human cytom
146	72.5	14.6	457	2	Q81VS6	human	219	68	13.7	587	2	Q61T62	CAEBR	Q61T62	caenorhabdi
147	72.5	14.6	461	1	TNR1B	human	220	68	13.7	587	2	Q6SW58	HCNV	Q6SW58	human cytom
148	72.5	14.6	461	2	Q5THJ6	human	221	68	13.7	593	2	Q4R529	NACFA	Q4R529	macaca faec
149	72.5	14.6	2715	1	MLL4	human	222	68	13.7	944	2	Q4SLX2	TETNG	Q4SLX2	tetraodon n
150	72.5	14.6	3377	2	Q6VU67	human	223	68	13.7	964	2	Q4STC1	TETNG	Q4STC1	tetraodon n
151	72.5	14.6	3377	2	Q76E14	homo sapien	224	68	13.7	1090	2	Q5SPG5	BRARE	Q5SPG5	brachydanio
152	72.5	14.6	3333	2	Q6VU68	homo sapien	225	68	13.7	1150	1	MA2A1	MOUSE	P27046	mus musculus
153	71.5	14.4	453	2	Q64767	adeno	226	68	13.7	1984	1	YL	DROME	P98163	drosophila
154	71.5	14.4	1170	1	TSP2	BOVIN	227	68	13.7	2359	2	Q59FG2	HUMAN	Q59FG2	homo sapien
155	71.5	14.4	1178	1	TSP2	CHICK	228	68	13.7	5147	1	FAT	DROME	P33450	drosophila
156	71.5	14.4	1574	1	EGFL3	RAT	229	67.5	13.6	89	2	Q5D232	HADSP	Q5D232	hadronyche
157	71.5	14.4	1809	1	FYV1	DROME	230	67.5	13.6	200	2	Q7PWB6	ANOAG	Q7PWB6	anopheles g
158	71	14.3	112	1	COL	RAT	231	67.5	13.6	269	2	Q4I3B1	GIBZE	Q4I3B1	gibberella
159	71	14.3	286	2	Q7JMU0	MELIC	232	67.5	13.6	269	2	Q583F5	9TRYP	Q583F5	trypanosoma
160	71	14.3	388	2	Q5R1P8	BRARE	233	67.5	13.6	303	2	Q3TTU9	MOUSE	Q3TTU9	mus musculus
161	71	14.3	305	2	Q25467	MELIC	234	67.5	13.6	413	2	Q6ZP14	HUMAN	Q6ZP14	homo sapien
162	71	14.3	438	2	Q53Y88	human	235	67.5	13.6	418	2	Q5ZMNA	CHICK	Q5ZMNA	gallus gall
163	71	14.3	457	2	Q8TEC5	homo sapien	236	67.5	13.6	490	1	TMPS2	MOUSE	Q3UKE3	mus musculus
164	71	14.3	593	1	GRN	HUMAN	237	67.5	13.6	490	2	Q3UKE3	MOUSE	Q3UKE3	mus musculus
165	71	14.3	593	2	Q53HQ8	human	238	67.5	13.6	490	2	Q7TN04	MOUSE	Q7TN04	mus musculus
166	71	14.3	593	2	Q540U8	homo sapien	239	67.5	13.6	540	2	Q4CXJ4	TRYCR	Q4CXJ4	trypanosoma
167	70.5	14.2	287	2	Q75Z12	brachydanio	240	67.5	13.6	729	2	Q8ANB7	CYNPY	Q8ANB7	cynops pyrr
168	70.5	14.2	555	2	Q4RN57	tetraodon n	241	67.5	13.6	729	2	Q8BNH3	MOUSE	Q8BNH3	mus musculus
169	70.5	14.2	591	1	GRN	CAVPO	242	67.5	13.6	787	2	Q8K061	MOUSE	Q8K061	mus musculus
170	70.5	14.2	919	2	Q61V24	CAEBR	243	67.5	13.6	1356	2	Q4NM7	THEPA	Q4NM7	thelateria p
171	70.5	14.2	966	2	Q22378	CAEBL	244	67.5	13.6	1637	2	Q9XSV8	BOVIN	Q9XSV8	bos taurus
172	70.5	14.2	2318	1	NOTC3	MOUSE	245	67.5	13.6	1744	2	Q8CHH1	MOUSE	Q8CHH1	mus musculus
173	70.5	14.2	2319	1	NOTC3	RAT	246	67.5	13.6	2013	2	Q6PHU4	MOUSE	Q6PHU4	mus musculus
174	70	14.1	68	2	TX16	PHONI	247	67.5	13.6	2713	2	Q5NU09	MOUSE	Q5NU09	mus musculus
175	70	14.1	92	2	Q2WCN5	HYDMA	248	67.5	13.6	4699	2	Q9V383	DROME	Q9V383	drosophila
176	70	14.1	113	1	COL	MOUSE	249	67.5	13.6	5146	2	Q8SPM4	BOVIN	Q8SPM4	bos taurus
177	70	14.1	251	2	Q24774	ENCHBU	250	67	13.5	113	2	Q8MKJ5	DROME	Q8MKJ5	drosophila

251	67	13.5	182	2	Q307E7_SHEEP	Q307e7 ovis aries	324	65.5	13.2	343	2	Q5XG84_HUMAN	Q5xg84 homo sapien
252	67	13.5	237	1	ALG14_YEAST	P38242 saccharomyc	325	65.5	13.2	356	2	Q96FY1_HUMAN	Q96fy1 homo sapien
253	67	13.5	495	2	Q54QC5_DICDI	P484c5 dictyosteli	326	65.5	13.2	589	2	Q3TWT4_MOUSE	Q3twt4 mus musculus
254	67	13.5	611	2	Q4SZ28_TETNG	Q4sz28 tetraodon n	327	65.5	13.2	722	1	DL11_MOUSE	DL11 mus musculus
255	67	13.5	749	2	Q86TP7_HUMAN	Q86tp7 homo sapien	328	65.5	13.2	722	2	Q6PFV7_MOUSE	Q6pfv7 mus musculus
256	67	13.5	993	1	EPHB3_MOUSE	P54754 mus musculus	329	65.5	13.2	724	2	Q32NV6_XENLA	Q32nv6 xenopus lae
257	67	13.5	993	2	Q91Y89_MOUSE	Q91y89 mus musculus	330	65.5	13.2	724	2	Q4ZJ75_XENLA	Q4zj75 xenopus lae
258	67	13.5	1050	2	Q71AG60_RSIV	Q71ag60 red sea bre	331	65.5	13.2	729	2	Q6GPT6_XENLA	Q6gpt6 xenopus lae
259	67	13.5	1168	2	Q60XC0_CAEBR	Q60xc0 caenorhabdi	332	65.5	13.2	768	2	Q36581_9RETR	Q36581 multiple sc
260	67	13.5	1239	1	EGFL3_HUMAN	Q75095 homo sapien	333	65.5	13.2	802	2	Q7JL02_CAEBL	Q7jl02 caenorhabdi
261	67	13.5	1289	2	Q59PL3_HUMAN	Q59pl3 homo sapien	334	65.5	13.2	804	2	Q3UK95_MOUSE	Q3uk95 mus musculus
262	67	13.5	1640	2	Q4AC86_HUMAN	Q4ac86 homo sapien	335	65.5	13.2	818	2	Q8CC59_MOUSE	Q8cc59 mus musculus
263	67	13.5	1761	2	Q86XN2_HUMAN	Q86xn2 homo sapien	336	65.5	13.2	818	2	Q8DBC8_MOUSE	Q8dbc8 mus musculus
264	67	13.5	2321	1	NOTC3_HUMAN	Q9UM47 homo sapien	337	65.5	13.2	887	2	Q3UMW1_MOUSE	Q3umw1 mus musculus
265	66.5	13.4	287	2	Q81PJ1_DROME	Q81pj1 drosophila	338	65.5	13.2	949	2	Q90956_CAEBL	Q90956 caenorhabdi
266	66.5	13.4	386	2	Q32NM5_XENLA	Q32nm5 xenopus lae	339	65.5	13.2	1114	2	Q3U2A7_MOUSE	Q3u2a7 mus musculus
267	66.5	13.4	388	2	Q68Y16_XENLA	Q68y16 xenopus lae	340	65.5	13.2	1114	2	Q9JKW7_MOUSE	Q9jkw7 mus musculus
268	66.5	13.4	388	2	Q6AJ22_XENLA	Q6aj22 xenopus lae	341	65.5	13.2	1235	2	Q6IQS0_HUMAN	Q6iqs0 homo sapien
269	66.5	13.4	462	2	Q3UDD6_MOUSE	Q3udd6 mus musculus	342	65.5	13.2	1465	2	Q4RN50_TETNG	Q4rn50 tetraodon n
270	66.5	13.4	480	2	Q34XA1_9GAMM	Q34xa1 alkallilimi	343	65.5	13.2	1847	2	Q76952_ARDAE	Q76952 aedes aegypt
271	66.5	13.4	511	2	Q61N42_RAT	Q61n42 rattus norv	344	65.5	13.2	2213	1	SORL_RABIT	Q95209 o sortilin-
272	66.5	13.4	588	1	GRN_RAT	P23785 r granulins	345	65.5	13.2	2471	1	NOTC2_HUMAN	Q04721 homo sapien
273	66.5	13.4	589	1	GRN_MOUSE	P28798 mus musculus	346	65.5	13.2	2471	2	QSVTD0_HUMAN	Qsvtd0 homo sapien
274	66.5	13.4	589	2	Q3TVQ3_MOUSE	Q3tvq3 mus musculus	347	65	13.1	111	1	COL_SPETR	Q9ix17 spermophili
275	66.5	13.4	589	2	Q3TX66_MOUSE	Q3tx66 mus musculus	348	65	13.1	147	2	Q6QXV5_ORYSA	Q6qxv5 oryza sativ
276	66.5	13.4	589	2	Q3UC19_MOUSE	Q3uc19 mus musculus	349	65	13.1	448	2	Q4UM87_XANC8	Q4um87 xanthomonas
277	66.5	13.4	589	2	Q544Y8_MOUSE	Q544y8 m adult mal	350	65	13.1	448	2	Q8P7W2_XANCP	Q8p7w2 xanthomonas
278	66.5	13.4	593	2	Q3U9K2_MOUSE	Q3u9k2 mus musculus	351	65	13.1	481	2	Q2WV02_CLOBE	Q2wv02 clostridium
279	66.5	13.4	602	2	Q3TW77_MOUSE	Q3tw77 mus musculus	352	65	13.1	794	2	Q8T4P0_LYTVZ	Q8t4p0 lytechinus
280	66.5	13.4	602	2	Q3U5Q6_MOUSE	Q3u5q6 mus musculus	353	65	13.1	893	2	Q9Y1Y3_9METZ	Q9y1y3 ephydacia f
281	66.5	13.4	602	2	Q3U8W3_MOUSE	Q3u8w3 mus musculus	354	65	13.1	1068	2	Q6QHS4_STRPU	Q6qh84 strongyloce
282	66.5	13.4	602	2	Q3U9N4_MOUSE	Q3u9n4 m bone marr	355	65	13.1	1123	2	Q4H346_CIOIN	Q4h346 ciona intes
283	66.5	13.4	602	2	Q9D2V3_MOUSE	Q9d2v3 mus musculus	356	65	13.1	3133	1	HMCT_BOMBO	P98092 bombyx mori
284	66.5	13.4	674	2	Q8T4N9_STRPU	Q8t4n9 strongyloce	357	65	13.1	3481	2	Q4DNC0_TYCR	Q4dnc0 trypanosoma
285	66.5	13.4	714	1	DL11_RAT	P97677 rattus norv	358	65	13.1	4599	1	LAP1B_MOUSE	Q9j118 mus musculus
286	66.5	13.4	907	2	Q4RI84_LEUMB	Q4rib4 leucophaea	359	65	13.1	23015	2	Q8IQ18_HUMAN	Q8iq18 drosophila
287	66.5	13.4	931	2	Q61FT4_CAEBR	Q61ft4 caenorhabdi	360	64.5	13.0	90	2	Q5T9G3_HUMAN	Q5t9g3 homo sapien
288	66.5	13.4	969	2	Q81V28_HUMAN	Q81v28 homo sapien	361	64.5	13.0	102	1	TXCA_CAEBR	Q8mtx1 caerostris
289	66.5	13.4	1180	2	Q5CZ12_HUMAN	Q5cz12 homo sapien	362	64.5	13.0	134	2	Q6ZR78_HUMAN	Q6zr78 homo sapien
290	66.5	13.4	1361	2	Q9NGV2_DROME	Q9ngv2 drosophila	363	64.5	13.0	170	2	Q52VJ8_CIOIN	Q52vj8 ciona intes
291	66.5	13.4	1361	2	Q9W714_DROME	Q9w714 drosophila	364	64.5	13.0	191	1	Y064_TREPA	Q83103 treponema p
292	66.5	13.4	1375	1	NID2_HUMAN	Q14112 homo sapien	365	64.5	13.0	245	2	Q6ZT26_HUMAN	Q6zt26 homo sapien
293	66.5	13.4	1379	2	Q59H72_HUMAN	Q59h72 homo sapien	366	64.5	13.0	256	1	FSTL3_MOUSE	Q542m9 mus musculus
294	66.5	13.4	1568	2	Q5VUP0_HUMAN	Q5vup0 homo sapien	367	64.5	13.0	325	2	Q542M9_MOUSE	Q542m9 mus musculus
295	66.5	13.4	1587	1	LAWC3_HUMAN	Q9y6n6 homo sapien	368	64.5	13.0	325	2	Q61423_CAEBR	Q61423 caenorhabdi
296	66.5	13.4	1587	2	Q5VUP1_HUMAN	Q5vup1 homo sapien	369	64.5	13.0	337	2	Q8NHD3_HUMAN	Q8nhd3 homo sapien
297	66.5	13.4	1945	2	Q4RQ96_TETNG	Q4rq96 tetraodon n	370	64.5	13.0	342	2	Q8NHD5_HUMAN	Q8nhd5 homo sapien
298	66.5	13.4	4545	2	Q61291_MOUSE	Q61291 mus musculus	371	64.5	13.0	375	2	Q7PR44_ANOGA	Q7pr44 anopheles g
299	66.5	13.4	4545	2	Q912X7_MOUSE	Q912x7 mus musculus	372	64.5	13.0	546	2	Q3UYW9_MOUSE	Q3uyw9 mus musculus
300	66.5	13.4	4545	2	Q920Y4_MOUSE	Q920y4 mus musculus	373	64.5	13.0	569	2	Q8NHD4_HUMAN	Q8nhd4 homo sapien
301	66	13.3	85	1	HEPC_MORCS	P82951 morone chry	374	64.5	13.0	656	1	EGFL3_MOUSE	Q8nv70 mus musculus
302	66	13.3	149	2	Q8GA35_ECOLI	Q8ga35 escherichia	375	64.5	13.0	744	2	Q8NHD7_HUMAN	Q8nhd7 homo sapien
303	66	13.3	208	2	Q6K6H7_ORYSA	Q6k6h7 oryza sativ	376	64.5	13.0	744	2	Q7Q8A1_ANOGA	Q7q8a1 anopheles g
304	66	13.3	598	1	FBLN1_CERAE	Q8mj19 cercopithe	377	64.5	13.0	772	2	Q4QBY8_LEIMA	Q4qby8 leishmania
305	66	13.3	1172	1	TSP2_HUMAN	P35442 homo sapien	378	64.5	13.0	804	2	Q7TPT4_MOUSE	Q7tpt4 mus musculus
306	66	13.3	1172	2	Q5RI52_HUMAN	Q5ri52 homo sapien	379	64.5	13.0	830	1	SREC_HUMAN	Q14162 homo sapien
307	66	13.3	1327	1	Y2006_MYCTU	Q10850 mycobacteri	380	64.5	13.0	841	2	Q4YVB8_PLABE	Q4yvb8 plasmodium
308	66	13.3	1327	2	Q7T261_MYCBO	Q7t261 mycobacteri	381	64.5	13.0	853	2	Q8I719_PLAF7	Q8i719 plasmodium
309	66	13.3	1599	2	Q616G7_CAEBR	Q616g7 caenorhabdi	382	64.5	13.0	853	2	Q8MMZ4_PLAF7	Q8mmz4 plasmodium
310	66	13.3	2289	2	Q4S3T6_TETNG	Q4s3t6 tetraodon n	383	64.5	13.0	873	2	Q8QGN9_BRARE	Q8qgn9 brachydanio
311	66	13.3	2884	2	Q4SHN1_TETNG	Q4shn1 tetraodon n	384	64.5	13.0	987	2	Q6XLI6_CALJA	Q6xli6 callithrix
312	66	13.3	3075	1	LAWA1_HUMAN	P25391 homo sapien	385	64.5	13.0	1021	2	Q3UGU1_MOUSE	Q3ugu1 mus musculus
313	66	13.3	3570	2	Q70737_ANOGA	Q70737 anopheles g	386	64.5	13.0	1051	2	Q5U4U1_XENLA	Q5u4u1 xenopus lae
314	66	13.3	3712	1	LAMA_DROME	Q00174 drosophila	387	64.5	13.0	1062	2	Q3UG73_MOUSE	Q3ug73 mus musculus
315	65.5	13.2	110	2	Q4PMX5_IXOSC	Q4pmx5 ixodes scap	388	64.5	13.0	1147	2	Q6DIB5_MOUSE	Q6dib5 mus musculus
316	65.5	13.2	176	2	Q4V4J0_DROME	Q4v4j0 drosophila	389	64.5	13.0	1211	2	Q83K66_9TRYP	Q83k66 trypanosoma
317	65.5	13.2	230	2	Q5VTG9_HUMAN	Q5vtg9 homo sapien	390	64.5	13.0	1214	2	Q90YD2_XENLA	Q90yd2 xenopus lae
318	65.5	13.2	236	2	Q7Z3S9_HUMAN	Q7z3s9 homo sapien	391	64.5	13.0	1216	2	Q5TZK7_BRARE	Q5tzk7 brachydanio
319	65.5	13.2	236	2	Q8WUQ9_HUMAN	Q8wuq9 homo sapien	392	64.5	13.0	1216	2	Q90Y55_BRARE	Q90y55 brachydanio
320	65.5	13.2	244	2	Q2Y7J9_NITMU	Q2y7j9 nitrospir	393	64.5	13.0	1254	2	Q5TZK8_BRARE	Q5tzk8 brachydanio
321	65.5	13.2	249	2	Q5BKT8_HUMAN	Q5bkt8 homo sapien	394	64.5	13.0	1254	2	Q90Y56_BRARE	Q90y56 brachydanio
322	65.5	13.2	269	2	Q8NC23_HUMAN	Q8nc23 homo sapien	395	64.5	13.0	1254	2	Q9YHU2_BRARE	Q9yhu2 brachydanio
323	65.5	13.2	342	2	Q6P192_HUMAN	Q6p192 homo sapien	396	64.5	13.0	1557	2	Q75412_HUMAN	Q75412 homo sapien

397	64.5	13.0	1587	2	O00508	HUMAN	000508	homo sapien
398	64.5	13.0	1624	2	O75413	HUMAN	075413	homo sapien
399	64.5	13.0	1722	2	Q19350	CABEL	Q19350	caenorhabdi
400	64.5	13.0	2214	1	SORL	HUMAN	Q92673	h. sortilin-
401	64.5	13.0	3718	1	LAMAS	DICDI	Q54hf8	dictyosteli
402	64	12.9	81	2	Q54HF8	DICDI	Q54231	hadronyche
403	64	12.9	84	2	Q5D231	HADSP	Q54233	hadronyche
404	64	12.9	90	2	Q5D233	HADIN	Q54233	hadronyche
405	64	12.9	116	2	Q5Q981	IXOSC	Q54233	hadronyche
406	64	12.9	117	2	Q9Yd41	AERPE	Q54233	hadronyche
407	64	12.9	146	1	TXVE	TRIFL	Q54233	hadronyche
408	64	12.9	163	2	Q4SFU4	TETNG	Q54233	hadronyche
409	64	12.9	217	2	O85613	ECOLI	Q54233	hadronyche
410	64	12.9	217	2	Q7A9R9	ECOS7	Q54233	hadronyche
411	64	12.9	225	2	Q8XCA3	ECOS7	Q54233	hadronyche
412	64	12.9	274	2	Q7Q953	ANOAG	Q54233	hadronyche
413	64	12.9	286	2	Q5CAG9	ORYSA	Q54233	hadronyche
414	64	12.9	315	2	Q616A1	CAEBR	Q54233	hadronyche
415	64	12.9	322	2	Q651I3	ORYSA	Q54233	hadronyche
416	64	12.9	425	1	TNR16	RAT	Q54233	hadronyche
417	64	12.9	581	2	Q5LU50	SILPO	Q54233	hadronyche
418	64	12.9	587	1	UL84	HCMT	Q54233	hadronyche
419	64	12.9	602	2	Q3UAJ3	MOUSE	Q54233	hadronyche
420	64	12.9	602	2	Q3UD85	MOUSE	Q54233	hadronyche
421	64	12.9	657	2	Q4PIC7	USTMA	Q54233	hadronyche
422	64	12.9	983	2	Q4T849	TETNG	Q54233	hadronyche
423	64	12.9	1037	2	Q3UV32	MOUSE	Q54233	hadronyche
424	64	12.9	1143	2	Q21010	CABEL	Q54233	hadronyche
425	64	12.9	1144	1	MA2A1	HUMAN	Q54233	hadronyche
426	64	12.9	1145	2	Q2PJ74	CABEL	Q54233	hadronyche
427	64	12.9	1818	2	Q2YI44	BLAGE	Q54233	hadronyche
428	64	12.9	1814	2	Q499U7	RAT	Q54233	hadronyche
429	64	12.9	2215	1	SORL	MOUSE	Q54233	hadronyche
430	64	12.9	2215	2	Q3UHM3	MOUSE	Q54233	hadronyche
431	64	12.9	2360	2	Q7YZP0	EIMMA	Q54233	hadronyche
432	64	12.9	2523	2	Q612I1	CAEBR	Q54233	hadronyche
433	64	12.9	2871	1	FBN1	PIG	Q54233	hadronyche
434	64	12.9	3857	2	O88840	MOUSE	Q54233	hadronyche
435	63.5	12.8	70	1	CLIX	CONBE	Q54233	hadronyche
436	63.5	12.8	92	2	KCP3	RAT	Q54233	hadronyche
437	63.5	12.8	240	1	Q9PUK3	CHICK	Q54233	hadronyche
438	63.5	12.8	320	2	Q4OHQ7	9RHOB	Q54233	hadronyche
439	63.5	12.8	349	2	Q9PVN4	CHICK	Q54233	hadronyche
440	63.5	12.8	362	2	Q5TV39	ANOAG	Q54233	hadronyche
441	63.5	12.8	395	2	Q3K7E8	PSEPF	Q54233	hadronyche
442	63.5	12.8	407	2	Q5SY22	HUMAN	Q54233	hadronyche
443	63.5	12.8	460	2	Q5RG03	BRARE	Q54233	hadronyche
444	63.5	12.8	536	2	Q90656	CHICK	Q54233	hadronyche
445	63.5	12.8	728	2	Q90656	CHICK	Q54233	hadronyche
446	63.5	12.8	747	2	Q4DFR4	TRYCR	Q54233	hadronyche
447	63.5	12.8	747	2	Q8VHF4	MOUSE	Q54233	hadronyche
448	63.5	12.8	841	1	TSIR1	HUMAN	Q54233	hadronyche
449	63.5	12.8	847	2	Q3JVB9	9VIRU	Q54233	hadronyche
450	63.5	12.8	871	2	Q626H3	CAEBR	Q54233	hadronyche
451	63.5	12.8	898	2	Q60UE2	CAEBR	Q54233	hadronyche
452	63.5	12.8	898	2	Q3URX7	MOUSE	Q54233	hadronyche
453	63.5	12.8	1004	2	Q8CGA7	MOUSE	Q54233	hadronyche
454	63.5	12.8	1034	2	Q8VHL7	MOUSE	Q54233	hadronyche
455	63.5	12.8	1034	2	Q8VHL7	MOUSE	Q54233	hadronyche
456	63.5	12.8	1285	1	CRUM2	HUMAN	Q54233	hadronyche
457	63.5	12.8	1505	2	O5S3N1	SALSA	Q54233	hadronyche
458	63.5	12.8	1519	2	Q8WPN0	9UROC	Q54233	hadronyche
459	63.5	12.8	1872	2	Q8JHV6	BRARE	Q54233	hadronyche
460	63.5	12.8	2672	2	Q3UHH3	MOUSE	Q54233	hadronyche
461	63.5	12.8	3695	1	LAMAS	HUMAN	Q54233	hadronyche
462	63.5	12.8	3695	2	O8TDF6	HUMAN	Q54233	hadronyche
463	63.5	12.8	3707	1	PCBM	MOUSE	Q54233	hadronyche
464	63	12.7	131	1	CHHB1	BOMMO	Q54233	hadronyche
465	63	12.7	319	2	Q4T826	TETNG	Q54233	hadronyche
466	63	12.7	371	2	Q5U215	RAT	Q54233	hadronyche
467	63	12.7	394	2	Q9NGP9	POLPA	Q54233	hadronyche
468	63	12.7	456	2	Q54IG3	DICDI	Q54233	hadronyche
469	63	12.7	459	2	Q62327	MOUSE	Q54233	hadronyche

Q3U2A9	mouse	musculus
Q4AQC1	chick	gallus
Q3T5U5	mouse	musculus
Q8S1M4	mouse	musculus
Q8ND91	human	homo sapien
Q9VJU4	mouse	musculus
Q4V526	mouse	musculus
Q86BL2	mouse	musculus
Q528V2	mouse	musculus
Q9WU23	mouse	musculus
Q8BRK9	mouse	musculus
Q6D1G4	mouse	musculus
Q8BKX7	mouse	musculus
Q86K96	mouse	musculus
Q4E977	mouse	musculus
Q614U4	mouse	musculus
Q4E961	mouse	musculus
Q80T91	mouse	musculus
Q8G111	mouse	musculus
Q4E7D3	mouse	musculus
Q9U350	mouse	musculus
Q4RW31	mouse	musculus
Q800E4	mouse	musculus
Q70465	mouse	musculus
P98133	mouse	musculus
P58455	mouse	musculus
Q3TRB8	mouse	musculus
Q63404	mouse	musculus
Q61KY7	mouse	musculus
Q56J11	mouse	musculus
Q3MZ10	mouse	musculus
Q3MCA3	mouse	musculus
Q565Y9	mouse	musculus
Q565Y9	mouse	musculus
Q510R0	mouse	musculus
Q6TMJ6	mouse	musculus
Q8WU13	mouse	musculus
Q3G137	mouse	musculus
Q02261	mouse	musculus
Q4S8K6	mouse	musculus
CADHF	mouse	musculus
Q9UB95	mouse	musculus
Q42124	mouse	musculus
Q8DE5	mouse	musculus
Q96K7	mouse	musculus
Q9Y7V5	mouse	musculus
Q60Y8	mouse	musculus
Q8C622	mouse	musculus
NID2	mouse	musculus
Q3TFN0	mouse	musculus
Q3US45	mouse	musculus
Q7TQF0	mouse	musculus
Q8CFA3	mouse	musculus
Q8R5G0	mouse	musculus
Q5RH37	mouse	musculus
Q4QHT5	mouse	musculus
Q4RVG6	mouse	musculus
MUC2	mouse	musculus
Q2MCN6	mouse	musculus
Q313L8	mouse	musculus
VP52	mouse	musculus
Q3LZQ0	mouse	musculus
Q5TAB1	mouse	musculus
Q9N2N0	mouse	musculus
CHHB2	mouse	musculus
Q8PPR1	mouse	musculus
Q6H8Q4	mouse	musculus
Q4S8K0	mouse	musculus
Q7XZ34	mouse	musculus
Q3U697	mouse	musculus
Q340C6	mouse	musculus
Q4TDM7	mouse	musculus

543	62	12.4	258	2	Q9Z548_TORAC	Q9Z448 nicotiana t	616	61.5	12.3	833	2	QSR654_PONPY	Q5r654 pongo pygma
544	62	12.4	282	1	END4_DESVH	Q72q99 desulfovibr	617	61.5	12.3	932	2	Q5Y4N8_RAT	Q5Y4n8 rattus norv
545	62	12.4	306	2	Q2KJ78_BOVIN	Q2KJ78 bos taurus	618	61.5	12.3	941	2	Q54YPO_DICTDI	Q54Yp0 dictyosteli
546	62	12.4	311	2	Q8R1G8_MOUSE	Q8R1g8 mus musculus	619	61.5	12.3	1045	2	Q8T3A6_CAEEL	Q8T3a6 caenorhabdi
547	62	12.4	315	2	Q4U3E1_HUMAN	Q4u3e1 homo sapien	620	61.5	12.3	1070	2	Q8T3A7_CAEEL	Q8T3a7 caenorhabdi
548	62	12.4	383	2	Q969Y6_HUMAN	Q969y6 homo sapien	621	61.5	12.3	1111	2	Q9XWD5_CAEEL	Q9Xwd5 caenorhabdi
549	62	12.4	388	2	Q66JUK_XENTR	Q66Juk xenopus tro	622	61.5	12.3	1316	2	Q96J07_HUMAN	Q96Ju7 homo sapien
550	62	12.4	389	2	Q8R226_MOUSE	Q8R226 mus musculus	623	61.5	12.3	1394	2	Q8MST1_DROME	Q8Mst1 drosophila
551	62	12.4	402	1	GUN1_HUMIN	P56800 humicola gr	624	61.5	12.3	1511	2	Q9VB21_DROME	Q9Vb21 drosophila
552	62	12.4	435	1	GUN1_HUMGT	Q12622 humicola in	625	61.5	12.3	1666	2	LTBP4_MOUSE	Q8k4g1 mus musculus
553	62	12.4	469	2	Q5BL53_BRARE	Q5bl53 brachydanio	626	61.5	12.3	1687	2	Q61204_MOUSE	Q61204 mus musculus
554	62	12.4	476	2	Q8R1H9_MOUSE	Q8R1h9 mus musculus	627	61.5	12.3	1721	2	Q614N6_CABBR	Q614n6 caenorhabdi
555	62	12.4	491	2	P90850_CAEEL	P90850 caenorhabdi	628	61.5	12.3	2030	2	Q9VXV3_DROME	Q9Vxv3 drosophila
556	62	12.4	493	2	Q7TNG6_MOUSE	Q7Tng6 mus musculus	629	61.5	12.3	2224	2	Q44131_CAEEL	Q44131 caenorhabdi
557	62	12.4	592	2	Q6IS34_MOUSE	Q6i34 mus musculus	630	61.5	12.3	2470	1	NOTC2_MOUSE	Q5516 mus musculus
558	62	12.4	601	2	Q52KT2_XENLA	Q52kt2 xenopus lae	631	61.5	12.3	2471	1	STAB1_HUMAN	Q9W330 rattus norv
559	62	12.4	615	2	Q58E52_MOUSE	Q58e52 mus musculus	632	61.5	12.3	2570	1	NOTC3_RAT	Q9W15 homo sapien
560	62	12.4	625	2	Q8QF9_9VIRU	Q8Qf9 adeno-assoc	633	61.5	12.3	2571	1	STAB1_MOUSE	Q8R44 mus musculus
561	62	12.4	657	2	Q8R0K8_MOUSE	Q8R0k8 mus musculus	634	61.5	12.3	2966	2	Q4RMT7_TETNG	Q4Rmt7 tetraodon n
562	62	12.4	737	2	Q8JZM4_MOUSE	Q8Jzm4 mus musculus	635	61.5	12.3	3333	1	LANA3_MOUSE	Q61789 mus musculus
563	62	12.4	737	2	Q8VD97_MOUSE	Q8Vd97 mus musculus	636	61.5	12.3	3457	2	Q4E0C7_TRYCR	Q4e0c7 trypanosoma
564	62	12.4	772	1	DLA4_BRARE	Q6di48 brachydanio	637	61.5	12.3	3548	2	Q5VTE4_HUMAN	Q5vte4 homo sapien
565	62	12.4	885	2	Q7R1C5_GIALA	Q7ric5 giardia lam	638	61.5	12.3	3574	2	Q4LDE5_HUMAN	Q4lde5 homo sapien
566	62	12.4	998	1	EPHB3_HUMAN	P54753 homo sapien	639	61.5	12.3	4260	2	Q4T3T2_TETNG	Q4T3t2 tetraodon n
567	62	12.4	1047	2	Q566K6_MOUSE	Q566k6 mus musculus	640	61.5	12.3	5374	2	Q9SND0_MOUSE	Q9Snd0 mus musculus
568	62	12.4	1065	2	Q810H2_MOUSE	Q810h2 mus musculus	641	61.5	12.3	5376	1	ZAN_MOUSE	Q8X799 mus musculus
569	62	12.4	1113	1	CORIN_MOUSE	Q9Z319 mus musculus	642	61	12.2	104	2	Q7XZ46_GRIJA	Q7Xz46 griffithsia
570	62	12.4	1170	1	TSPI_HUMAN	P07996 homo sapien	643	61	12.2	111	1	COL_MYOCO	P42889 myocastor c
571	62	12.4	1170	1	TSPI_MOUSE	P35441 mus-musculus	644	61	12.2	112	1	COL_PIG	P02703 sus scrofa
572	62	12.4	1170	2	Q3TR40_MOUSE	Q3tr40 mus-musculus	645	61	12.2	112	1	Q315G6_PIG	Q315g6 sus scrofa
573	62	12.4	1170	2	Q71SA3_RAT	Q71sa3 rattus norv	646	61	12.2	115	1	MERT_SHEPU	Q54462 shewanella
574	62	12.4	1171	2	Q80YQ1_MOUSE	Q80Yq1 mus musculus	647	61	12.2	116	2	Q5T6Z9_HUMAN	Q5T6z9 homo sapien
575	62	12.4	1171	2	Q8QGB2_MOUSE	Q8Qgb2 mus musculus	648	61	12.2	146	1	TXVE_BOTIN	Q90x24 bothrops in
576	62	12.4	1174	2	Q3TGL4_MOUSE	Q3tg4 mus musculus	649	61	12.2	156	2	Q2IVF9_RHOPA	Q2ivf9 rhodopseudo
577	62	12.4	1174	2	Q9PKS8_MOUSE	Q9Pk8 mus musculus	650	61	12.2	173	2	Q9RJ35_STRCO	Q9Rj35 streptomyce
578	62	12.4	1205	2	Q8KOP6_MOUSE	Q8Kop6 mus musculus	651	61	12.2	205	2	Q9T700_HUMAN	Q9T700 homo sapien
579	62	12.4	1221	1	FBLN2_MOUSE	P37889 mus musculus	652	61	12.2	211	2	Q9RK27_STRCO	Q9Rk27 streptomyce
580	62	12.4	1225	2	Q59E99_HUMAN	Q59e99 homo sapien	653	61	12.2	307	2	Q4C965_CROWT	Q4C965 crocospaer
581	62	12.4	1308	2	Q9GPM8_CABRE	Q9Gpm8 caenorhabdi	654	61	12.2	369	2	Q7QDZ6_ANOGA	Q7Qdz6 anopheles g
582	62	12.4	1361	2	Q6PD18_MOUSE	Q6pd18 mus musculus	655	61	12.2	380	2	Q60214_METCA	Q60214 methylococc
583	62	12.4	1403	2	Q70E20_MOUSE	Q70e20 mus musculus	656	61	12.2	409	2	Q3TV46_MOUSE	Q3tv46 mus musculus
584	62	12.4	1813	1	LTBP2_MOUSE	Q08999 mus musculus	657	61	12.2	413	2	Q23015_CAEEL	Q23015 caenorhabdi
585	62	12.4	1935	2	Q6QHS3_LYTVA	Q6qhs3 lytechinus	658	61	12.2	442	2	Q55GL3_DICTDI	Q55gl3 dictyosteli
586	62	12.4	2043	2	Q4Q510_LEITMA	Q4q510 leishmania	659	61	12.2	442	2	Q569T8_XENLA	Q569t8 xenopus lae
587	62	12.4	2067	2	Q59ED8_HUMAN	Q59ed8 homo sapien	660	61	12.2	443	2	Q2TAU8_XENLA	Q2tau8 xenopus lae
588	62	12.4	2282	1	ZAN_RABIT	P57999 oryctolagus	661	61	12.2	447	2	Q4J3W1_AZOVI	Q4j3w1 azotobacter
589	62	12.4	2437	1	NOTC1_BRARE	P46530 brachydanio	662	61	12.2	456	2	Q3WTR3_9RHIZ	Q3Wtr3 mesorhizobi
590	62	12.4	2511	2	Q4T9V2_TETNG	Q4T9v2 tetraodon n	663	61	12.2	506	2	Q8C7W2_MOUSE	Q8C7w2 mus musculus
591	62	12.4	2555	2	Q5SXM3_HUMAN	Q5sxm3 homo sapien	664	61	12.2	525	2	P92162_BOMMO	P92162 bombyx mori
592	62	12.4	2556	1	NOTC1_HUMAN	P46531 homo sapien	665	61	12.2	538	2	Q8CC86_MOUSE	Q8cc86 m adult mal
593	62	12.4	5141	2	Q700K0_RAT	Q700k0 rattus norv	666	61	12.2	563	2	Q7TP82_RAT	Q7tp82 rattus norv
594	61.5	12.3	83	2	Q9XTK6_CAEEL	Q9xkt6 caenorhabdi	667	61	12.2	571	2	Q8C1E3_MOUSE	Q8c1e3 mus musculus
595	61.5	12.3	110	2	Q5TA82_HUMAN	Q5ta82 homo sapien	668	61	12.2	610	2	Q4B0K0_POLARONAS	Q4B0k0 polaromonas
596	61.5	12.3	128	2	Q52VH7_CIOIN	Q52vh7 ciona intes	669	61	12.2	657	2	Q4T6N0_TETNG	Q4ten0 tetraodon n
597	61.5	12.3	159	2	Q7XZ75_GRIJA	Q7xz75 griffithsia	670	61	12.2	703	2	Q8C122_MOUSE	Q8c122 mus musculus
598	61.5	12.3	166	1	ZCH13_HUMAN	Q8ww36 homo sapien	671	61	12.2	705	1	FBLN1_MOUSE	Q08879 mus musculus
599	61.5	12.3	176	2	Q87WA2_PSESM	Q87wa2 pseudomonas	672	61	12.2	723	2	Q3TWK8_MOUSE	Q3twk8 mus musculus
600	61.5	12.3	190	2	Q3ZDR4_PIG	Q3zdr4 sus scrofa	673	61	12.2	735	2	Q8E2T2_MOUSE	Q8e2t2 mus musculus
601	61.5	12.3	228	2	Q9LNG9_9PARA	Q9lng9 ciona viru	674	61	12.2	735	2	Q8E2T2_MOUSE	Q8e2t2 mus musculus
602	61.5	12.3	277	1	TNR4_HUMAN	P43489 homo sapien	675	61	12.2	881	2	Q9W0A0_DROME	Q9Woa0 drosophila
603	61.5	12.3	277	1	Q2M312_HUMAN	Q2m312 homo sapien	676	61	12.2	903	2	Q44397_TRITR	Q44397 trichuris t
604	61.5	12.3	368	2	Q82VZ2_NITEU	Q82vz2 nitrosomona	677	61	12.2	1037	2	Q616G9_CABBR	Q616g9 caenorhabdi
605	61.5	12.3	373	2	Q5SNS5_BRARE	Q5sns5 brachydanio	678	61	12.2	1037	2	Q5VY43_HUMAN	Q5vy43 homo sapien
606	61.5	12.3	452	2	Q51SL2_MACFA	Q5isl2 macaca fasc	679	61	12.2	1057	2	Q4N4P8_THEPA	Q4n4p8 theileria p
607	61.5	12.3	469	2	Q52V41_CIOIN	Q52v41 ciona intes	680	61	12.2	1111	2	Q8OYN4_RAT	Q8Oyn4 rattus norv
608	61.5	12.3	587	2	Q5C3P1_SCHJA	Q5c3p1 schistosoma	681	61	12.2	1123	2	Q5RDI5_PONPY	Q5Rdi5 pongo pygma
609	61.5	12.3	720	2	Q2U318_ASPOR	Q2u318 aspergillus	682	61	12.2	1162	2	Q2Q422_CANFA	Q2Q422 canis famil
610	61.5	12.3	735	2	Q498M5_RAT	Q498m5 rattus norv	683	61	12.2	1212	2	Q42347_CHICK	Q42347 gallus gall
611	61.5	12.3	774	2	Q3SEM5_PARTE	Q3sem2 paramecium	684	61	12.2	1249	2	Q8VI66_RAT	Q8vi66 rattus norv
612	61.5	12.3	782	2	Q7PDS2_PLAYO	Q7pds2 paramecium	685	61	12.2	1396	2	Q4RPLY_TETNG	Q4Rpy1 tetraodon n
613	61.5	12.3	812	2	Q7PDS2_PLAYO	Q7pds2 plasmodium	686	61	12.2	1418	2	Q93457_SCOMX	Q93457 scophthalmu
614	61.5	12.3	812	2	Q77779_BOVIN	Q77779 bos taurus	687	61	12.2	1476	2	Q90285_CARAU	Q90285 carassius a
615	61.5	12.3	816	2	Q5R449_PONPY	Q5r449 pongo pygma	688	61	12.2	1599	2	Q09983_CAEEL	Q09983 caenorhabdi

689	61	12.2	1790	2	Q55P41_DICDI	Q55F41 dictyosteli
690	61	12.2	2476	1	ZAN_PIG	Q28983 sus scrofa
691	61	12.2	2532	2	Q629H6_CABR	Q629h6 caenorhabdi
692	61	12.2	2806	2	Q4DH79_TRYCR	Q4dh79 trypanosoma
693	61	12.2	4998	2	Q8CG65_MOUSE	Q8cg65 mus musculus
694	60.5	12.1	92	2	Q8GX9_ARATH	Q8gx9 arabidopsis
695	60.5	12.1	96	2	Q8CJ11_LACLA	Q8cj11 lactococcus
696	60.5	12.1	106	2	Q33AQ5_ORYSA	Q33aq5 oryza sativ
697	60.5	12.1	113	2	Q8H3W9_ORYSA	Q8h3w9 oryza sativ
698	60.5	12.1	129	2	Q9YCE5_AERPE	Q9yce5 aeropyrum p
699	60.5	12.1	168	2	Q8T2Z9_TRYCR	Q8t2z9 trypanosoma
700	60.5	12.1	189	2	Q3F736_9BURK	Q3f736 burkholderi
701	60.5	12.1	234	2	Q5C033_SCHJA	Q5c033 schistosoma
702	60.5	12.1	261	2	Q39TH1_GEOMG	Q39th1 geobacter m
703	60.5	12.1	296	2	Q5M8H8_XENTR	Q5m8h8 xenopus tro
704	60.5	12.1	316	1	IBP2_PIG	P24853 sus scrofa
705	60.5	12.1	368	2	Q86IM1_DICDI	Q86im1 dictyosteli
706	60.5	12.1	383	2	Q70534_RAT	Q70534 rattus norv
707	60.5	12.1	383	2	Q62779_RAT	Q62779 rattus norv
708	60.5	12.1	386	2	Q53LE2_ORYSA	Q53le2 oryza sativ
709	60.5	12.1	395	2	Q559Z3_DICDI	Q559z3 dictyosteli
710	60.5	12.1	401	2	Q81IK6_MOUSE	Q81ik6 mus musculus
711	60.5	12.1	407	2	Q961I3_DROME	Q961i3 drosophila
712	60.5	12.1	452	2	Q499Z4_HUMAN	Q499z4 homo sapien
713	60.5	12.1	452	2	Q9H6G5_HUMAN	Q9h6g5 homo sapien
714	60.5	12.1	510	2	Q3QRX7_9RHOB	Q3qrx7 silicibacte
715	60.5	12.1	515	1	NAGPA_HUMAN	Q9uk23 homo sapien
716	60.5	12.1	544	2	Q5BW73_SCHJA	Q5bw73 schistosoma
717	60.5	12.1	556	2	Q5VXW6_HUMAN	Q5vxw6 homo sapien
718	60.5	12.1	637	2	Q7PFQ7_ANOGA	Q7pfq7 anopheles g
719	60.5	12.1	723	1	DL11_HUMAN	O0548 homo sapien
720	60.5	12.1	767	2	Q9DGR2_XENLA	Q9dgr2 xenopus lae
721	60.5	12.1	780	2	Q3U2X9_MOUSE	Q3u2x9 mus musculus
722	60.5	12.1	790	2	Q4R728_MACFA	Q4r728 macaca fasc
723	60.5	12.1	871	2	Q4SCX8_TETNG	Q4scx8 tetraodon n
724	60.5	12.1	905	2	O18260_CAEEL	O18260 caenorhabdi
725	60.5	12.1	917	2	Q9VE20_DROME	Q9ve20 drosophila
726	60.5	12.1	978	1	MCR_MOUSE	Q8vii8 mus musculus
727	60.5	12.1	1024	2	Q9BX11_HUMAN	Q9bx11 homo sapien
728	60.5	12.1	1104	1	NFX1_HUMAN	Q12986 homo sapien
729	60.5	12.1	1120	2	Q96EL5_HUMAN	Q96el5 homo sapien
730	60.5	12.1	1389	1	LTB1S_MOUSE	Q8cg18 mus musculus
731	60.5	12.1	1394	2	Q505C9_MOUSE	Q505c9 mus musculus
732	60.5	12.1	1622	2	Q3ZTN4_SALSC	Q3ztn4 salmuri sci
733	60.5	12.1	1713	1	LTB1L_MOUSE	Q8cgn4 mus musculus
734	60.5	12.1	1914	2	Q4WHJ5_ASPPU	Q4whj5 aspergillus
735	60.5	12.1	2038	2	Q7QFS2_ANOGA	Q7qfs2 anopheles g
736	60.5	12.1	2653	2	Q25253_LUCCU	Q25253 lucilia cup
737	60.5	12.1	2703	1	NORCH_DROME	P07207 drosophila
738	60.5	12.1	2771	2	Q9WTS7_MOUSE	Q9wts7 mus musculus
739	60.5	12.1	2783	2	Q7M559_BRARE	Q7m559 brachydanio
740	60.5	12.1	2796	2	Q3UHK6_MOUSE	Q3uhk6 mus musculus
741	60.5	12.1	2833	2	Q3UH52_MOUSE	Q3uh52 mus musculus
742	60.5	12.1	3486	2	Q4DGM4_TRYCR	Q4dgm4 trypanosoma
743	60	12.0	125	2	Q4WZP5_ASPPU	Q4wzp5 aspergillus
744	60	12.0	126	2	Q8T5W4_CABRE	Q8t5w4 caenorhabdi
745	60	12.0	127	2	Q8T5X2_CABRE	Q8t5x2 caenorhabdi
746	60	12.0	128	2	Q8T5W8_CABRE	Q8t5w8 caenorhabdi
747	60	12.0	129	2	Q8T5W7_CABRE	Q8t5w7 caenorhabdi
748	60	12.0	146	2	Q5K4F7_SCHGR	Q5k4f7 schistocerc
749	60	12.0	181	2	Q4APAF_9CHLB	Q4afa9 chlorobium
750	60	12.0	184	1	ESW1_HUMAN	Q9nq30 homo sapien
751	60	12.0	185	2	Q6XIW9_DROYA	Q6xiw9 drosophila
752	60	12.0	211	2	Q6TPK5_CHICK	Q6tpk5 gallus gall
753	60	12.0	309	2	Q74ZS4_ASHGO	Q74zsa ashbya goss
754	60	12.0	318	2	Q6A853_PROAC	Q6a853 propionibac
755	60	12.0	320	2	Q8N780_HUMAN	Q8n780 homo sapien
756	60	12.0	348	2	Q54XB6_DICDI	Q54xb6 dictyosteli
757	60	12.0	366	2	Q46SU2_RALEJ	Q46su2 ralstonia e
758	60	12.0	383	2	Q3KA04_PSEPP	Q3ka04 pseudomonas
759	60	12.0	397	2	Q52VK2_CIOIN	Q52vk2 ciona intes
760	60	12.0	398	2	Q52VK3_CIOIN	Q52vk3 ciona intes
761	60	12.0	403	2	Q4R3X4_MACFA	Q4r3x4 macaca fasc

Q4kfp7	pseudomonas
Q91zm6	rattus norv
Q98173	molluscum c
Q8ABx6	brachydanio
Q6vau8	rattus norv
Q6phh5	brachydanio
Q642b2	rattus norv
Q80wy6	rattus norv
Q5ylp0	rattus norv
Q4h3q6	ciona intes
Q617P3	caenorhabdi
Q6J2K6	oryza sativ
Q6p2g0	homo sapien
Q5Y9B3	adeno-associ
Q5Y9B5	adeno-associ
Q56136	adeno-associ
Q9wbp7	adeno-associ
Q4REW4	tetradon n
Q81pp3	drosophila
Q3w1k0	frankia sp.
Q4t4w9	tetradon n
Q91bd5	anguilla ja
Q99965	homo sapien
Q28478	macaca fasc
Q4r6r6	macaca fasc
Q9r0g6	mus musculus
Q8v154	mus musculus
Q89py0	bradyrhizob
Q8mjk0	cercopithe
Q22685	caenorhabdi
Q6btq2	debaromyce
Q5bi10	drosophila
Q28178	bos taurus
Q3508	caenorhabdi
Q9n815	homo sapien
Q8K3k1	rattus norv
P20951	papaya mosa
Q61k66	caenorhabdi
P30432	drosophila
P31696	gallus gall
Q59E86	homo sapien
Q7pf90	anopheles g
Q4rhf2	tetradon n
P35556	homo sapien
Q3V514	mus musculus
Q4rj20	tetradon n
Q35452	mus musculus
O54796	mus musculus
Q9byr6	homo sapien
O521P0	homo sapien
Q6ntd3	homo sapien
Q65313	lavatera th
Q5azi7	urtica dioi
Q92P51	urtica dioi
Q2izf4	rhodopseudo
Q08429	bacillus su
Q2qlp4	pan troglod
Q2wai5	magnecospir
Q6n0u5	rhodopseudo
Q5LKG8	silicibacte
Q7rtn5	neurospora
Q4at93	poliaronas
Q59v7	anaplama m
Q2jsw8	cyanobacter
Q61hi4	caenorhabdi
Q3v1i2	mus musculus
Q31vr3	rhodobacter
O57079	cowpox viru
Q4q266	leishmania
Q54xk1	dictyosteli
Q3Rxt6	ralstonia m
Q62434	oryza sativ
O51g05	bacteroides

835	59.5	11.9	402	2	Q64W1_BACFR	Q64w1 bacteroides	908	59	11.8	550	2	Q4QAE0_LEIMA	Q4qae0 leishmania
836	59.5	11.9	411	2	Q89YQ3_BACTN	Q89yq3 bacteroides	909	59	11.8	551	2	Q61MD2_CAEBR	Q61md2 caenorhabdi
837	59.5	11.9	421	2	Q9DEY1_CYPCA	Q9dey1 cypinus ca	910	59	11.8	570	2	Q2UNP0_ASPOR	Q2unp0 aspergillus
838	59.5	11.9	433	2	Q7ZX39_XENLA	Q7zx39 xenopus lae	911	59	11.8	573	2	Q5W9G8_HUMAN	Q5w9g8 homo sapien
839	59.5	11.9	438	2	Q6INJ1_XENLA	Q6inj1 xenopus lae	912	59	11.8	576	2	Q4RG87_TETNG	Q4rg87 tetraodon n
840	59.5	11.9	448	2	Q9VUJ8_DROME	Q9vju8 drosophila	913	59	11.8	579	2	Q3BUC0_XANC5	Q3buc0 xanthomonas
841	59.5	11.9	484	2	Q5C268_HUMAN	Q5c268 homo sapien	914	59	11.8	579	2	Q2PIT6_XANOR	Q2pit6 xanthomonas
842	59.5	11.9	491	2	Q8TEK2_HUMAN	Q8tek2 homo sapien	915	59	11.8	579	2	Q5GYT3_XANOR	Q5gyt3 xanthomonas
843	59.5	11.9	533	2	Q66HB8_RAT	Q66hb8 rattus norv	916	59	11.8	579	2	Q8P9L1_XANCP	Q8p9l1 xanthomonas
844	59.5	11.9	564	2	Q9TTS4_BOVIN	Q9tte4 bos taurus	917	59	11.8	582	2	Q4UU77_XANCP	Q4uu77 xanthomonas
845	59.5	11.9	587	2	Q3QV05_PROAE	Q3qv05 prothecocho	918	59	11.8	582	2	Q9L4D5_XANCA	Q9l4d5 xanthomonas
846	59.5	11.9	658	2	Q4RLS7_TETNG	Q4rls7 tetraodon n	919	59	11.8	616	2	Q20852_CAEEL	Q20852 caenorhabdi
847	59.5	11.9	712	2	Q5OUF9_CAEEL	Q5ouf9 caenorhabdi	920	59	11.8	674	2	Q87JU0_PHLRA	Q87ju0 phlebia rad
848	59.5	11.9	765	2	Q4SWJ3_TETNG	Q4swj3 tetraodon n	921	59	11.8	702	2	Q5S3M7_9APHY	Q5s3m7 fomitopsis
849	59.5	11.9	836	2	Q49HJ0_CANFA	Q49hj0 canie famil	922	59	11.8	712	2	Q5S3M5_9AGAR	Q5s3m5 grifola sor
850	59.5	11.9	856	2	Q4H557_9DEIO	Q4h557 d fad-depen	923	59	11.8	719	2	Q5S3M6_GRIFR	Q5s3m6 grifola fro
851	59.5	11.9	886	2	EMR1_HUMAN	Q14246 homo sapien	924	59	11.8	740	2	Q6PIA2_HUMAN	Q6pia2 homo sapien
852	59.5	11.9	886	2	Q217G5_HUMAN	Q2i7g5 homo sapien	925	59	11.8	801	2	Q87J88_9HOMO	Q87j88 sterium hir
853	59.5	11.9	917	1	LRP8_CHICK	Q98931 gallus gall	926	59	11.8	803	2	Q87J83_9HOMO	Q87j83 coltricia p
854	59.5	11.9	917	1	Q65XH7_ORYSA	Q65xh7 oryza sativ	927	59	11.8	806	1	ADM1B_MOUSE	Q8r534 mus musculu
855	59.5	11.9	925	2	Q9UB94_CAEEL	Q9ub94 caenorhabdi	928	59	11.8	809	2	Q3V095_MOUSE	Q3v095 mus musculu
856	59.5	11.9	1070	2	Q4RJ74_TETNG	Q4rjt4 tetraodon n	929	59	11.8	823	2	Q61GU3_CAEER	Q61gu3 caenorhabdi
857	59.5	11.9	1117	2	Q6EOK3_DIDMA	Q6eok3 didelphis m	930	59	11.8	836	2	Q61CHI_HUMAN	Q61chl homo sapien
858	59.5	11.9	1144	2	Q4WGE0_ASEFGU	Q4wge0 aspergillus	931	59	11.8	859	2	Q7ZZR6_ORYLA	Q7zzr6 oryzias lat
859	59.5	11.9	1191	2	Q7QH41_ANOGA	Q7qh41 anopheles g	932	59	11.8	859	2	Q98UH9_ORYLA	Q98uh9 oryzias lat
860	59.5	11.9	1620	2	Q3ZTN2_SAGOE	Q3ztn2 saguinus oe	933	59	11.8	871	2	Q87V33_9AGAR	Q87v33 echinodonti
861	59.5	11.9	1621	2	Q3ZTN8_MACMU	Q3ztn8 macaca mula	934	59	11.8	886	2	Q5U7W2_9HOMO	Q5u7w2 clinacodon
862	59.5	11.9	3102	2	Q45614_CAEEL	Q45614 caenorhabdi	935	59	11.8	891	2	Q9ULT6_HUMAN	Q9ult6 homo sapien
863	59.5	11.9	3108	2	Q6OUW4_CAEER	Q6ouw4 caenorhabdi	936	59	11.8	907	2	Q9XTS9_CAEEL	Q9xte9 caenorhabdi
864	59.5	11.9	4135	2	Q18977_BOVIN	Q18977 bos taurus	937	59	11.8	913	2	Q5U7W8_9HOMO	Q5u7w8 albatrellus
865	59.5	11.9	4544	1	LRP1_HUMAN	Q07954 homo sapien	938	59	11.8	913	2	Q5SSZ7_MOUSE	Q5ssz7 mus musculu
866	59.5	11.9	4544	1	Q2PPI2_HUMAN	Q2ppi2 homo sapien	939	59	11.8	937	1	DGRM_CAEEL	Q10024 caenorhabdi
867	59	11.8	88	2	Q5UAZ1_PAGWA	Q5uaz1 pagrus majo	940	59	11.8	949	2	Q4S2B5_TETNG	Q4s2b5 tetraodon n
868	59	11.8	88	2	Q6PW54_PAGWA	Q6pw54 pagrus majo	941	59	11.8	990	2	Q4RMV7_TETNG	Q4rmv7 tetraodon n
869	59	11.8	96	2	Q9S199_CHLRE	Q9s199 chlamydomon	942	59	11.8	1119	2	Q18034_CAEEL	Q18034 caenorhabdi
870	59	11.8	107	2	Q8RKW5_PRORE	Q8rkw5 providencia	943	59	11.8	1123	2	Q7S5Y0_HUMAN	Q7s5y0 homo sapien
871	59	11.8	109	2	Q9S987_HUMAN	Q9s987 homo sapien	944	59	11.8	1146	2	Q60M26_CAEER	Q60m26 caenorhabdi
872	59	11.8	115	2	Q3G626_9GAMU	Q3g626 shewanella	945	59	11.8	1154	2	Q3U1W7_MOUSE	Q3u1w7 m b6-derive
873	59	11.8	116	2	Q3E1Y8_CHLAU	Q3e1y8 chloroflexu	946	59	11.8	1167	2	Q6KAT1_MOUSE	Q6kat1 mus musculu
874	59	11.8	130	2	Q6IE42_RAT	Q6ie42 rattus norv	947	59	11.8	1175	2	Q50TW3_ENTHI	Q50tw3 entamoeba h
875	59	11.8	150	2	Q443U5_SOLUS	Q443u5 solibacter	948	59	11.8	1268	1	LTBP3_MOUSE	Q61810 mus musculu
876	59	11.8	159	1	KRA98_HUMAN	Q9byq0 homo sapien	949	59	11.8	1270	2	Q9GPN0_CAEER	Q9gpn0 caenorhabdi
877	59	11.8	186	1	AG13_WHEAT	P10969 triticum ae	950	59	11.8	1314	2	Q8UZJ7_9GAMA	Q8uzj7 cercopthec
878	59	11.8	209	2	P93029_ARATH	P93029 arabidopsis ae	951	59	11.8	1674	2	Q2R3L7_ORYSA	Q2r3l7 oryza sativ
879	59	11.8	215	2	Q8OW51_MOUSE	Q8ow51 mus musculu	952	59	11.8	1764	1	LTBP2_RAT	Q35806 rattus norv
880	59	11.8	218	1	YR661_MIMIV	Q5uq61 mimivirus	953	59	11.8	1827	2	Q4CQ43_TRYCR	Q4cq43 trypanosoma
881	59	11.8	220	2	Q4TF08_TETNG	Q4tf08 tetraodon n	954	59	11.8	2370	2	Q4UJ22_THEAN	Q4uj22 theleria a
882	59	11.8	225	2	Q7XZ30_GRIJA	Q7xz30 griffithsia	955	59	11.8	2428	2	Q816X6_BOOMI	Q816x6 boophilus m
883	59	11.8	234	2	Q7QG32_ANOGA	Q7qgy2 anopheles g	956	59	11.8	2549	2	Q2L697_CTOIN	Q2l697 ciona intes
884	59	11.8	261	2	Q4OMY0_DESAC	Q4omy0 desulfuroco	957	59	11.8	2871	1	FBN1_MOUSE	Q61554 mus musculu
885	59	11.8	269	2	Q9U2B8_CAEEL	Q9u2b8 caenorhabdi	958	59	11.8	2872	2	Q9WU8_RAT	Q9wuh8 rattus norv
886	59	11.8	272	2	Q61BN9_CAEER	Q61bn9 caenorhabdi	959	59	11.8	3843	2	Q9U5D0_DROME	Q9u5d0 drosophila
887	59	11.8	300	2	Q84BD4_MYXXA	Q84bd4 myxococcus	960	59	11.8	3843	2	Q9VU94_DROME	Q9vu94 drosophila
888	59	11.8	306	2	Q3WRH0_9RHIZ	Q3wrh0 mesorhizobi	961	59	11.8	4349	1	FAT2_HUMAN	Q9nyq8 homo sapien
889	59	11.8	315	2	Q8LA97_ARATH	Q8la97 arabidopsis	962	58.5	11.7	50	2	Q64DV8_9ARCH	Q64dv8 uncultured
890	59	11.8	315	2	Q82307_ARATH	Q82307 arabidopsis	963	58.5	11.7	76	2	Q64AE9_9ARCH	Q64ae9 uncultured
891	59	11.8	317	2	Q4TF09_TETNG	Q4tf09 tetraodon n	964	58.5	11.7	99	2	Q9CPW1_MOUSE	Q9cpw1 m adult mal
892	59	11.8	343	2	Q6PAL1_MOUSE	Q6pal1 mus musculu	965	58.5	11.7	99	2	Q9D638_MOUSE	Q9d638 mus musculu
893	59	11.8	343	2	Q8C3D8_MOUSE	Q8c3d8 mus musculu	966	58.5	11.7	99	2	Q9D7P0_MOUSE	Q9d7p0 mus musculu
894	59	11.8	348	2	Q6UWK8_HUMAN	Q6uwk8 homo sapien	967	58.5	11.7	128	2	Q6ZWD3_HUMAN	Q6zwd3 homo sapien
895	59	11.8	349	1	XRCC3_MOUSE	Q9cxe6 mus musculu	968	58.5	11.7	138	2	Q6UTY0_BOVIN	Q6uty0 bos taurus
896	59	11.8	349	2	Q5SNX0_HUMAN	Q5snx0 homo sapien	969	58.5	11.7	139	2	Q70PB6_9GEMI	Q70pb6 sida micran
897	59	11.8	349	2	Q8NB13_HUMAN	Q8nb13 homo sapien	970	58.5	11.7	181	2	Q39923_BURSI	Q39923 burkholderi
898	59	11.8	386	1	AMPW1_MOUSE	Q8bp48 mus musculu	971	58.5	11.7	200	2	Q5TUY6_ANOGA	Q5tuy6 anopheles g
899	59	11.8	386	2	Q4VAA9_MOUSE	Q4vaa9 m methionyl	972	58.5	11.7	214	2	Q58FY3_ARATH	Q58fy3 arabidopsis
900	59	11.8	414	2	Q61BN4_CAEER	Q61bn4 caenorhabdi	973	58.5	11.7	214	2	Q84RKO_ARATH	Q84rko arabidopsis
901	59	11.8	419	2	Q92043_CROAT	Q92043 crotalus at	974	58.5	11.7	252	2	Q3X2T3_9ACTN	Q3x2t3 rubrobacter
902	59	11.8	435	2	Q616G8_CAEER	Q616g8 caenorhabdi	975	58.5	11.7	254	2	Q4DN16_TRYCR	Q4dn16 trypanosoma
903	59	11.8	454	2	Q7F8X9_ORYSA	Q7f8x9 oryza sativ	976	58.5	11.7	276	2	Q4PL95_ARATH	Q4pl95 arabidopsis
904	59	11.8	459	1	PROC_PIG	Q9gip2 s vitamin k	977	58.5	11.7	291	2	Q3B3Y5_PELLD	Q3b3y5 pelodictyon
905	59	11.8	474	1	TNR1B_MOUSE	P25119 mus musculu	978	58.5	11.7	308	2	Q46370_BOVIN	Q46370 bos taurus
906	59	11.8	474	2	Q545P4_MOUSE	Q545p4 m adult mal	979	58.5	11.7	318	2	Q4A672_MYC5S	Q4a672 mycoplasma
907	59	11.8	524	2	Q6QJD5_9APHY	Q6qjd5 cylindrobac	980	58.5	11.7	325	1	VT2_SFVKA	P25943 shope fibro

981	58.5	11.7	325	2	Q77PB3_9POXV	Q77pb3 rabbit fibr	1054	58	11.6	116	2	Q40LW6_DESAC	Q40lw6 desulfuromo
982	58.5	11.7	327	2	Q37PR3_SPHAR	Q37pr9 novosphingo	1055	58	11.6	125	2	Q62T15_HUMAN	Q62t15 homo sapien
983	58.5	11.7	328	2	Q8MQG2_CABEL	Q8mqg3 caenorhabdi	1056	58	11.6	126	2	Q6F4F7_TRISC	Q6f4f7 triakie ey
984	58.5	11.7	358	2	Q18392_CABEL	Q18392 caenorhabdi	1057	58	11.6	127	2	Q8T5W9_CAERE	Q8t5w9 caenorhabdi
985	58.5	11.7	361	2	Q4V7M2_XENLA	Q4v7m2 xenopus lae	1058	58	11.6	128	2	Q8T5X1_CAERE	Q8t5x1 caenorhabdi
986	58.5	11.7	375	2	Q4TC52_TETNG	Q4tc52 tetraodon n	1059	58	11.6	129	2	Q8T5X4_CAERE	Q8t5x4 caenorhabdi
987	58.5	11.7	407	2	Q4WAJ6_ASPFU	Q4waj6 aspergillus	1060	58	11.6	168	2	Q2L2N5_DROPS	Q2l2n5 drosophila
988	58.5	11.7	429	2	Q8UZP9_9GAMA	Q8uzf9 cercopithec	1061	58	11.6	170	2	Q912H3_PSEAE	Q912h3 pseudomonas
989	58.5	11.7	463	2	Q88QF3_LITFO	Q88qf3 lithobius f	1062	58	11.6	190	2	Q33518_AGKHB	Q33518 agkistrodon
990	58.5	11.7	492	1	F3CN2_BOVIN	Q18728 bos taurus	1063	58	11.6	199	2	Q9H557_HUMAN	Q9h557 homo sapien
991	58.5	11.7	513	2	Q9VJW7_DROME	Q9vjw7 drosophila	1064	58	11.6	210	2	Q8WSM7_PLACH	Q8wsm7 plasmodium
992	58.5	11.7	534	2	Q91VM8_MOUSE	Q91vm8 mus musculu	1065	58	11.6	212	2	Q90Y44_AGKRP	Q90y44 agkistrodon
993	58.5	11.7	559	2	Q9HBQ2_HUMAN	Q9hbq2 homo sapien	1066	58	11.6	227	2	Q3X072_AACTN	Q3x072 agkrobacter
994	58.5	11.7	565	2	Q8RBP1_PONPY	Q8rbp1 pongo pygma	1067	58	11.6	228	2	Q39X70_GEOMG	Q39x70 geobacter m
995	58.5	11.7	575	2	Q729Y7_DESVH	Q729y7 desulfovibr	1068	58	11.6	229	2	Q4PN05_XOSMC	Q4pn05 ixodes scap
996	58.5	11.7	581	2	Q40Y44_KINRA	Q40y44 kineococcus	1069	58	11.6	238	2	Q3V1G0_MOUSE	Q3v1g0 mus musculu
997	58.5	11.7	583	2	Q6A008_MOUSE	Q6a008 mus musculu	1070	58	11.6	275	2	Q7TGA5_EAV	Q7tga5 equine arte
998	58.5	11.7	591	2	Q5AKX6_CANAL	Q5akx6 candida alb	1071	58	11.6	277	2	Q31ZR9_RHOS4	Q31zr9 rhodobacter
999	58.5	11.7	654	2	Q4RYU0_TETNG	Q4ryu0 tetraodon n	1072	58	11.6	288	2	Q9XYV5_TOXCA	Q9xyv5 toxocara ca
1000	58.5	11.7	671	2	Q6BET7_CABEL	Q6bet7 caenorhabdi	1073	58	11.6	288	2	Q3HJX3_TRIER	Q3hjx3 trichodesmi
1001	58.5	11.7	675	2	Q4RYT9_TETNG	Q4ryt9 tetraodon n	1074	58	11.6	296	2	Q2QJC9_9CYAN	Q2qjc9 symploca at
1002	58.5	11.7	678	2	Q6NX58_HUMAN	Q6nx58 homo sapien	1075	58	11.6	296	2	Q2QJD1_9CYAN	Q2qjd1 symploca at
1003	58.5	11.7	684	2	Q9BIM7_TOXGO	Q9bim7 toxoplasma	1076	58	11.6	299	2	Q9FRP5_ORYSA	Q9frp5 oryza sativ
1004	58.5	11.7	701	1	TRE_XENLA	P20233 xenopus lae	1077	58	11.6	299	2	Q7XBT0_ORYSA	Q7xbt0 oryza sativ
1005	58.5	11.7	712	2	Q8IGX5_DROME	Q8igx5 drosophila	1078	58	11.6	305	2	Q7Z7Y8_9AGAR	Q7z7y8 mallocybe s
1006	58.5	11.7	712	2	Q9VG15_DROME	Q9vg15 drosophila	1079	58	11.6	305	2	Q6D150_BRARE	Q6d150 brachydanio
1007	58.5	11.7	721	2	Q3JG10_BURP1	Q3jg10 burkholderi	1080	58	11.6	318	2	Q90Z81_BRARE	Q90z81 brachydanio
1008	58.5	11.7	721	2	Q91902_XENLA	Q91902 xenopus lae	1081	58	11.6	331	2	Q6R7N8_9AGAR	Q6r7n8 phaecoallyb
1009	58.5	11.7	731	2	Q47254_COLP3	Q47254 colwellia p	1082	58	11.6	332	2	Q7Z816_9AGAR	Q7z816 inocybe gla
1010	58.5	11.7	762	2	Q4V6V0_DROME	Q4v6v0 drosophila	1083	58	11.6	334	2	Q7Z727_9AGAR	Q7z727 inocybe que
1011	58.5	11.7	764	2	Q215S0_GLOIN	Q215s0 glomus intr	1084	58	11.6	334	2	Q7Z818_9AGAR	Q7z818 inocybe flo
1012	58.5	11.7	787	1	ADA32_HUMAN	Q8c27 homo sapien	1085	58	11.6	334	2	Q7Z856_9AGAR	Q7z856 inocybe cal
1013	58.5	11.7	813	2	Q9ULN3_HUMAN	Q9uln3 homo sapien	1086	58	11.6	335	2	Q7Z856_9AGAR	Q7z856 inocybe cer
1014	58.5	11.7	841	2	Q3KQ33_HUMAN	Q3kq33 homo sapien	1087	58	11.6	342	2	Q68FN3_MOUSE	Q68fn3 mus musculu
1015	58.5	11.7	847	2	Q6R6C8_LISIV	Q6r6c8 listeria iv	1088	58	11.6	357	2	Q2HX77_9AGAR	Q2hx77 tricholoma
1016	58.5	11.7	882	2	Q5EWZ4_TRITU	Q5ewz4 triticum tu	1089	58	11.6	357	2	Q2HX22_9AGAR	Q2hx22 asterophora
1017	58.5	11.7	894	2	Q17429_CABEL	Q17429 caenorhabdi	1090	58	11.6	358	2	Q2HXY9_9AGAR	Q2hxy9 lyophyllum
1018	58.5	11.7	895	2	Q91X23_ARATH	Q91x23 arabidopsis	1091	58	11.6	358	2	Q2HX20_9AGAR	Q2hx20 calocybe ca
1019	58.5	11.7	898	2	Q8MQG2_CABEL	Q8mqg2 caenorhabdi	1092	58	11.6	358	2	Q2HX21_9AGAR	Q2hx21 tetraodon n
1020	58.5	11.7	901	2	Q6AV10_ORYSA	Q6av10 oryza sativ	1093	58	11.6	367	2	Q4RUJ5_TETNG	Q4ruj5 brachydanio
1021	58.5	11.7	907	2	Q5EWZ0_WHEAT	Q5ewz0 triticum ae	1094	58	11.6	415	2	Q90ZE3_BRARE	Q90ze3 brachydanio
1022	58.5	11.7	907	2	Q947C9_TRIMO	Q947c9 triticum mo	1095	58	11.6	418	2	Q6NP02_DROME	Q6np02 drosophila
1023	58.5	11.7	925	2	Q44191_CABEL	Q44191 caenorhabdi	1096	58	11.6	422	2	Q39ZC0_GEOMG	Q39zc0 geobacter m
1024	58.5	11.7	925	2	Q9U4E4_CABEL	Q9u4e4 caenorhabdi	1097	58	11.6	432	2	Q9NPM2_HUMAN	Q9npm2 homo sapien
1025	58.5	11.7	960	2	Q8WM07_CABEL	Q8wm07 caenorhabdi	1098	58	11.6	448	2	Q8PJ71_XANAC	Q8pj71 xanthomonas
1026	58.5	11.7	962	1	KR73_FCHV1	Q00094 ictalurid h	1099	58	11.6	461	2	Q3BRR0_XANAC	Q3br0 xanthomonas
1027	58.5	11.7	974	2	Q6DI14_XENTR	Q6di14 xenopus tro	1100	58	11.6	465	2	Q2KGU4_MAGGR	Q2kgu4 magnaporthe
1028	58.5	11.7	1033	2	Q7QK54_ANOGA	Q7qk54 anopheles g	1101	58	11.6	479	2	Q6MGL5_BDEBA	Q6mgl5 bdellovibri
1029	58.5	11.7	1061	2	Q478L6_TETNG	Q4t8l6 tetraodon n	1102	58	11.6	491	2	Q2K017_RHIET	Q2k017 rhizobium e
1030	58.5	11.7	1238	1	JAG2_HUMAN	Q9y219 homo sapien	1103	58	11.6	504	2	Q7QJ41_ANOGA	Q7qj41 anopheles g
1031	58.5	11.7	1592	1	SORL_CHICK	Q98930 g sortilin-	1104	58	11.6	515	2	Q6QF59_HETAN	Q6qf59 heterobasid
1032	58.5	11.7	1712	1	LTBP1_RAT	Q09918 rattus norv	1105	58	11.6	525	2	Q24433_ARATH	Q24433 arabidopsis
1033	58.5	11.7	2019	2	Q68FE0_MOUSE	Q68fe0 mus musculu	1106	58	11.6	551	2	Q99677_CABEL	Q99677 caenorhabdi
1034	58.5	11.7	2146	1	CRB_DROME	P10040 drosophila	1107	58	11.6	569	2	Q7PMF9_ANOGA	Q7pmf9 anopheles g
1035	58.5	11.7	2146	2	Q4T7A2_TETNG	Q4t7a2 tetraodon n	1108	58	11.6	576	2	Q9Y3V7_HUMAN	Q9y3v7 homo sapien
1036	58.5	11.7	2189	2	Q95105_EIMTE	Q9bi05 einertia ten	1109	58	11.6	578	2	Q8PLD7_XANAC	Q8pld7 xanthomonas
1037	58.5	11.7	2414	2	Q6DFL6_XENLA	Q6df16 xenopus lae	1110	58	11.6	608	2	Q4P9C1_USTMA	Q4p9c1 ustilago ma
1038	58.5	11.7	2427	2	Q8MQ36_CABEL	Q8mq36 caenorhabdi	1111	58	11.6	608	2	Q627A0_CABER	Q627a0 caenorhabdi
1039	58.5	11.7	2764	2	Q9WTS5_MOUSE	Q9wt55 mus musculu	1112	58	11.6	628	2	Q9VER6_DROME	Q9ver6 drosophila
1040	58.5	11.7	2764	2	Q5NBW8_MOUSE	Q5nbw8 mus musculu	1113	58	11.6	639	2	Q5RL27_9AGAR	Q5rl27 mallocybe d
1041	58.5	11.7	2774	2	Q4Z799_PLABE	Q4z799 plasmodium	1114	58	11.6	645	2	Q5S3M1_PLEOS	Q5s3m1 pleutetus o
1042	58.5	11.7	3004	2	Q24550_DROME	Q24550 drosophila	1115	58	11.6	646	2	Q5S3M0_9AGAR	Q5s3m0 pluteus rom
1043	58.5	11.7	3004	2	Q9VYN8_DROME	Q9vyn8 drosophila	1116	58	11.6	654	2	Q5U7W6_9AGAR	Q5u7w6 ampullocit
1044	58.5	11.7	3019	2	Q4RU98_TETNG	Q4ru98 tetraodon n	1117	58	11.6	669	2	Q5S316_9AGAR	Q5s316 oudemansst
1045	58.5	11.7	3087	2	Q8WRD2_PLABE	Q8wrd2 plasmodium	1118	58	11.6	671	2	Q5S2B9_9APHY	Q5s2b9 hyphoderm
1046	58.5	11.7	3222	2	Q6V017_HUMAN	Q6v017 homo sapien	1119	58	11.6	677	2	Q5S319_RAMAR	Q5s319 ramaria rub
1047	58.5	11.7	3589	2	Q7PPF9_ANOGA	Q7ppf9 anopheles g	1120	58	11.6	686	2	Q5RM01_9AGAR	Q5rm01 hygrocybe c
1048	58.5	11.7	4391	1	PGBM_HUMAN	P98160 homo sapien	1121	58	11.6	687	2	Q7Z8B0_9AGAR	Q7z8b0 phaeonaraam
1049	58.5	11.7	4391	1	PGBM_HUMAN	Q9vu27 homo sapien	1122	58	11.6	691	2	Q5S3M8_PLAVE	Q5s3m8 flammulina
1050	58.5	11.7	4981	2	Q2PZL6_MOUSE	Q2pzl6 mus musculu	1123	58	11.6	693	2	Q5U7W1_9AGAR	Q5u7w1 clitocybe s
1051	58.5	11.7	5255	1	Q2PC93_CHICK	Q2pc93 gallus gall	1124	58	11.6	694	2	Q5U7W3_9HOMO	Q5u7w3 clavaria zo
1052	58	11.6	46	1	ENAI_HORSE	P80930 equus cabal	1125	58	11.6	694	2	Q5U7W7_9AGAR	Q5u7w7 amanita bru
1053	58	11.6	98	2	Q2J8I9_9ACTO	Q2j8i9 frankia ep.	1126	58	11.6				

1127	58	11.6	694	2	Q5TWT0_ANOGA	Q5TWT0 anopheles g	1200	58	11.6	2660	2	Q7QL19_ANOGA	Q7ql19 anopheles g
1128	58	11.6	698	2	Q5US90_9APHY	Q5us90 athelia bom	1201	58	11.6	2812	1	ZAN_HUMAN	Q9v493 homo sapien
1129	58	11.6	699	2	Q5UTW9_COPCM	Q5utw9 coprinus co	1202	58	11.6	2824	2	Q9W7R3_BRARE	Q9w7r3 brachydanio
1130	58	11.6	700	2	Q5S2C1_9AGAR	Q5s2c1 collybia tu	1203	58	11.6	2906	1	Q9WUH9_RAT	Q9wuh9 rattus norv
1131	58	11.6	705	2	Q5S3M3_9AGAR	Q5s3m3 marasmus a	1204	58	11.6	2907	1	Q9N2_MOUSE	Q9n2 mus musculu
1132	58	11.6	721	2	Q5S2C0_9AGAR	Q5s2c0 rhodocollyb	1205	58	11.6	3301	1	CELR3_MOUSE	Q9tzi0 mus musculu
1133	58	11.6	728	1	FBLN1_CAEEL	Q77r69 caenorhabdi	1206	58	11.6	3452	2	Q4D8D4_TRYCR	Q4d8d4 trypanosoma
1134	58	11.6	728	2	Q515Q9_CAEEL	Q515q9 caenorhabdi	1207	58	11.6	4056	2	Q2PDM3_DROME	Q2pdm3 drosophila
1135	58	11.6	741	2	Q33HS7_METHU	Q33hs7 methanospir	1208	58	11.6	4573	2	Q5TMP0_ANOGA	Q5tmp0 anopheles g
1136	58	11.6	741	2	Q4DJ56_TRYCR	Q4dj56 trypanosoma	1209	58	11.6	4856	2	Q61EJ2_CAEBR	Q61ej2 caenorhabdi
1137	58	11.6	750	2	Q4RTV7_TETNG	Q4rtv7 tetraodon n	1210	58	11.6	4856	2	Q7PZB3_ANOGA	Q7pzb3 anopheles g
1138	58	11.6	754	2	Q5TNY8_ANOGA	Q5tny8 anopheles g	1211	57.5	11.5	68	1	TTF17_HADVE	P81803 nadronyche
1139	58	11.6	755	1	COMP_RAT	P35444 rattus norv	1212	57.5	11.5	98	1	KRA32_HUMAN	Q9pyr7 homo sapien
1140	58	11.6	770	2	Q473V7_9AGAR	Q473v7 chondroster	1213	57.5	11.5	101	2	Q9XGJ3_GERHY	Q9xgj3 gerbera hyb
1141	58	11.6	801	2	Q4D260_TRYCR	Q4d260 trypanosoma	1214	57.5	11.5	110	1	LCE2B_HUMAN	Q14633 homo sapien
1142	58	11.6	820	2	Q9FEK8_9ARATH	Q9ffk8 arabidopsis	1215	57.5	11.5	110	2	Q5TA80_HUMAN	Q5ta80 homo sapien
1143	58	11.6	848	2	Q873T2_9AGAR	Q873t2 heningsomy	1216	57.5	11.5	114	2	Q4XQB6_PLACH	Q4xqb6 plasmodium
1144	58	11.6	849	2	Q873U3_9HOMO	Q873u3 lycoperdon	1217	57.5	11.5	123	2	Q83078_9VIRU	Q83078 lychnis rin
1145	58	11.6	863	2	Q5S3M4_9HOMO	Q5s3m4 hygrophorop	1218	57.5	11.5	132	2	Q4RD47_TETNG	Q4rd47 tetraodon n
1146	58	11.6	869	2	Q42126_XENLA	Q42126 xenopus lae	1219	57.5	11.5	139	2	Q61L01_DROME	Q61l01 drosophila
1147	58	11.6	869	2	Q6NS01_XENLA	Q6ns01 xenopus lae	1220	57.5	11.5	157	2	Q5ISQ5_MACFA	Q5isq5 macaca fasc
1148	58	11.6	878	2	Q6QJD4_9AGAR	Q6qjd4 crotinarius	1221	57.5	11.5	170	2	Q52VK0_CIOIN	Q52vk0 ciona intes
1149	58	11.6	884	2	Q5U7W5_ARMME	Q5u7w5 armillaria	1222	57.5	11.5	176	2	Q59K89_CANAL	Q59k89 candida alb
1150	58	11.6	889	2	Q5S3M2_9APHY	Q5s3m2 phylloctopi	1223	57.5	11.5	176	2	Q4ZNF7_PSEU2	Q4znf7 pseudomonas
1151	58	11.6	891	2	Q5SHG9_9ARATH	Q5shg9 arabidopsis	1224	57.5	11.5	205	2	Q96LP4_HUMAN	Q96lp4 homo sapien
1152	58	11.6	892	2	Q5RGJ2_9HOMO	Q5rgj2 cotyldia s	1225	57.5	11.5	217	2	Q8NEE7_HUMAN	Q8nee7 homo sapien
1153	58	11.6	898	2	Q5RM00_9HOMO	Q5rm00 fomitiporia	1226	57.5	11.5	222	2	Q7XZ47_GRIJA	Q7xz47 griffithsia
1154	58	11.6	898	2	Q9UF24_HUMAN	Q9uf24 homo sapien	1227	57.5	11.5	226	2	Q8BYT9_MOUSE	Q8byt9 mus musculu
1155	58	11.6	898	2	Q5S2C2_9HOMO	Q5s2c2 boletellus	1228	57.5	11.5	237	1	UTL1_9ARATH	Q8w92 arabidopsis
1156	58	11.6	908	2	Q5S3L8_9HOMO	Q5s3l8 streptolomyc	1229	57.5	11.5	257	2	Q6NW92_BRARE	Q6nw92 brachydanio
1157	58	11.6	913	2	Q8AY18_RANES	Q8ay18 rana esculi	1230	57.5	11.5	269	2	Q6AL36_DESPS	Q6al36 desulfotale
1158	58	11.6	914	2	Q9UVA3_AGABI	Q9uva3 agaricus bi	1231	57.5	11.5	275	2	Q7M9D7_WOLSU	Q7m9d7 wolinnella s
1159	58	11.6	917	2	Q6RY19_9AMAPH	Q6ry19 amanita pha	1232	57.5	11.5	298	2	Q4CR12_TRYCR	Q4cr12 trypanosoma
1160	58	11.6	949	2	Q3V7A7_9PRIM	Q3v7a7 macaca fusc	1233	57.5	11.5	298	2	Q5PLX1_AZOSE	Q5plx1 azoarcus sp
1161	58	11.6	980	1	TSP4_RAT	P49744 rattus norv	1234	57.5	11.5	300	2	Q4RKB9_TETNG	Q4rkb9 tetraodon n
1162	58	11.6	1015	2	Q3UGT7_MOUSE	Q3ugt7 mus musculu	1235	57.5	11.5	308	2	Q5YUP0_NOCFA	Q5yup0 nocardia fa
1163	58	11.6	1026	2	Q8SWY0_DROME	Q8swy0 drosophila	1236	57.5	11.5	319	2	Q9V6U6_DROME	Q9v6u6 drosophila
1164	58	11.6	1121	2	Q966P9_CAEEL	Q966p9 caenorhabdi	1237	57.5	11.5	322	2	Q72761_COWPX	Q72761 cowpx viru
1165	58	11.6	1123	2	Q6V7X2_OROMI	Q6v7x2 orobanche m	1238	57.5	11.5	367	2	Q9ZVY4_9ARATH	Q9zvy4 arabidopsis
1166	58	11.6	1148	2	Q966Q0_CAEEL	Q966q0 caenorhabdi	1239	57.5	11.5	368	2	Q3NBU8_9PROT	Q3nbu8 nitrosomona
1167	58	11.6	1184	1	FBLN2_HUMAN	P98095 homo sapien	1240	57.5	11.5	368	2	Q3RUPA_RALME	Q3rup4 raistonia m
1168	58	11.6	1184	2	Q86V58_HUMAN	Q86v58 homo sapien	1241	57.5	11.5	368	2	Q46U28_RALEJ	Q46u28 raistonia e
1169	58	11.6	1200	2	Q8VD07_MOUSE	P01132 mus musculu	1242	57.5	11.5	371	2	Q5Z0J9_NOCFA	Q5z0j9 nocardia fa
1170	58	11.6	1217	1	EGF_MOUSE	Q569w5 mus musculu	1243	57.5	11.5	373	2	Q4UEJ5_THEAN	Q4uej5 theileria a
1171	58	11.6	1217	2	Q569W5_MOUSE	Q569w5 mus musculu	1244	57.5	11.5	383	2	Q6XVW4_CRYNV	Q6xvw4 cryptococcu
1172	58	11.6	1231	2	Q81U10_HUMAN	Q81u10 homo sapien	1245	57.5	11.5	434	2	Q5HRJ3_STAEQ	Q5hrj3 staphylococ
1173	58	11.6	1231	2	Q81U11_HUMAN	Q81u11 homo sapien	1246	57.5	11.5	434	2	Q8CTS4_STAES	Q8cts4 staphylococ
1174	58	11.6	1249	1	APAF_RAT	Q9epv5 rattus norv	1247	57.5	11.5	450	2	Q869J7_9MYRI	Q869j7 glomeria ma
1175	58	11.6	1275	2	Q61PE4_CAEBR	Q61pe4 caenorhabdi	1248	57.5	11.5	458	2	Q8Z7P8_SALTI	Q8z7p8 salmonella
1176	58	11.6	1296	2	Q6AWM6_DROME	Q6awm6 drosophila	1249	57.5	11.5	472	1	FSCN27_9AGAR	Q68st7 pleurotus d
1177	58	11.6	1311	2	Q4RUS3_TETNG	Q4rus3 tetraodon n	1250	57.5	11.5	492	1	FSCN27_9AGAR	Q68st7 pleurotus d
1178	58	11.6	1420	2	Q45YJ8_SCHMD	Q45yj8 schmidtea m	1251	57.5	11.5	499	2	Q3H183_9ACTO	Q3h183 nocardioid
1179	58	11.6	1428	2	Q43441_HALURU	Q43441 halictis ru	1252	57.5	11.5	507	2	Q56BV3_9CAUD	Q56bv3 enterobacte
1180	58	11.6	1469	2	Q6PD04_MOUSE	Q6pd04 mus musculu	1253	57.5	11.5	508	2	Q6DHG1_BRARE	Q6dhg1 brachydanio
1181	58	11.6	1477	2	Q4H3A4_CIOIN	Q4h3a4 ciona intes	1254	57.5	11.5	527	2	Q4SRF3_TETNG	Q4srf3 tetraodon n
1182	58	11.6	1483	2	Q4CNR3_TRYCR	Q4cnr3 trypanosoma	1255	57.5	11.5	542	2	Q80T13_MOUSE	Q80t13 mus musculu
1183	58	11.6	1517	2	Q6KAS1_MOUSE	Q6kas1 mus musculu	1256	57.5	11.5	544	2	Q8VCG2_MOUSE	Q8vcg2 mus musculu
1184	58	11.6	1517	2	Q3UPH7_MOUSE	Q3uph7 mus musculu	1257	57.5	11.5	581	2	Q8NAV8_HUMAN	Q8nav8 homo sapien
1185	58	11.6	1673	2	Q4RSP7_TETNG	Q4rsp7 tetraodon n	1258	57.5	11.5	586	2	Q4RJE7_TETNG	Q4rje7 tetraodon n
1186	58	11.6	1686	2	Q6P7J9_HUMAN	Q6p7j9 homo sapien	1259	57.5	11.5	591	2	Q6LBN5_HUMAN	Q6lbn5 homo sapien
1187	58	11.6	1790	1	LAMB1_DROME	P11046 drosophila	1260	57.5	11.5	594	1	CHDH_HUMAN	Q8ne62 homo sapien
1188	58	11.6	1805	2	Q7QVW0_GIALA	Q7qvwo giardia lam	1261	57.5	11.5	601	2	Q656X3_ORYSA	Q656x3 oryza sativ
1189	58	11.6	2030	2	Q2WBY6_PLADU	Q2wby6 platynereis	1262	57.5	11.5	604	1	ENR1_HUMAN	Q14264 h herv-r 7q
1190	58	11.6	2061	2	Q4SRM9_TETNG	Q4srm9 tetraodon n	1263	57.5	11.5	604	2	Q4W2L3_PANTR	Q4w2l3 pan troglod
1191	58	11.6	2192	2	Q804R1_BRARE	Q804r1 brachydanio	1264	57.5	11.5	625	2	Q2Q863_ORYSA	Q2qe63 oryza sativ
1192	58	11.6	2225	2	Q571J3_MOUSE	Q571j3 mus musculu	1265	57.5	11.5	642	2	Q8MPM6_GIALA	Q8mpm6 giardia lam
1193	58	11.6	2277	2	Q4CRW2_TRYCR	Q4crw2 trypanosoma	1266	57.5	11.5	644	2	Q5NKM3_CRYNV	Q5nkm3 cryptococcu
1194	58	11.6	2506	2	Q9WJD2_9VIRU	Q9wj22 venezuelan	1267	57.5	11.5	667	2	Q7RVRO_NEUCR	Q7rvro neurospora
1195	58	11.6	2516	2	Q7TQ52_MOUSE	Q7tq52 mus musculu	1268	57.5	11.5	680	2	Q9QWL5_9MURI	Q9qwl5 mus sp bet
1196	58	11.6	2526	2	Q7TQ51_MOUSE	Q7tq51 mus musculu	1269	57.5	11.5	689	2	Q2PFZ7_MACFA	Q2pfz7 macaca fasc
1197	58	11.6	2531	1	NOTC1_MOUSE	Q01705 mus musculu	1270	57.5	11.5	710	2	Q14407_NEUCR	Q14407 neurospora
1198	58	11.6	2531	2	Q7TQ50_MOUSE	Q7tq50 mus musculu	1271	57.5	11.5	719	2	Q5XG79_HUMAN	Q5xg79 homo sapien
1199	58	11.6	2531	2	Q8K428_MOUSE	Q8k428 mus musculu	1272	57.5	11.5	719	2	Q459K7_TETNG	Q459k7 tetraodon n

1273	57.5	11.5	745	2	Q6UXK2_HUMAN	Q6uxk2 homo sapien	1346	57	11.4	250	2	Q3U4X0_MOUSE	Q3u4x0 m 2 days ne
1274	57.5	11.5	763	2	Q4VB88_HUMAN	Q4vb88 homo sapien	1347	57	11.4	251	2	Q95Y21_CAEBL	Q95y21 caenorhabdi
1275	57.5	11.5	763	2	Q4VB99_HUMAN	Q4vb99 homo sapien	1348	57	11.4	252	2	Q6L2P3_PICTO	Q6l2p3 picrophilus
1276	57.5	11.5	773	2	Q3VA95_9SPHN	Q3va95 sphingopyxi	1349	57	11.4	263	2	Q3I347_ONCMY	Q3i347 oncorhynchus
1277	57.5	11.5	778	2	Q91BG4_XENLA	Q91bg4 xenopus lae	1350	57	11.4	265	2	Q4V9H3_BRARE	Q4v9h3 brachydanio
1278	57.5	11.5	785	2	Q9P263_HUMAN	Q9p263 homo sapien	1351	57	11.4	266	2	Q9R1K1_RAT	Q9r1k1 rattus norv
1279	57.5	11.5	787	1	ITB3_MOUSE	O54890 mus musculus	1352	57	11.4	281	2	Q4CTN3_TRYCR	Q4ctn3 trypanosoma
1280	57.5	11.5	787	2	Q3TZC6_MOUSE	Q3tzc6 mus musculus	1353	57	11.4	291	2	Q9UDM2_HUMAN	Q9udm2 homo sapien
1281	57.5	11.5	810	1	NELL1_HUMAN	Q92832 mus musculus	1354	57	11.4	299	2	Q8BX64_MOUSE	Q8bx64 mus musculus
1282	57.5	11.5	810	1	NELL1_RAT	Q62919 rattus norv	1355	57	11.4	320	2	Q6IQ75_BRARE	Q6iq75 brachydanio
1283	57.5	11.5	810	2	Q4VB90_HUMAN	Q4vb90 homo sapien	1356	57	11.4	327	2	Q86J05_DICDI	Q86j05 dictyosteli
1284	57.5	11.5	810	2	Q6NSY8_HUMAN	Q6nsy8 homo sapien	1357	57	11.4	328	2	Q76B99_XENLA	Q76b99 xenopus lae
1285	57.5	11.5	810	2	Q2VMQ2_MOUSE	Q2vmq2 mus musculus	1358	57	11.4	344	2	Q9VY49_DROME	Q9vy49 drosophila
1286	57.5	11.5	817	2	Q4E1D8_TRYCR	Q4e1d9 trypanosoma	1359	57	11.4	360	2	Q5RLJ3_PIG	Q5rlj3 sus scrofa
1287	57.5	11.5	830	2	Q59HB9_HUMAN	Q59hb9 homo sapien	1360	57	11.4	374	2	Q9VVK0_DROME	Q9vvk0 drosophila
1288	57.5	11.5	846	2	Q8CIL3_MOUSE	Q8cil3 mus musculus	1361	57	11.4	394	2	Q4SYL1_TETNG	Q4syll1 tetraodon n
1289	57.5	11.5	852	2	Q5CZB3_HUMAN	Q5czb3 homo sapien	1362	57	11.4	402	2	Q2UIE8_ASPOR	Q2uie8 aspergillus
1290	57.5	11.5	870	2	O02660_BOVIN	O02660 bos taurus	1363	57	11.4	410	2	Q3G7I9_9DEL1	Q3g7i9 pelobacter
1291	57.5	11.5	872	2	Q62A49_ORYSA	Q62a49 oryza sativ	1364	57	11.4	414	2	Q9XVJ1_CAEBL	Q9xvj1 caenorhabdi
1292	57.5	11.5	874	2	Q73VQ0_MYCPA	Q73vq0 mycobacteri	1365	57	11.4	421	2	Q86RJ7_CAEBL	Q86rj7 caenorhabdi
1293	57.5	11.5	880	2	Q8NAU9_HUMAN	Q8na9 homo sapien	1366	57	11.4	423	2	Q4WX56_ASPFU	Q4wx56 aspergillus
1294	57.5	11.5	927	2	Q5DLW0_9VIRU	Q5dlw0 sea perch i	1367	57	11.4	432	2	Q75G89_ORYSA	Q75g89 oryza sativ
1295	57.5	11.5	942	2	Q7QYW9_GIALA	Q7qyw9 giardia lam	1368	57	11.4	454	2	Q8TB42_HUMAN	Q8tb42 homo sapien
1296	57.5	11.5	976	2	Q90ZN9_BRARE	Q90zn9 brachydanio	1369	57	11.4	468	2	Q7L1K8_HUMAN	Q7l1k8 homo sapien
1297	57.5	11.5	992	2	Q86UZ9_HUMAN	Q86uz9 homo sapien	1370	57	11.4	470	2	Q9NSH4_HUMAN	Q9nsh4 homo sapien
1298	57.5	11.5	993	2	Q81X30_HUMAN	Q81x30 homo sapien	1371	57	11.4	474	2	Q95LW7_MACPA	Q95lw7 macaca faec
1299	57.5	11.5	1055	2	Q4CMG1_TRYCR	Q4cmg1 trypanosoma	1372	57	11.4	475	2	Q6KAQ6_MOUSE	Q6kaq6 mus musculus
1300	57.5	11.5	1107	2	Q4CML1_TRYCR	Q4cml1 trypanosoma	1373	57	11.4	491	2	Q4T2B4_TETNG	Q4t2b4 tetraodon n
1301	57.5	11.5	1131	2	Q75DJ5_ASHGO	Q75dj5 ashbya goss	1374	57	11.4	502	2	Q6IPC7_HUMAN	Q6ipc7 homo sapien
1302	57.5	11.5	1234	2	Q91CH6_9ALPH	Q91ch6 macropodid	1375	57	11.4	514	2	Q9LD86_ARATH	Q9ld86 arabidopsis
1303	57.5	11.5	1247	1	JAC2_MOUSE	Q9gye5 mus musculus	1376	57	11.4	516	2	Q60SB4_CAEBR	Q60se4 caenorhabdi
1304	57.5	11.5	1280	2	Q6QHS1_LYTTA	Q6qhs1 lytechinus	1377	57	11.4	543	2	Q4P8Y4_USTMA	Q4p8y4 ustilago ma
1305	57.5	11.5	1355	2	Q2XPT7_CANFA	Q2xpt7 canis famli	1378	57	11.4	558	2	Q32SR8_BRARE	Q32sk8 brachydanio
1306	57.5	11.5	1356	1	VGPR2_HUMAN	Q35968 homo sapien	1379	57	11.4	560	2	Q314M8_DESDF	Q314m8 desulfovibr
1307	57.5	11.5	1451	2	Q59EB0_HUMAN	Q59eb0 homo sapien	1380	57	11.4	576	2	Q6YID6_PENMO	Q6yid6 penaeus mon
1308	57.5	11.5	1461	2	Q9JLP3_MOUSE	Q9jlp3 mus musculus	1381	57	11.4	610	2	Q9YI20_AKGHP	Q9yi20 agkistrodon
1309	57.5	11.5	1504	1	SLIT_DROME	P24014 drosophila	1382	57	11.4	612	1	MCR_XENLA	Q91573 xenopus lae
1310	57.5	11.5	1569	2	Q6W4X9_HUMAN	Q6w4x9 homo sapien	1383	57	11.4	623	2	Q8JGG1_9VIRU	Q8jgg1 adeno-associ
1311	57.5	11.5	1594	2	Q6PAL7_MOUSE	Q6pal7 mus musculus	1384	57	11.4	643	2	Q7PULO_ANOGA	Q7pulo anopheles g
1312	57.5	11.5	1595	2	Q5USN7_MOUSE	Q5usn7 mus musculus	1385	57	11.4	655	1	TNR21_HUMAN	Q75509 homo sapien
1313	57.5	11.5	1603	2	Q5TGJ3_HUMAN	Q5tgj3 homo sapien	1386	57	11.4	656	2	Q86PQ8_CRYPV	Q86pq8 cryptospori
1314	57.5	11.5	1619	2	Q7QJR9_ANOGA	Q7qjr9 anopheles g	1387	57	11.4	657	2	Q564H7_HUMAN	Q564h7 homo sapien
1315	57.5	11.5	1619	2	Q3UH23_MOUSE	Q3uh23 mus musculus	1388	57	11.4	669	2	Q4SC13_TETNG	Q4sc13 tetraodon n
1316	57.5	11.5	1620	1	DNWT1_MOUSE	P13864 mus musculus	1389	57	11.4	704	2	Q4T8B6_TETNG	Q4t8be tetraodon n
1317	57.5	11.5	1623	2	Q9J3U7_ANOGA	Q9j3u7 anopheles g	1390	57	11.4	705	1	CTL2_CAVPO	Q810f1 cavia porce
1318	57.5	11.5	1627	2	Q7TBJ0_MOUSE	Q7tj0 mus musculus	1391	57	11.4	706	2	Q7S578_NEUCR	Q7s578 neurospora
1319	57.5	11.5	1783	2	Q5XHI6_XENLA	Q5xhi6 xenopus lae	1392	57	11.4	710	2	Q5VX00_HUMAN	Q5vx00 homo sapien
1320	57.5	11.5	1913	2	Q5SVA2_HUMAN	Q5sva2 homo sapien	1393	57	11.4	710	2	Q9H6A2_HUMAN	Q9h6a2 homo sapien
1321	57.5	11.5	2045	1	AGRN_HUMAN	O00468 homo sapien	1394	57	11.4	721	2	Q2VPC6_HUMAN	Q2vpc6 homo sapien
1322	57.5	11.5	2045	2	Q6PFI1_HUMAN	Q6ofel1 homo sapien	1395	57	11.4	722	1	ADA21_HUMAN	Q9ukj8 homo sapien
1323	57.5	11.5	2223	2	Q61T23_CAEBR	Q61t23 caenorhabdi	1396	57	11.4	722	2	Q32MR0_HUMAN	Q32mr0 homo sapien
1324	57.5	11.5	2352	2	Q61240_HALRO	Q61240 halocynthia	1397	57	11.4	737	2	Q81YT0_HUMAN	Q81yt0 homo sapien
1325	57.5	11.5	2871	1	FBN1_HUMAN	P35555 homo sapien	1398	57	11.4	737	2	Q8NFT8_HUMAN	Q8nft8 homo sapien
1326	57.5	11.5	3475	2	Q4DF73_TRYCR	Q4df73 trypanosoma	1399	57	11.4	749	2	Q7Z391_HUMAN	Q7z391 mus musculus
1327	57.5	11.5	3482	2	Q4DDN1_TRYCR	Q4ddn1 trypanosoma	1400	57	11.4	757	2	Q3TD36_MOUSE	Q3td36 mus musculus
1328	57.5	11.5	4071	2	Q6KDZ1_CHICK	Q6kdz1 gallus gall	1401	57	11.4	757	2	Q2KFT3_WAGR	Q2kft3 magnaporthe
1329	57.5	11.5	5193	2	Q2Q147_MOUSE	Q2q147 mus musculus	1402	57	11.4	760	2	Q7Q7D9_ANOGA	Q7q7d9 anopheles g
1330	57	11.4	92	1	LCM_LOCM1	P80060 locusta mig	1403	57	11.4	777	2	Q4T9G3_TETNG	Q4t9g3 tetraodon n
1331	57	11.4	147	2	Q90ZC8_BRARE	Q90zch8 brachydanio	1404	57	11.4	780	2	Q6DJD9_XENLA	Q6djd9 xenopus lae
1332	57	11.4	147	2	Q90ZC8_BRARE	Q90zch8 brachydanio	1405	57	11.4	805	2	Q5YF64_9VIRU	Q5yf64 rock bream
1333	57	11.4	153	2	O11434_9ADEN	O11434 duck adenov	1406	57	11.4	809	2	Q9U3W7_DROME	Q9u3w7 drosophila
1334	57	11.4	172	2	Q95XJ5_CAEBL	Q95xj8 caenorhabdi	1407	57	11.4	830	2	Q4RTY8_TETNG	Q4rty8 tetraodon n
1335	57	11.4	173	2	Q62217_CAEBR	Q62217 caenorhabdi	1408	57	11.4	860	2	Q8WYI1_HUMAN	Q8wyi1 homo sapien
1336	57	11.4	175	2	Q9PD10_XYLFA	Q9pd10 xyella fas	1409	57	11.4	915	2	Q4RS15_TETNG	Q4rs15 tetraodon n
1337	57	11.4	191	1	WAP_MACEU	Q9n018 macropus eu	1410	57	11.4	917	1	TBCD2_HUMAN	Q9byx2 homo sapien
1338	57	11.4	195	2	Q4P521_USTMA	Q4p521 ustilago ma	1411	57	11.4	917	2	Q5VWZ8_HUMAN	Q5vwz8 homo sapien
1339	57	11.4	195	2	Q9NDT4_BALAM	Q9ndt4 balanus amp	1412	57	11.4	921	2	Q969A3_BRARE	Q969a3 branchiosteo
1340	57	11.4	212	1	AGI_HORVU	P15312 hordeum vul	1413	57	11.4	946	2	Q4DUD9_TRYCR	Q4dud9 trypanosoma
1341	57	11.4	214	2	Q4S2C4_TETNG	Q4s2c4 tetraodon n	1414	57	11.4	1012	2	Q6KAR4_MOUSE	Q6kar4 mus musculus
1342	57	11.4	217	2	Q7QDE4_ANOGA	Q7qde4 anopheles g	1415	57	11.4	1014	2	Q4KSD1_9VIRU	Q4ksd1 orange-spot
1343	57	11.4	219	2	Q8SC14_9VIRU	Q8sc14 propionibac	1416	57	11.4	1042	2	Q8B4N0_9VIRU	Q8b4n0 rock bream
1344	57	11.4	231	2	Q5MD86_MACMU	Q5md86 macaca mula	1417	57	11.4	1044	2	Q6SXU0_BAMOL	Q6sxu0 bambusa old
1345	57	11.4	250	1	TNR7_MOUSE	P41272 mus musculus	1418	57	11.4	1074	2		

1419	57	11.4	1103	2	Q6MZF4_HUMAN	Q6mf4 homo sapien	1492	56.5	11.3	353	2	Q7LD55_HUMAN	Q7ld55 homo sapien
1420	57	11.4	1152	2	Q6PHP3_MOUSE	Q6php3 mus musculus	1493	56.5	11.3	353	2	Q96GX4_HUMAN	Q96gx4 homo sapien
1421	57	11.4	1210	1	EGF_FELCA	Q95nd4 felis silve	1494	56.5	11.3	366	2	Q35A74_9BRAD	Q35a74 bradyrhizob
1422	57	11.4	1218	2	Q4SRP3_TETNG	Q4srp3 tetraodon n	1495	56.5	11.3	369	2	Q8VI97_MOUSE	Q8vi97 mus musculus
1423	57	11.4	1230	2	Q4RPT6_USTMA	Q4rpt6 ustilago ma	1496	56.5	11.3	373	2	Q9PUD2_XENLA	Q9pud2 xenopus lae
1424	57	11.4	1249	1	APAF_MOUSE	Q88879 mus musculus	1497	56.5	11.3	375	2	Q3PNK7_NITHA	Q3pnk7 nitrobaacter
1425	57	11.4	1251	2	QSDU30_MOUSE	Qsd30 mus musculus	1498	56.5	11.3	399	2	Q7MXS6_PORGI	Q7mxs6 porphyromon
1426	57	11.4	1346	2	Q3TXV8_MOUSE	Q3txv8 mus musculus	1499	56.5	11.3	404	2	Q7RLK8_PLAYO	Q7rlk8 plasmodium
1427	57	11.4	1346	2	Q3UD14_MOUSE	Q3ud14 mus musculus	1500	56.5	11.3	418	2	Q4T4X0_TETNG	Q4t4x0 tetraodon n
1428	57	11.4	1378	2	Q6S5J2_CRYPV	Q6s5j2 cryptospori							
1429	57	11.4	1395	2	Q4SHU0_TETNG	Q4shu0 tetraodon n							
1430	57	11.4	1409	2	Q5W7N6_BOMMO	Q5w7n6 bombyx mori							
1431	57	11.4	1522	1	BAT3_HUMAN	Q60242 homo sapien							
1432	57	11.4	1522	2	Q5VY37_HUMAN	Q5vy37 homo sapien							
1433	57	11.4	1522	2	Q2KNK6_HUMAN	Q2knk6 homo sapien							
1434	57	11.4	1641	2	Q6SA9_MOUSE	Q6sa9 mus musculus							
1435	57	11.4	1680	2	Q4IAH2_GIBZE	Q4iah2 gibberella							
1436	57	11.4	1776	2	Q5BG13_EMENI	Q5bg13 aspergillus							
1437	57	11.4	1877	1	PCSK5_MOUSE	Q04592 mus musculus							
1438	57	11.4	2217	2	Q585T2_HUMAN	Q585t2 homo sapien							
1439	57	11.4	2240	2	Q68DP8_HUMAN	Q68dp8 homo sapien							
1440	57	11.4	2351	1	FINC_BOVIN	P07589 bos taurus							
1441	57	11.4	2365	2	Q6OFE4_HUMAN	Q6ofe4 homo sapien							
1442	57	11.4	2365	2	Q68DP9_HUMAN	Q68dp9 homo sapien							
1443	57	11.4	2396	2	Q6NOA6_HUMAN	Q6noa6 homo sapien							
1444	57	11.4	2351	2	Q59EH1_HUMAN	Q59eh1 homo sapien							
1445	57	11.4	2357	2	Q68DT4_HUMAN	Q68dt4 homo sapien							
1446	57	11.4	2386	1	FINC_HUMAN	P02751 homo sapien							
1447	57	11.4	2444	2	Q6NO25_HUMAN	Q6no25 homo sapien							
1448	57	11.4	2475	2	Q501R6_XENTR	Q501r6 xenopus tro							
1449	57	11.4	2477	2	Q6MZU5_HUMAN	Q6mzu5 homo sapien							
1450	57	11.4	2481	1	FINC_XENLA	Q91740 xenopus lae							
1451	57	11.4	2481	2	Q6GQA5_XENLA	Q6gqa5 xenopus lae							
1452	57	11.4	2869	2	Q4CU21_TRYCR	Q4cu21 trypanosoma							
1453	57	11.4	2970	2	Q4SFW8_TETNG	Q4sfw8 tetraodon n							
1454	57	11.4	3313	1	CELR3_RAT	Q88278 ratus norv							
1455	57	11.4	3447	2	Q4DUJ6_TRYCR	Q4dja6 trypanosoma							
1456	57	11.4	3482	2	Q4DKJ7_TRYCR	Q4dkj7 trypanosoma							
1457	57	11.4	3487	2	Q4DL83_TRYCR	Q4dl83 trypanosoma							
1458	56.5	11.3	99	1	GASA3_ARATH	P46687 arabidopsis							
1459	56.5	11.3	103	2	Q5YR2_URTDI	Q9sy2 urtica dioi							
1460	56.5	11.3	113	1	IMM1_SHISO	P22558 shigella so							
1461	56.5	11.3	121	2	Q4HAA3_9DEIO	Q4haa3 deinococcus							
1462	56.5	11.3	127	2	Q725U4_DESVH	Q725u4 desulfovibr							
1463	56.5	11.3	130	1	KRA3A_SHEEP	P02443 ovie aries							
1464	56.5	11.3	133	2	Q4SUJ2_TETNG	Q4su2 tetraodon n							
1465	56.5	11.3	148	2	Q57093_COMPX	Q57093 compox viru							
1466	56.5	11.3	153	2	Q8GVR8_ORYSA	Q8gvr8 oryza sativ							
1467	56.5	11.3	161	2	Q35KP7_9BRAD	Q35kp7 bradyrhizob							
1468	56.5	11.3	168	2	Q6SGZ0_9BACT	Q6sgz0 uncultured							
1469	56.5	11.3	178	2	Q4SD48_9BURK	Q4sd48 burkholderi							
1470	56.5	11.3	178	2	Q4LV70_9BURK	Q4lv70 burkholderi							
1471	56.5	11.3	184	2	Q8SZ05_DROME	Q8sz05 drosophila							
1472	56.5	11.3	204	2	Q8ANN2_ORYSA	Q8ann2 oryza sativ							
1473	56.5	11.3	236	2	Q9U7T7_DESVH	Q9u7t7 desulfovibr							
1474	56.5	11.3	236	2	Q9U7H7_PLAFA	Q9u7h7 plasmodium							
1475	56.5	11.3	237	2	Q75DJ3_ASAGO	Q75dj3 aethya gos							
1476	56.5	11.3	238	2	Q4QAV2_LEIMA	Q4qav2 leishmania							
1477	56.5	11.3	238	2	Q4Z2P2_PLAEMOD	Q4z2p2 plasmodium							
1478	56.5	11.3	246	2	Q5TNY6_ANOGA	Q5tny6 anopheles g							
1479	56.5	11.3	258	2	Q44179_CABEL	Q44179 caenorhabd							
1480	56.5	11.3	267	2	Q3E8H0_ARATH	Q3e8h0 arabidopsis							
1481	56.5	11.3	276	2	Q4DBR0_TRYCR	Q4db00 trypanosoma							
1482	56.5	11.3	294	2	Q9FHE4_ARATH	Q9fhe4 arabidopsis							
1483	56.5	11.3	295	2	Q9BKP2_CABEL	Q9bkp2 caenorhabd							
1484	56.5	11.3	310	2	Q4SG28_TETNG	Q4sg28 tetraodon n							
1485	56.5	11.3	329	2	Q9DEY0_CYPCA	Q9dey0 cyprinus ca							
1486	56.5	11.3	336	2	Q6L513_ORYSA	Q6l513 oryza sativ							
1487	56.5	11.3	342	2	Q18744_BOVIN	Q18744 bos taurus							
1488	56.5	11.3	349	2	Q4FT3T_TETNG	Q4ft3t tetraodon n							
1489	56.5	11.3	351	2	Q2VPA1_HUMAN	Q2vpa1 homo sapien							
1490	56.5	11.3	351	2	Q37HL4_RHOFA	Q37hl4 rhodopseudo							
1491	56.5	11.3	353	2	Q8TX46_METKA	Q8tx46 methanopyru							

ALIGNMENTS

RESULT 1

ID	PROK1_HUMAN	STANDARD;	PRT;	105 AA.
AC	P58294			
DT	26-SEP-2001,	integrated into UniProtKB/Swiss-Prot.		
DT	26-SEP-2001,	sequence version 1.		
DT	21-FEB-2006,	entry version 35.		
DE	Prokineticin-1 precursor (Endocrine-gland-derived vascular endothelial growth factor) [EG-VEGF] (Mambakine).			
DE	growth factor) [EG-VEGF] (Mambakine).			
GN	Name=PROK1; ORFNames=UNQ600/PRO1186;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RX	MEDLINE=21160229; PubMed=11259612;			
RA	Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.-Y.;			
RT	"Identification of two prokineticin cDNAs: recombinant proteins			
RT	potentially contract gastrointestinal smooth muscle.";			
RL	Mol. Pharmacol. 59:692-698(2001).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RX	MEDLINE=21419730; PubMed=11528470; DOI=10.1038/35091000;			
RA	LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z.,			
RA	Dillard-Telm L., Prantz G., Rangell L., DeGuzman L., Keller G.-A.,			
RA	Peale F., Gurney A., Hillan K.J., Ferrara N.;			
RT	"Identification of an angiogenic mitogen selective for endocrine gland			
RT	endothelium.";			
RL	Nature 412:877-884(2001).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RA	Fraser C.;			
RT	"Mambakine, a snake venom related endocrine hormone that controls			
RT	macrophages.";			
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Baton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,			
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,			
RA	Wood W.I., Godowski P.J., Gray A.M.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[5]			
RP	PROTEIN SEQUENCE OF 20-34.			
RX	PubMed=15340161; DOI=10.1110/ps.04682504;			
RA	Zhang Z., Hensel W.J.;			
RT	"Signal peptide prediction based on analysis of experimentally			
RT	verified cleavage sites.";			

Protein Sci. 13:2819-2824 (2004).

-!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle. of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types.

-!- SUBCELLULAR LOCATION: Secreted protein.

-!- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary, testis, adrenal and placenta.

-!- SIMILARITY: Belongs to the prokinectin family.

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EMBL; AF333024; AAK49918.1; -; mRNA.
DR EMBL; AY029225; AAK33111.1; -; mRNA.
DR EMBL; AY358683; AAK89046.1; -; mRNA.
DR HSP; P25687; 1IMT.
DR Ensembl; ENSG00000143125; Homo sapiens.
DR H-InvDB; HTX0000868; -.
DR HGNC; HGNC:18454; PROK1.
DR MIM; 606233; gene.
DR InterPro; IPR009523; Prokinectin.
DR PANTHER; PTHR18821; Prokinectin; 1.
DR Pfam; PF06607; Prokinectin; 1.
KW Direct protein sequencing; Growth factor; Mitogen; Signal.
FT SIGNAL 1 19
FT CHAIN 20 105
FT FT FT Prokinectin-1.
FT FT FT /FTIG=PRO 0000025807.
FT FT FT By similarity.
FT FT FT By similarity.
FT FT FT By similarity.
FT FT FT By similarity.
FT FT FT By similarity.
FT FT FT By similarity.
SQ SEQUENCE 105 AA; 11715 MW; C7E3FDE30EFB416A CRC64;

Query Match 100.0%; Score 498; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKHKHTCP 60
DQ 20 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKHKHTCP 79
DQ 61 CLPNLLCSRFPDGRYRCSDMLKKNIF 86
DQ 80 CLPNLLCSRFPDGRYRCSDMLKKNIF 105

RESULT 2
Q5VWD4_HUMAN
ID Q5VWD4_HUMAN PRELIMINARY; PRT; 105 AA.
AC Q5VWD4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Prokinectin 1.
GN Name=PROK1; ORFNames=RP11-470L19.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wallis J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBSJ databases.
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EMBL; BC025399; AAK25399.1; -; mRNA.

Protein Sci. 13:2819-2824 (2004).

-!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle. of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types.

-!- SUBCELLULAR LOCATION: Secreted protein.

-!- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary, testis, adrenal and placenta.

-!- SIMILARITY: Belongs to the prokinectin family.

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EMBL; AF333024; AAK49918.1; -; mRNA.
DR EMBL; AY029225; AAK33111.1; -; mRNA.
DR EMBL; AY358683; AAK89046.1; -; mRNA.
DR HSP; P25687; 1IMT.
DR Ensembl; ENSG00000143125; Homo sapiens.
DR H-InvDB; HTX0000868; -.
DR HGNC; HGNC:18454; PROK1.
DR MIM; 606233; gene.
DR InterPro; IPR009523; Prokinectin.
DR PANTHER; PTHR18821; Prokinectin; 1.
DR Pfam; PF06607; Prokinectin; 1.
KW Direct protein sequencing; Growth factor; Mitogen; Signal.
FT SIGNAL 1 19
FT CHAIN 20 105
FT FT FT Prokinectin-1.
FT FT FT /FTIG=PRO 0000025807.
FT FT FT By similarity.
FT FT FT By similarity.
FT FT FT By similarity.
FT FT FT By similarity.
FT FT FT By similarity.
FT FT FT By similarity.
SQ SEQUENCE 105 AA; 11715 MW; C7E3FDE30EFB416A CRC64;

Query Match 100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKHKHTCP 60
DQ 20 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKHKHTCP 79
DQ 61 CLPNLLCSRFPDGRYRCSDMLKKNIF 86
DQ 80 CLPNLLCSRFPDGRYRCSDMLKKNIF 105

RESULT 3
Q5VWD4_HUMAN
ID Q5VWD4_HUMAN PRELIMINARY; PRT; 105 AA.
AC Q5VWD4;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Prokinectin 1.
GN Name=PROK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Schenkman Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RG NIH MGC Project;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.
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EMBL; BC025399; AAK25399.1; -; mRNA.

RESULT 6

```
Q3ZF12_BOVIN
ID Q3ZF12_BOVIN PRELIMINARY; PRT; 81 AA.
AC Q3ZF12;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Prokineticin-1 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX PubMed=159329; DOI=10.1210/en.2005-0297;
RA Kislouk T., Podlovni H., Spindel-Borowski K., Ovadia O., Zhou Q.Y.,
RA Meidan R.;
RT "Prokineticins (endocrine gland-derived vascular endothelial growth
RT factor and Bv8) in the bovine ovary: expression and role as mitogens
RT and survival factors for corpus luteum-derived endothelial cells.";
RL Endocrinology 146:3950-3958(2005).
CC -----
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CC -----
DE EMBL; AY877432; AAX81517.1; -; mRNA.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
FT NON TER 1
SQ SEQUENCE 81 AA; 9086 MW; 228834A7B83BA536 CRC64;

Query Match 83.7%; Score 417; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 6.9e-38;
Matches 71; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 ACERDVQCCAGTCCATSLWLRGLRMCTPLGRGEECHPGSHKVPFFRKRRKHTTCTCLPNL 65
DB 1 ACERDVQCCAGTCCATSLWLRGLRMCTPLGRGEECHPGSHKVPFFRKRRKHTTCTCLPNL 60

QY 66 LCSRPDPGRYCSMDLKNIF 86
DB 61 LCSRGLDGRYCSMDLKNIF 81

RESULT 7
Q2XXR8 VARVA
ID Q2XXR8 VARVA PRELIMINARY; PRT; 104 AA.
AC Q2XXR8;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 21-FEB-2006, entry version 4.
DE AVIToxin-VAR1 precursor.
OS Varanus varius (Lace monitor).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
NCBI_TaxID=8559;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16292255;
RA Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F.,
RA Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C.,
RA Ignjatovic V., Summerhayes R., Kochva E.;
RT "Early evolution of the venom system in lizards and snakes.";
RL Nature 439:584-588(2006).
CC -----
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CC -----
DE EMBL; DQ139878; AAZ75584.1; -; mRNA.
DR SIGNAL 1 19 Potential.
FT CHAIN 20 104 AVIToxin-VAR2.
FT SIGNAL 1 19 Potential.
SQ SEQUENCE 104 AA; 11191 MW; C25A83A6B59D3AA3 CRC64;

Query Match 68.3%; Score 340; DB 2; Length 104;
Best Local Similarity 63.1%; Pred. No. 2.4e-29;
Matches 53; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCCAGTCCATSLWLRGLRMCTPLGRGEECHPGSHKVPFFRKRRKHTTCTCP 60
DB 20 AVITGACERDVQCCAGTCCATSLWLRGLRMCTPLGRGEECHPGSHKVPFFRKRRKHTTCTCP 60
QY 61 CLPNLLCSRFPDGRYCSMDLKNII 84
DB 80 CLPNLLVCGQTSPGKYKCLPFPKQV 103

RESULT 9
VPRA_DENPO
ID VPRA_DENPO STANDARD; PRT; 81 AA.
AC P25687;
DT 01-MAY-1992, integrated into UniProtKB/Swiss-Prot.
DT 19-JUL-2005, sequence version 3.
DT 07-MAR-2006, entry version 37.
DE Intestinal toxin 1 (Mamba intestinal toxin 1) (MIT 1) (MIT1) (Venom
DE protein A).
OS Dendroaspis polylepis polylepis (Black mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
NCBI_TaxID=8620;

SQ SEQUENCE 104 AA; 11217 MW; C25A96B3B59D3AA3 CRC64;

Query Match 69.3%; Score 345; DB 2; Length 104;
Best Local Similarity 64.3%; Pred. No. 6.8e-30;
Matches 54; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCCAGTCCATSLWLRGLRMCTPLGRGEECHPGSHKVPFFRKRRKHTTCTCP 60
DB 20 AVITGACERDVQCCAGTCCATSLWLRGLRMCTPLGRGEECHPGSHKVPFFRKRRKHTTCTCP 79
QY 61 CLPNLLCSRFPDGRYCSMDLKNII 84
DB 80 CLPNLLVCGQTSPGKYKCLPFPKQV 103
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Query Match      63.3%; Score 315; DB 1; Length 81;
Best Local Similarity 62.3%; Pred. NO. 1e-26;
Matches 48; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY    1 AVITGACERDVCGAGTCCAISLWLRLGLRMCTPLRGREGBCHPGSHKVPFRKRKHHTCP 60
       ||||| : |:: : |:| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     1 AVITGACERDLGGKGTCCAVSLWIKSVRVCTPVGTSGDGCDHPASHKIPIPSQGQMHHHTCP 60
       ||||| : |:: : |:| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY    61 CLPNLLCSRFPDGRYC 77
       ||||| : |:: :|||
Db     61 CAPNLACVTSPKKPKC 77
       ||||| : |:: :|||

RESULT 10
Q4RUV3 TETNG PRELIMINARY; PRT; 106 AA.
AC Q4RUV3_
DT 19-JUL-2005, integrated into UniProtKB/TREMBL.
DT 19-JUL-2005, sequence version 1.
DE Chromosome 9 SCAF14991, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG00028169001;
OS Tetraodon nigroviridis [Green puffer].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neoceratrygii; Teleostei; Euteleostei; Notoeleostei;
OC Acanthomorpha; Apocrypterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
OX OX
XX [ ] _TaxIDE SEQUENCE.
RN RP
RP PUBMED=15496914; DOI=10.1038/nature03025;
RX Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lucifala G., Dosset C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boulet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blument C., Skalli Z., Cattolicio L., Poultain J., De Berardinis V.,
RA Cruad C., Duprat S., Brottier P., Coutanceau J.-P., Gouzay J.,
RA Parza G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Landier E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RW Nature 431:946-957(2004).
RR [2]
RN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEBS-2004) to the EMBL/GenBank/DDBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
Cc EMBL; CAAE01014991; CAG07489.1; -: Genomic_DNA.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PFHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
DR NON TER 106 106
SQ SEQUENCE 106 AA; 12098 MW; 8DA4DC1B388B3052 CRC64;

Query Match      62.4%; Score 311; DB 2; Length 106;
Best Local Similarity 62.4%; Pred. No. 3.7e-26;
Matches 53; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY    1 AVITGACERDVCGAGTCCAISLWLRLGLRMCTPLRGREGBCHPGSHKVPFRKRKHHTCP 60
       ||||| : |:: : |:| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     21 AVITGAREXHMQGLEFLPCSVLLLLGLRCMCAPRGLEGDECIFFSHKVIPGQRQHHTCP 80
       ||||| : |:: : |:~::~||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```


RX MEDLINS=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohtaki T., Onda H., Fujino M.,
RT "Isolation and identification of EG-VEGF/prokineticins as cognate
RT ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
[2]
RN EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
RP MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
RX Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.,
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
CC -1- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potentially contracts gastrointestinal (GI) smooth muscle (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed at high levels in testis and at
CC lower levels in brain, lung, ovary, spleen, thymus and uterus.
CC -1- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC genes (CRY1 and CRY2) (Probable).
CC -1- SIMILARITY: Belongs to the prokineticin family.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AY089984; AA09105.1; -; mRNA.
CC HSP: P25687; ILMT.
CC Ensembl: ENSRNOG0000010898; Rattus norvegicus.
CC RGD: 620280; Prok2.
CC GO: GO:0001664; FcG-protein-coupled receptor binding; IDA.
CC InterPro: IPR009523; Prokineticin.
CC PANTHER: PTHR18821; Prokineticin; 1.
CC Pfam: PF06607; Prokineticin; 1.
CC Biological rhythms; Neuropeptide; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 107 Prokineticin-2.
FT FTID=PRO_0000025811.
FT DISULFID 33 45 By similarity.
FT DISULFID 39 57 By similarity.
FT DISULFID 44 85 By similarity.
FT DISULFID 67 93 By similarity.
FT DISULFID 87 103 By similarity.
SQ SEQUENCE 107 AA; 11594 MW; BDF316CDB5FED0 CRC64;

Query Match 57.4%; Score 286; DB 1; Length 107;
Best Local Similarity 57.1%; Pred. No. 2e-23;
Matches 44; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGECCHPGSHKVPFFRKRKHTCP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 27 AVITGACDKDSQCGGMCACVSIWKSIRICTPMGQVGDSCPLTRKVPFWGRMHTCP 86

QY 61 CLPNLLCSRPDPGRYRC 77
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 CLPGLACLRTSFNRFC 103

RESULT 14
Q50E37_9MURI PRELIMINARY; PRT; 107 AA.
AC Q50E37;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE Prokineticin 2 variant 1S/2/4.
GN Names=Prok2;
OS Arvicantthis niloticus (African grass rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Arvicanthis.
OX NCBI_TaxID=61156;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15851527; DOI=10.1177/0748730405275135;
RA Lambert C.M., Machida K.K., Smale L., Nunez A.A., Weaver D.R.;
RT "Analysis of the Prokineticin 2 System in a Diurnal Rodent, the
RT Unstriped Nile Grass Rat (Arvicantthis niloticus).";
RL J. Biol. Rhythms 20:206-218(2005).
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CC -----
CC EMBL: AY820154; AAV73830.1; -; mRNA.
CC InterPro: IPR009523; Prokineticin.
CC PANTHER: PTHR18821; Prokineticin; 1.
CC Pfam: PF06607; Prokineticin; 1.
SQ SEQUENCE 107 AA; 11581 MW; DDBDB472B5C8045 CRC64;

Query Match 57.4%; Score 286; DB 2; Length 107;
Best Local Similarity 57.1%; Pred. No. 2e-23;
Matches 44; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGECCHPGSHKVPFFRKRKHTCP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 27 AVITGACDKDSQCGGMCACVSIWKSIRICTPMGQVGDSCPLTRKVPFWGRMHTCP 86

QY 61 CLPNLLCSRPDPGRYRC 77
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DT 07-FEB-2006, sequence version 1.
DE Prokineticin 2 variant 1A/2/4.
GN Names=Prok2;
OS Arvicantthis niloticus (African grass rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Arvicanthis.
OX NCBI_TaxID=61156;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15851527; DOI=10.1177/0748730405275135;
RA Lambert C.M., Machida K.K., Smale L., Nunez A.A., Weaver D.R.;
RT "Analysis of the Prokineticin 2 System in a Diurnal Rodent, the
RT Unstriped Nile Grass Rat (Arvicantthis niloticus).";
RL J. Biol. Rhythms 20:206-218(2005).
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CC EMBL: AY820154; AAV73830.1; -; mRNA.
CC InterPro: IPR009523; Prokineticin.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Arvicanthis.
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RL J. Biol. Rhythms 20:206-218(2005).
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CC -----
CC EMBL: AY820155; AAV73831.1; -; mRNA.
CC InterPro: IPR009523; Prokineticin.
CC PANTHER: PTHR18821; Prokineticin; 1.
CC Pfam: PF06607; Prokineticin; 1.
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Db 87 CLPGLACLRTSFNRFC 103

RESULT 15
Q50E38_9MURI PRELIMINARY; PRT; 107 AA.
AC Q50E38;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE Prokineticin 2 variant 1A/2/4.
GN Names=Prok2;
OS Arvicantthis niloticus (African grass rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Arvicanthis.
OX NCBI_TaxID=61156;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15851527; DOI=10.1177/0748730405275135;
RA Lambert C.M., Machida K.K., Smale L., Nunez A.A., Weaver D.R.;
RT "Analysis of the Prokineticin 2 System in a Diurnal Rodent, the
RT Unstriped Nile Grass Rat (Arvicantthis niloticus).";
RL J. Biol. Rhythms 20:206-218(2005).
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CC -----
CC EMBL: AY820154; AAV73830.1; -; mRNA.
CC InterPro: IPR009523; Prokineticin.
CC PANTHER: PTHR18821; Prokineticin; 1.
CC Pfam: PF06607; Prokineticin; 1.
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Search completed: December 14, 2006, 14:13:40
Job time : 193.602 secs

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; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-5

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ALIGNMENTS

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 : Patent No. 6485938

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ALIGNMENTS

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; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-5

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; Sequence 5, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14

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